

Glu Asp Pro Arg Val Ser Ile Ile Val Asp Asp Ala Phe Thr Trp Leu  
 345 350 355  
 cgc tcc ggc gga aat aat ggc gaa act tac gat tcc atc atc atc gat 1219  
 Arg Ser Gly Gly Asn Asn Gly Glu Thr Tyr Asp Ser Ile Ile Ile Asp  
 360 365 370  
 ctt ccc gac cca aac aac gac acc atg gcc agg ctg tat tca gaa gag 1267  
 Leu Pro Asp Pro Asn Asn Asp Thr Met Ala Arg Leu Tyr Ser Glu Glu  
 375 380 385  
 ttc tac acc ttg gcc cga gca cga ctg aac gaa caa ggc cgc atg gtg 1315  
 Phe Tyr Thr Leu Ala Arg Ala Arg Leu Asn Glu Gln Gly Arg Met Val  
 390 395 400 405  
 gtg caa tcc tcc agc gcc tac acc act cca gat gtg ttc tgg cga gtt 1363  
 Val Gln Ser Ser Ser Ala Tyr Thr Thr Pro Asp Val Phe Trp Arg Val  
 410 415 420  
 gga gca acc ttg aaa tcg gcg ggc tgt gaa caa gtc atc cca tat cac 1411  
 Gly Ala Thr Leu Lys Ser Ala Gly Cys Glu Gln Val Ile Pro Tyr His  
 425 430 435  
 gtg cat gtt ccc aca ttt ggc gac tgg ggc ttc caa ctg tgt ggc cct 1459  
 Val His Val Pro Thr Phe Gly Asp Trp Gly Phe Gln Leu Cys Gly Pro  
 440 445 450  
 gcc gac atg gaa tta gag ctt cgg gaa gac acc ccg cca ctg act ttc 1507  
 Ala Asp Met Glu Leu Glu Leu Arg Glu Asp Thr Pro Pro Leu Thr Phe  
 455 460 465  
 ctt aat gat gaa gtt ctg gtg gct gct ggg gtg ttt ggg ttg gat aat 1555  
 Leu Asn Asp Glu Val Leu Val Ala Ala Gly Val Phe Gly Leu Asp Asn  
 470 475 480 485  
 cag cct cgt gaa ttg gaa cct tcc acg ctg gat cat ccc cgc gtg gtg 1603  
 Gln Pro Arg Glu Leu Glu Pro Ser Thr Leu Asp His Pro Arg Val Val  
 490 495 500  
 gag gat ctg cgc aag gga tac cgc gaa tca ggc gac tagctgcaac 1649  
 Glu Asp Leu Arg Lys Gly Tyr Arg Glu Ser Gly Asp  
 505 510  
 gatgcgctgt gtg 1662

&lt;210&gt; 348

&lt;211&gt; 513

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 348

Met Ser Asp Leu Gly Pro Ile Trp Arg Trp Leu Leu Leu Val Ser Val  
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 20 25 30  
 Leu Ser Thr Ser Leu Asn Gly Gly Gly Ile Val Glu Thr Ser Leu Ile  
 35 40 45

Val Ala Gly Tyr Val Ala Leu Gly Leu Gly Ala Leu Leu Val Lys  
 50 55 60  
 Pro Phe Leu Asn Trp Pro Ala Gln Thr Phe Leu Gly Val Glu Thr Leu  
 65 70 75 80  
 Leu Gly Leu Ile Gly Gly Cys Ser Ala Leu Val Leu Tyr Phe Thr Phe  
 85 90 95  
 Ala Thr Ile Gly Gln Ser Leu Trp Ile Leu Val Ile Ala Thr Ala Ala  
 100 105 110  
 Ile Gly Ile Leu Val Gly Ala Glu Leu Pro Leu Leu Met Thr Met Ile  
 115 120 125  
 Gln Gln Gly Arg Leu Ala Asp Ala Lys Thr Thr Gly Ser Leu Val Ala  
 130 135 140  
 Thr Leu Asn Ala Ala Asp Tyr Leu Gly Ala Leu Leu Gly Gly Leu Ala  
 145 150 155 160  
 Trp Pro Phe Val Leu Leu Pro Trp Leu Gly Met Met Arg Gly Ala Ala  
 165 170 175  
 Ala Ala Gly Met Ile Asn Leu Val Ala Ala Leu Phe Val Gly Cys Val  
 180 185 190  
 Leu Leu Arg His Leu Leu Pro Arg Thr His Phe Phe Val Ser Val Val  
 195 200 205  
 Ala Leu Leu Leu Ala Ile Ala Ala Leu Ala Thr Val Leu Val Lys Ser  
 210 215 220  
 Asp Gly Ile Val Ala Thr Ala Arg Ala Gln Leu Tyr Arg Asp Pro Val  
 225 230 235 240  
 Ile Tyr Ser His Gln Ser Asp Tyr Gln Asp Ile Val Val Thr Glu Arg  
 245 250 255  
 Gly Lys Asp Arg Arg Leu Tyr Leu Asn Gly Gly Leu Gln Tyr Ser Thr  
 260 265 270  
 Arg Asp Gln His Arg Tyr Thr Glu Ser Leu Val Tyr Pro Ser Leu Asn  
 275 280 285  
 Pro Glu Ala Glu Ser Val Leu Ile Ile Gly Gly Gly Asp Gly Leu Ala  
 290 295 300  
 Ala Arg Glu Leu Leu Arg Phe Pro Ser Met Gln Ile Thr Gln Val Glu  
 305 310 315 320  
 Leu Asp Pro Glu Val Ile Glu Val Ala Asn Thr Val Leu Arg Ser Asp  
 325 330 335  
 Asn Gly Gly Ala Met Glu Asp Pro Arg Val Ser Ile Ile Val Asp Asp  
 340 345 350  
 Ala Phe Thr Trp Leu Arg Ser Gly Gly Asn Asn Gly Glu Thr Tyr Asp  
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 Ser Ile Ile Ile Asp Leu Pro Asp Pro Asn Asn Asp Thr Met Ala Arg



Asp

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<220>  
<221> CDS  
<222> (101)..(901)  
<223> RXA01757
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70	75	80	85
atc gag ggt gat gcg ctt ttt gag acg ctt gtc gac gcc ccg agc cgc			403
Ile Glu Gly Asp Ala Leu Phe Glu Thr Leu Val Asp Ala Pro Ser Arg			
	90	95	100
ctg cgg ggt aac ccc ata gac gct gct tca ggc agg ttc caa gca ggg			451
Leu Arg Gly Asn Pro Ile Asp Ala Ala Ser Gly Arg Phe Gln Ala Gly			
	105	110	115
gcc tcc tcg ctt gcg ctc ggg ctt gca gcc cag ctc aag cca gga gtt			499
Ala Ser Ser Leu Ala Leu Gly Leu Ala Ala Gln Leu Lys Pro Gly Val			
	120	125	130
tta gaa ctc ggg gac ccc gtc cat tct ctc agt gag gaa gat ggg gaa			547
Leu Glu Leu Gly Asp Pro Val His Ser Leu Ser Glu Glu Asp Gly Glu			
	135	140	145
atc gtt gtg aag tct tcc aaa cag att gtg agg gca aag cac gtc atc			595
Ile Val Val Lys Ser Ser Lys Gln Ile Val Arg Ala Lys His Val Ile			
	150	155	160
att gcg gtt cca ccg gca ctc gct gcc gag ttg att ggt ttc acc cta			643
Ile Ala Val Pro Pro Ala Leu Ala Ala Glu Leu Ile Gly Phe Thr Leu			
	170	175	180
gat tta cca gct gac gtg cga aaa gca gcg cat cca caa cat ata gct			691
Asp Leu Pro Ala Asp Val Arg Lys Ala Ala His Pro Gln His Ile Ala			
	185	190	195
gtg atg aat tgg gca aag gag aaa tac acc tta ccc aca caa gcc gca			739
Val Met Asn Trp Ala Lys Glu Lys Tyr Thr Leu Pro Thr Gln Ala Ala			
	200	205	210
tcg gct ggg ggt ttt ggg cat gag ctg ttc caa caa cca ctc gga cat			787
Ser Ala Gly Gly Phe Gly His Glu Leu Phe Gln Gln Pro Leu Gly His			
	215	220	225
ggg cga att cat tgg gca tca acg gaa gtt gcc act gag ttt ggt gga			835
Gly Arg Ile His Trp Ala Ser Thr Glu Val Ala Thr Glu Phe Gly Gly			
	230	235	240
cac ctt gaa ggc gca gtt cgt gca gga att cag gct gcg ctt caa aca			883
His Leu Glu Gly Ala Val Arg Ala Gly Ile Gln Ala Ala Leu Gln Thr			
	250	255	260
gga ttt aat cta aaa tct taaacctcgt attttccctg ata			924
Gly Phe Asn Leu Lys Ser			
	265		

&lt;210&gt; 350

&lt;211&gt; 267

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 350

Met Pro Thr Ala Ser Pro Ile Tyr Asp Val Val Val Val Gly Ala Gly  
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 Ile Ser Gly Leu Ile Ala Thr Gln Leu Leu Asp Arg Ala Gly Leu Asn  
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 Ile Lys Cys Phe Glu Ala Cys Ser Arg Val Gly Gly Arg Ala Val Ser  
 35 40 45  
 Val Gln Gln Ser Asp Leu Phe Leu Asp Leu Gly Ala Thr Trp Phe Trp  
 50 55 60  
 Leu Asn Glu Pro Leu Val Gln Gln Leu Val Asn Asn Leu Gly Leu Gly  
 65 70 75 80  
 Thr Phe Pro Gln Ala Ile Glu Gly Asp Ala Leu Phe Glu Thr Leu Val  
 85 90 95  
 Asp Ala Pro Ser Arg Leu Arg Gly Asn Pro Ile Asp Ala Ala Ser Gly  
 100 105 110  
 Arg Phe Gln Ala Gly Ala Ser Ser Leu Ala Leu Gly Leu Ala Ala Gln  
 115 120 125  
 Leu Lys Pro Gly Val Leu Glu Leu Gly Asp Pro Val His Ser Leu Ser  
 130 135 140  
 Glu Glu Asp Gly Glu Ile Val Val Lys Ser Ser Lys Gln Ile Val Arg  
 145 150 155 160  
 Ala Lys His Val Ile Ile Ala Val Pro Pro Ala Leu Ala Ala Glu Leu  
 165 170 175  
 Ile Gly Phe Thr Leu Asp Leu Pro Ala Asp Val Arg Lys Ala Ala His  
 180 185 190  
 Pro Gln His Ile Ala Val Met Asn Trp Ala Lys Glu Lys Tyr Thr Leu  
 195 200 205  
 Pro Thr Gln Ala Ala Ser Ala Gly Gly Phe Gly His Glu Leu Phe Gln  
 210 215 220  
 Gln Pro Leu Gly His Gly Arg Ile His Trp Ala Ser Thr Glu Val Ala  
 225 230 235 240  
 Thr Glu Phe Gly Gly His Leu Glu Gly Ala Val Arg Ala Gly Ile Gln  
 245 250 255  
 Ala Ala Leu Gln Thr Gly Phe Asn Leu Lys Ser  
 260 265

&lt;210&gt; 351

&lt;211&gt; 636

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(613)

&lt;223&gt; RXA02159

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				Met Ser Leu Gly Ser	5	
				1		
acc ccg tca aca ccg gaa aac tta aat ccc gtg act cgc act gca cgc	163					
Thr Pro Ser Thr	10	Glu Asn Leu Asn	15	Thr Arg Thr	20	
caa gct ctc att ttg cag att ttg gac aaa caa aaa gtc acc agc cag	211					
Gln Ala Leu Ile Leu Gln Ile Leu Asp Lys Gln Lys Val Thr Ser Gln	25		30		35	
gta caa ctg tct gaa ttg ctg ctg gat gaa ggc atc gat atc acc cag	259					
Val Gln Leu Ser Glu Leu Leu Leu Asp Glu Gly Ile Asp Ile Thr Gln	40		45		50	
gcc acc ttg tcc cga gat ctc gat gaa ctc ggt gca cgc aag gtt cgc	307					
Ala Thr Leu Ser Arg Asp Leu Asp Glu Leu Gly Ala Arg Lys Val Arg	55		60		65	
ccc gat ggg gga cgc gcc tac tac gcg gtc ggc cca gta gat agc atc	355					
Pro Asp Gly Gly Arg Ala Tyr Tyr Ala Val Gly Gly cca gta gat agc atc	70		75		80	
					85	
gcc cgc gaa gat ctc cgg ggt ccg tcg gag aag ctg cgc cgc atg ctt	403					
Ala Arg Glu Asp Leu Arg Gly Pro Ser Glu Lys Leu Arg Arg Met Leu	90		95		100	
gat gaa ctg ctg gtt tct aca gat cat tcc ggc aac atc gcg atg ctg	451					
Asp Glu Leu Val Ser Thr Asp His Ser Gly Asn Ile Ala Met Leu	105		110		115	
cgc acc ccg ccg gga gct gcc cag tac ctg gca agt ttc atc gat agg	499					
Arg Thr Pro Pro Gly Ala Ala Gln Tyr Leu Ala Ser Phe Ile Asp Arg	120		125		130	
gtg ggg ctg aaa gaa gtc gtt ggc acc atc gct ggt gat gac acc gtt	547					
Val Gly Leu Lys Glu Val Val Gly Thr Ile Ala Gly Asp Asp Thr Val	135		140		145	
ttc gtt ctc gcc cgt gat ccg ctc aca ggt aaa gaa cta ggt gaa tta	595					
Phe Val Leu Ala Arg Asp Pro Leu Thr Gly Lys Glu Leu Gly Glu Leu	150		155		160	
					165	
ctc agc ggg cgc acc act taaagcgccc ctagttcaag gct	636					
Leu Ser Gly Arg Thr	170					

Met Ser Leu Gly Ser Thr Pro Ser Thr Pro Glu Asn Leu Asn Pro Val  
1 5 10 15

gtt ctt ggc tcc aac atg tgc cac gtg cag gta gaa att gat gag gaa 259  
Val Leu Gly Ser Asn Met Cys His Val Gln Val Glu Ile Asp Glu Glu  
40 45 50

ccttaaagcg gcg 414

Pro

acc acc tac cag gga gtc acc gag atc gga tcc gtt ccg gca tac ctg 163

Thr	Thr	Tyr	Gln	Gly	Val	Thr	Glu	Ile	Gly	Ser	Val	Pro	Ala	Tyr	Leu	
				10					15					20		
gtt	ctt	gca	gac	gga	cgt	acc	ttc	acc	gga	ttt	ggc	ttt	gga	gct	atc	211
Val	Leu	Ala	Asp	Gly	Arg	Thr	Phe	Thr	Gly	Phe	Gly	Phe	Gly	Ala	Ile	
			25					30					35			
ggc	acc	acc	ctt	ggt	gag	gca	gtg	ttc	act	acc	gcc	atg	acc	ggt	tac	259
Gly	Thr	Thr	Leu	Gly	Glu	Ala	Val	Phe	Thr	Thr	Ala	Met	Thr	Gly	Tyr	
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caa	gaa	acc	atg	acc	gat	cct	tcc	tat	cac	cgc	cag	att	gtt	gtg	gct	307
Gln	Glu	Thr	Met	Thr	Asp	Pro	Ser	Tyr	His	Arg	Gln	Ile	Val	Val	Ala	
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acc	gca	cca	cag	atc	ggc	aac	acc	ggc	tgg	aac	gat	gag	gac	aac	gag	355
Thr	Ala	Pro	Gln	Ile	Gly	Asn	Thr	Gly	Trp	Asn	Asp	Glu	Asp	Asn	Glu	
			70			75				80					85	
tcc	cgc	gac	ggc	aag	att	tgg	gtt	gca	ggc	ctt	gtt	atc	cgc	gac	ctc	403
Ser	Arg	Asp	Gly	Lys	Ile	Trp	Val	Ala	Gly	Leu	Val	Ile	Arg	Asp	Leu	
				90					95					100		
gca	gca	cgt	gtg	tcc	aac	tgg	cgc	gcc	acc	acc	tcc	ttg	cag	cag	gaa	451
Ala	Ala	Arg	Val	Ser	Asn	Trp	Arg	Ala	Thr	Thr	Ser	Leu	Gln	Gln	Glu	
			105					110					115			
atg	gca	ggc	cag	ggc	atc	gtc	ggc	atc	ggc	gga	atc	gac	acc	cgc	gca	499
Met	Ala	Gly	Gln	Gly	Ile	Val	Gly	Ile	Gly	Gly	Ile	Asp	Thr	Arg	Ala	
			120				125					130				
ctg	gtt	cgc	cac	ctg	cgc	aat	gaa	ggt	tcc	att	gca	gcg	ggc	atc	ttc	547
Leu	Val	Arg	His	Leu	Arg	Asn	Glu	Gly	Ser	Ile	Ala	Ala	Gly	Ile	Phe	
			135				140				145					
tcc	ggc	gct	gac	gca	cag	cgc	cca	gtt	gaa	gaa	ctc	gta	gag	atc	gtc	595
Ser	Gly	Ala	Asp	Ala	Gln	Arg	Pro	Val	Glu	Glu	Leu	Val	Glu	Ile	Val	
					155					160					165	
aag	aat	cag	cca	gca	atg	acc	ggc	gca	aac	ctc	tcc	gtt	gag	gtc	tct	643
Lys	Asn	Gln	Pro	Ala	Met	Thr	Gly	Ala	Asn	Leu	Ser	Val	Glu	Val	Ser	
				170					175					180		
gct	gat	gaa	acc	tac	gtc	atc	gaa	gct	gaa	ggc	gaa	gag	cgc	cac	acc	691
Ala	Asp	Glu	Thr	Tyr	Val	Ile	Glu	Ala	Glu	Gly	Glu	Glu	Arg	His	Thr	
			185					190					195			
gtc	gtg	gcc	tac	gac	ctg	ggc	att	aag	caa	aac	acc	cca	cgt	cgt	ttc	739
Val	Val	Ala	Tyr	Asp	Leu	Gly	Ile	Lys	Gln	Asn	Thr	Pro	Arg	Arg	Phe	
			200				205					210				
tct	gca	cgc	ggt	gtt	cgc	acc	gtc	atc	gtg	cct	gct	gaa	acc	cca	ttc	787
Ser	Ala	Arg	Gly	Val	Arg	Thr	Val	Ile	Val	Pro	Ala	Glu	Thr	Pro	Phe	
			215				220				225					
gag	gat	atc	aag	cag	tac	aac	cca	tca	ggc	gtg	ttc	atc	tcc	aac	ggc	835
Glu	Asp	Ile	Lys	Gln	Tyr	Asn	Pro	Ser	Gly	Val	Phe	Ile	Ser	Asn	Gly	
			230			235				240					245	
cct	ggc	gat	cct	gca	gca	gca	gac	gtc	atg	gtt	gat	atc	gtc	cgc	gaa	883
Pro	Gly	Asp	Pro	Ala	Ala	Ala	Asp	Val	Met	Val	Asp	Ile	Val	Arg	Glu	

250										255					260					
gtt	ctt	gaa	gcc	gac	att	cca	ttc	ttt	ggc	atc	tgc	ttc	ggc	aac	cag	931				
Val	Leu	Glu	Ala	Asp	Ile	Pro	Phe	Phe	Gly	Ile	Cys	Phe	Gly	Asn	Gln					
265					270					275										
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Ile	Leu	Gly	Arg	Ala	Phe	Gly	Met	Glu	Thr	Tyr	Lys	Leu	Lys	Phe	Gly					
280					285					290										
cac	cgc	ggc	atc	aac	gtt	cca	gtg	aag	aac	cac	atc	acc	ggc	aag	atc	1027				
His	Arg	Gly	Ile	Asn	Val	Pro	Val	Lys	Asn	His	Ile	Thr	Gly	Lys	Ile					
295					300					305										
gac	atc	acc	gcc	cag	aac	cac	ggc	ttc	gca	ctc	aag	ggt	gaa	gca	ggc	1075				
Asp	Ile	Thr	Ala	Gln	Asn	His	Gly	Phe	Ala	Leu	Lys	Gly	Glu	Ala	Gly					
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Gln	Glu	Phe	Glu	Thr	Asp	Phe	Gly	Thr	Ala	Ile	Val	Thr	His	Thr	Cys					
330					335					340										
ctc	aac	gac	ggc	gtc	gtt	gaa	ggt	att	gcg	ctg	aag	tcc	gga	cgc	gca	1171				
Leu	Asn	Asp	Gly	Val	Val	Glu	Gly	Ile	Ala	Leu	Lys	Ser	Gly	Arg	Ala					
345					350					355										
tac	tcc	gtt	cag	tac	cac	cca	gag	gcc	gct	gcc	ggc	cca	aat	gat	gca	1219				
Tyr	Ser	Val	Gln	Tyr	His	Pro	Glu	Ala	Ala	Ala	Gly	Pro	Asn	Asp	Ala					
360					365					370										
agc	ccc	ctg	ttt	gac	cag	ttt	gtt	gag	ctg	atg	gat	gca	gac	gct	cag	1267				
Ser	Pro	Leu	Phe	Asp	Gln	Phe	Val	Glu	Leu	Met	Asp	Ala	Asp	Ala	Gln					
375					380					385										
aag	aaa	ggc	gca	taaataacat	gccaaagcgt tca										1302					
Lys	Lys	Gly	Ala																	
390																				

&lt;210&gt; 356

&lt;211&gt; 393

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 356

Val	Ser	Lys	Asp	Thr	Thr	Thr	Tyr	Gln	Gly	Val	Thr	Glu	Ile	Gly	Ser
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Val	Pro	Ala	Tyr	Leu	Val	Leu	Ala	Asp	Gly	Arg	Thr	Phe	Thr	Gly	Phe
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Gly	Phe	Gly	Ala	Ile	Gly	Thr	Thr	Leu	Gly	Glu	Ala	Val	Phe	Thr	Thr
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Ala	Met	Thr	Gly	Tyr	Gln	Glu	Thr	Met	Thr	Asp	Pro	Ser	Tyr	His	Arg
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Gln	Ile	Val	Val	Ala	Thr	Ala	Pro	Gln	Ile	Gly	Asn	Thr	Gly	Trp	Asn
65					70					75					80

Asp	Glu	Asp	Asn	Glu	Ser	Arg	Asp	Gly	Lys	Ile	Trp	Val	Ala	Gly	Leu
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85								90				95				
Val	Ile	Arg	Asp	Leu	Ala	Ala	Arg	Val	Ser	Asn	Trp	Arg	Ala	Thr	Thr	
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Ser	Leu	Gln	Gln	Glu	Met	Ala	Gly	Gln	Gly	Ile	Val	Gly	Ile	Gly	Gly	
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Ile	Asp	Thr	Arg	Ala	Leu	Val	Arg	His	Leu	Arg	Asn	Glu	Gly	Ser	Ile	
130								135				140				
Ala	Ala	Gly	Ile	Phe	Ser	Gly	Ala	Asp	Ala	Gln	Arg	Pro	Val	Glu	Glu	
145								150				155				
Leu	Val	Glu	Ile	Val	Lys	Asn	Gln	Pro	Ala	Met	Thr	Gly	Ala	Asn	Leu	
				165								170				
Ser	Val	Glu	Val	Ser	Ala	Asp	Glu	Thr	Tyr	Val	Ile	Glu	Ala	Glu	Gly	
180								185				190				
Glu	Glu	Arg	His	Thr	Val	Val	Ala	Tyr	Asp	Leu	Gly	Ile	Lys	Gln	Asn	
195								200				205				
Thr	Pro	Arg	Arg	Phe	Ser	Ala	Arg	Gly	Val	Arg	Thr	Val	Ile	Val	Pro	
210								215				220				
Ala	Glu	Thr	Pro	Phe	Glu	Asp	Ile	Lys	Gln	Tyr	Asn	Pro	Ser	Gly	Val	
225								230				235				
Phe	Ile	Ser	Asn	Gly	Pro	Gly	Asp	Pro	Ala	Ala	Ala	Asp	Val	Met	Val	
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Asp	Ile	Val	Arg	Glu	Val	Leu	Glu	Ala	Asp	Ile	Pro	Phe	Phe	Gly	Ile	
260								265				270				
Cys	Phe	Gly	Asn	Gln	Ile	Leu	Gly	Arg	Ala	Phe	Gly	Met	Glu	Thr	Tyr	
275								280				285				
Lys	Leu	Lys	Phe	Gly	His	Arg	Gly	Ile	Asn	Val	Pro	Val	Lys	Asn	His	
290								295				300				
Ile	Thr	Gly	Lys	Ile	Asp	Ile	Thr	Ala	Gln	Asn	His	Gly	Phe	Ala	Leu	
305								310				315				
Lys	Gly	Glu	Ala	Gly	Gln	Glu	Phe	Glu	Thr	Asp	Phe	Gly	Thr	Ala	Ile	
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Val	Thr	His	Thr	Cys	Leu	Asn	Asp	Gly	Val	Val	Glu	Gly	Ile	Ala	Leu	
340								345				350				
Lys	Ser	Gly	Arg	Ala	Tyr	Ser	Val	Gln	Tyr	His	Pro	Glu	Ala	Ala	Ala	
355								360				365				
Gly	Pro	Asn	Asp	Ala	Ser	Pro	Leu	Phe	Asp	Gln	Phe	Val	Glu	Leu	Met	
370								375				380				
Asp	Ala	Asp	Ala	Gln	Lys	Lys	Gly	Ala								
385				390												

&lt;210&gt; 357

<211> 924  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(901)  
 <223> RXS00905

<400> 357

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aac gcg caa gta ctt aaa gag aac atc gaa aac caa cgc gag cag atc 163
Asn Ala Gln Val Leu Lys Glu Asn Ile Glu Asn Gln Arg Glu Gln Ile
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Pro Asn Leu Leu Glu Asp Tyr Ala Gly Ala Lys Glu Trp Val Lys Glu
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aca ctg acc aac gca ggt ctc acc gtc agc gaa ttc gct gcc gaa gat 307
Thr Leu Thr Asn Ala Gly Leu Thr Val Ser Glu Phe Ala Ala Glu Asp
                               55                               60                               65

gga acc acc aac ttc atc ggc acc cgc aag ggc tcc gaa ggt gca cca 355
Gly Thr Thr Asn Phe Ile Gly Thr Arg Lys Gly Ser Glu Gly Ala Pro
   70                               75                               80                               85

aag gta ctg ctg tac agc cac ttc gac gtt gtc cca tcc ggc cct ttg 403
Lys Val Leu Leu Tyr Ser His Phe Asp Val Val Pro Ser Gly Pro Leu
                               90                               95                               100

gat ctc tgg gac acc aat cct ttt gaa ctc acc gag cgc gac gct ggc 451
Asp Leu Trp Asp Thr Asn Pro Phe Glu Leu Thr Glu Arg Asp Ala Gly
                               105                               110                               115

cac ggc acc cgc tgg tac ggc cgc ggc gcc gct gac tgc aag ggc aac 499
His Gly Thr Arg Trp Tyr Gly Arg Gly Ala Ala Asp Cys Lys Gly Asn
                               120                               125                               130

ctg gtc atg cac ctc gca gca ctg cgc gcc gtc gaa gcc agc ggc gac 547
Leu Val Met His Leu Ala Ala Leu Arg Ala Val Glu Ala Ser Gly Asp
                               135                               140                               145

acc aca ctc aac ctc acc tac gtg gtc gag ggc tcc gag gaa atg gga 595
Thr Thr Leu Asn Leu Thr Tyr Val Val Glu Gly Ser Glu Glu Met Gly
   150                               155                               160                               165

ggc gga gcg ctc agc gcg ctc atc aag gac aag cct gag ctt ttc gac 643
Gly Gly Ala Leu Ser Ala Leu Ile Lys Asp Lys Pro Glu Leu Phe Asp
                               170                               175                               180

gca gat gtc atc ttg att gca gac agc gga aac gct tcc gtg ggc acc 691

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Ala Asp Val Ile Leu Ile Ala Asp Ser Gly Asn Ala Ser Val Gly Thr  
 185 190 195

cca acc ttg acc act acc ctg cgc ggt ggc gga cag gtc acc gtc acc 739  
 Pro Thr Leu Thr Thr Thr Leu Arg Gly Gly Gly Gln Val Thr Val Thr  
 200 205 210

gtg gac acc ctt gaa ggc gct gtt cac tcc ggc cag aac ggt ggc gct 787  
 Val Asp Thr Leu Glu Gly Ala Val His Ser Gly Gln Asn Gly Gly Ala  
 215 220 225

gcc cca gat gct gtt gct gct ctc gtg cgc gtt ctg gat act ttg cgc 835  
 Ala Pro Asp Ala Val Ala Ala Leu Val Arg Val Leu Asp Thr Leu Arg  
 230 235 240 245

gat gaa cac gga cgc acc gtt atc gac ggc tgt caa cac cac cgc aaa 883  
 Asp Glu His Gly Arg Thr Val Ile Asp Gly Cys Gln His His Arg Lys  
 250 255 260

ctg gaa ggg cga gcc tta tgatccagag actttccgca gcg 924  
 Leu Glu Gly Arg Ala Leu  
 265

&lt;210&gt; 358

&lt;211&gt; 267

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 358

Met Thr Gln Phe Glu Asn Ala Gln Val Leu Lys Glu Asn Ile Glu Asn  
 1 5 10 15

Gln Arg Glu Gln Ile Phe Thr Gln Leu Lys Glu Ile Val Ser Phe Asn  
 20 25 30

Ser Val His Ser Asp Pro Asn Leu Leu Glu Asp Tyr Ala Gly Ala Lys  
 35 40 45

Glu Trp Val Lys Glu Thr Leu Thr Asn Ala Gly Leu Thr Val Ser Glu  
 50 55 60

Phe Ala Ala Glu Asp Gly Thr Thr Asn Phe Ile Gly Thr Arg Lys Gly  
 65 70 75 80

Ser Glu Gly Ala Pro Lys Val Leu Leu Tyr Ser His Phe Asp Val Val  
 85 90 95

Pro Ser Gly Pro Leu Asp Leu Trp Asp Thr Asn Pro Phe Glu Leu Thr  
 100 105 110

Glu Arg Asp Ala Gly His Gly Thr Arg Trp Tyr Gly Arg Gly Ala Ala  
 115 120 125

Asp Cys Lys Gly Asn Leu Val Met His Leu Ala Ala Leu Arg Ala Val  
 130 135 140

Glu Ala Ser Gly Asp Thr Thr Leu Asn Leu Thr Tyr Val Val Glu Gly  
 145 150 155 160

Ser Glu Glu Met Gly Gly Gly Ala Leu Ser Ala Leu Ile Lys Asp Lys

165										170					175				
Pro	Glu	Leu	Phe	Asp	Ala	Asp	Val	Ile	Leu	Ile	Ala	Asp	Ser	Gly	Asn				
			180					185					190						
Ala	Ser	Val	Gly	Thr	Pro	Thr	Leu	Thr	Thr	Thr	Leu	Arg	Gly	Gly	Gly				
		195					200					205							
Gln	Val	Thr	Val	Thr	Val	Asp	Thr	Leu	Glu	Gly	Ala	Val	His	Ser	Gly				
	210					215					220								
Gln	Asn	Gly	Gly	Ala	Ala	Pro	Asp	Ala	Val	Ala	Ala	Leu	Val	Arg	Val				
225					230					235					240				
Leu	Asp	Thr	Leu	Arg	Asp	Glu	His	Gly	Arg	Thr	Val	Ile	Asp	Gly	Cys				
				245					250					255					
Gln	His	His	Arg	Lys	Leu	Glu	Gly	Arg	Ala	Leu									
			260					265											

&lt;210&gt; 359

&lt;211&gt; 627

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(604)

&lt;223&gt; RXS00906

&lt;400&gt; 359

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gctgttgctg	ctctcgtg	cggttctggat	actttgcgcg	atg	aac	acg	gac	gca		115
				Met	Asn	Thr	Asp	Ala		
				1				5		

ccg	tta	tcg	acg	gct	gtc	aac	acc	acc	gca	aac	tgg	aag	ggc	gag	cct		163
Pro	Leu	Ser	Thr	Ala	Val	Asn	Thr	Thr	Ala	Asn	Trp	Lys	Gly	Glu	Pro		
			10						15					20			

tat	gat	cca	gag	act	ttc	cgc	agc	gat	gcc	ggc	atc	ctc	gac	ggt	gta		211
Tyr	Asp	Pro	Glu	Thr	Phe	Arg	Ser	Asp	Ala	Gly	Ile	Leu	Asp	Gly	Val		
			25					30					35				

gac	atc	atg	ggc	gac	ggc	gac	aac	cca	gca	agc	atg	ctg	tgg	tcc	agg		259
Asp	Ile	Met	Gly	Asp	Gly	Asp	Asn	Pro	Ala	Ser	Met	Leu	Trp	Ser	Arg		
		40					45					50					

cct	gca	atc	tcc	atc	acc	gga	ttc	act	tcc	acc	cca	gtg	gca	gaa	gca		307
Pro	Ala	Ile	Ser	Ile	Thr	Gly	Phe	Thr	Ser	Thr	Pro	Val	Ala	Glu	Ala		
		55				60					65						

ctc	aac	gca	gtg	ccc	gca	acg	gcg	tcc	gcc	aag	cta	aac	ctt	cgc	gtg		355
Leu	Asn	Ala	Val	Pro	Ala	Thr	Ala	Ser	Ala	Lys	Leu	Asn	Leu	Arg	Val		
	70				75				80					85			

cca	gca	ggc	ctg	gaa	gca	aac	gat	gtg	gcc	gag	aag	ctg	aag	cag	cac		403
Pro	Ala	Gly	Leu	Glu	Ala	Asn	Asp	Val	Ala	Glu	Lys	Leu	Lys	Gln	His		
			90					95						100			

ctg atc aat cac aca cct tgg ggc gca aag atc acg gtg gag atc gat 451  
 Leu Ile Asn His Thr Pro Trp Gly Ala Lys Ile Thr Val Glu Ile Asp  
                   105                                  110                                  115  
  
 gac att aac caa ccg ttc tcc acc gat att acc ggc cct gca atg tcc 499  
 Asp Ile Asn Gln Pro Phe Ser Thr Asp Ile Thr Gly Pro Ala Met Ser  
                   120                                  125                                  130  
  
 acc ctg gcg tcc tgc ctg agc gct gcg tac gag ggc aag gat ctt gtc 547  
 Thr Leu Ala Ser Cys Leu Ser Ala Ala Tyr Glu Gly Lys Asp Leu Val  
                   135                                  140                                  145  
  
 acc gaa ggc agc ggc gga tcc att cca ctg tgt acc gaa ctg att gag 595  
 Thr Glu Gly Ser Gly Gly Ser Ile Pro Leu Cys Thr Glu Leu Ile Glu  
 150                                  155                                  160                                  165  
  
 gtc aac cca taagcagaat tggcactcta cgg 627  
 Val Asn Pro

<210> 360  
 <211> 168  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 360  
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 Trp Lys Gly Glu Pro Tyr Asp Pro Glu Thr Phe Arg Ser Asp Ala Gly  
                   20                                  25                                  30  
  
 Ile Leu Asp Gly Val Asp Ile Met Gly Asp Gly Asp Asn Pro Ala Ser  
                   35                                  40                                  45  
  
 Met Leu Trp Ser Arg Pro Ala Ile Ser Ile Thr Gly Phe Thr Ser Thr  
   50                                  55                                  60  
  
 Pro Val Ala Glu Ala Leu Asn Ala Val Pro Ala Thr Ala Ser Ala Lys  
   65                                  70                                  75                                  80  
  
 Leu Asn Leu Arg Val Pro Ala Gly Leu Glu Ala Asn Asp Val Ala Glu  
                   85                                  90                                  95  
  
 Lys Leu Lys Gln His Leu Ile Asn His Thr Pro Trp Gly Ala Lys Ile  
                   100                                  105                                  110  
  
 Thr Val Glu Ile Asp Asp Ile Asn Gln Pro Phe Ser Thr Asp Ile Thr  
                   115                                  120                                  125  
  
 Gly Pro Ala Met Ser Thr Leu Ala Ser Cys Leu Ser Ala Ala Tyr Glu  
   130                                  135                                  140  
  
 Gly Lys Asp Leu Val Thr Glu Gly Ser Gly Gly Ser Ile Pro Leu Cys  
 145                                  150                                  155                                  160  
  
 Thr Glu Leu Ile Glu Val Asn Pro  
                   165

gatatgccag catagaccgt gctttatcga aggtgaaccc atg ccc gtt atc aat 115

											Met	Pro	Val	Ile	Asn		
											1					5	
agt	atc	gcc	agt	ttt	tcc	gac	gag	atg	acc	cgc	tgg	cgg	cgt	cac	ctg	163	
Ser	Ile	Ala	Ser	Phe	Ser	Asp	Glu	Met	Thr	Arg	Trp	Arg	Arg	His	Leu		
				10					15					20			
cat	caa	aac	ccc	gaa	atc	agc	ttt	gat	tgt	gtg	gaa	act	gcg	gcc	ttc	211	
His	Gln	Asn	Pro	Glu	Ile	Ser	Phe	Asp	Cys	Val	Glu	Thr	Ala	Ala	Phe		
				25					30					35			
gtg	gcc	gag	cag	ctg	cgc	agc	ttc	ggg	gtg	gat	gaa	att	cac	acc	ggc	259	
Val	Ala	Glu	Gln	Leu	Arg	Ser	Phe	Gly	Val	Asp	Glu	Ile	His	Thr	Gly		
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atc	gcg	aaa	acc	ggg	atc	atc	gcc	ctg	att	cac	ggg	cgc	gag	gct	ggc	307	
Ile	Ala	Lys	Thr	Gly	Ile	Ile	Ala	Leu	Ile	His	Gly	Arg	Glu	Ala	Gly		
				55					60					65			
ccc	gtc	gtc	ggc	ctg	cgc	gcc	gat	atg	gac	gcg	ctg	ccg	ctg	acc	gag	355	
Pro	Val	Val	Gly	Leu	Arg	Ala	Asp	Met	Asp	Ala	Leu	Pro	Leu	Thr	Glu		
				70					75					80			
att	acc	ggc	gtc	gac	tat	gcc	tcg	acc	acc	ccc	gga	aaa	atg	cac	gcc	403	
Ile	Thr	Gly	Val	Asp	Tyr	Ala	Ser	Thr	Thr	Pro	Gly	Lys	Met	His	Ala		
				90					95					100			
tgc	ggc	cac	gac	ggc	cac	acg	acc	atg	ctg	ctg	ggc	gcc	gcc	aaa	tat	451	
Cys	Gly	His	Asp	Gly	His	Thr	Thr	Met	Leu	Leu	Gly	Ala	Ala	Lys	Tyr		
				105					110					115			
ctg	gcc	gag	acg	cgc	aat	ttc	gca	ggg	acc	gtc	gcg	ctg	atc	ttc	cag	499	
Leu	Ala	Glu	Thr	Arg	Asn	Phe	Ala	Gly	Thr	Val	Ala	Leu	Ile	Phe	Gln		
				120					125					130			
cct	gcg	gaa	gaa	aac	ggc	ggc	ggc	gcg	ggc	gtt	atg	gtc	gat	gaa	ggc	547	
Pro	Ala	Glu	Glu	Asn	Gly	Gly	Gly	Ala	Gly	Val	Met	Val	Asp	Glu	Gly		
				135					140					145			
gtc	ctc	gac	cgc	ttt	gcc	atc	gcc	gaa	gtc	tac	gcc	ctg	cac	aac	cag	595	
Val	Leu	Asp	Arg	Phe	Ala	Ile	Ala	Glu	Val	Tyr	Ala	Leu	His	Asn	Gln		
				150					155					160			
ccc	ggc	ctg	ccg	ctt	ggc	cat	ttt	atg	acg	aca	gcc	ggc	ccg	atc	atg	643	
Pro	Gly	Leu	Pro	Leu	Gly	His	Phe	Met	Thr	Thr	Ala	Gly	Pro	Ile	Met		
				170					175					180			
gcc	gct	gtc	gac	acg	ttc	gac	atc	aac	att	acc	gga	cgc	ggc	ggc	cac	691	
Ala	Ala	Val	Asp	Thr	Phe	Asp	Ile	Asn	Ile	Thr	Gly	Arg	Gly	Gly	His		
				185					190					195			
ggg	gcc	aaa	ccg	cac	caa	acc	cgc	gac	ccc	atc	gtc	gca	gcc	gtc	gga	739	
Gly	Ala	Lys	Pro	His	Gln	Thr	Arg	Asp	Pro	Ile	Val	Ala	Ala	Val	Gly		
				200					205					210			
att	gtc	caa	gcg	ttt	caa	acg	ata	gtc	agc	cgg	aat	cac	aat	ccg	gtc	787	
Ile	Val	Gln	Ala	Phe	Gln	Thr	Ile	Val	Ser	Arg	Asn	His	Asn	Pro	Val		
				215					220					225			
gag	gac	ctt	gtc	gtg	tcg	gtc	acg	caa	atc	cac	acc	ggc	agc	gcc	gat	835	
Glu	Asp	Leu	Val	Val	Ser	Val	Thr	Gln	Ile	His	Thr	Gly	Ser	Ala	Asp		

230	235	240	245	
aat atc atc ccc gaa acc gcc tat atc aac ggc act gtc cgc acc ttc				883
Asn Ile Ile Pro Glu Thr Ala Tyr Ile Asn Gly Thr Val Arg Thr Phe				
250		255	260	
aac aaa gac gtg cag gcc atg gtc atc acg cgg atg gaa gaa atc gtc				931
Asn Lys Asp Val Gln Ala Met Val Ile Thr Arg Met Glu Glu Ile Val				
265		270	275	
gcg ggc caa gct gca gcc tat ggg gtc gag gcg acg ctg acc tac aac				979
Ala Gly Gln Ala Ala Ala Tyr Gly Val Glu Ala Thr Leu Thr Tyr Asn				
280		285	290	
cgc aac tat ccc gcc acc att aac gac gcc gcc aaa gcc gcc atc gct				1027
Arg Asn Tyr Pro Ala Thr Ile Asn Asp Ala Ala Lys Ala Ala Ile Ala				
295		300	305	
gcc gaa gtc gcg ggc gag gtc ggc ctc ggg gtc aac ccg aac ggc tcg				1075
Ala Glu Val Ala Gly Glu Val Gly Leu Gly Val Asn Pro Asn Gly Ser				
310		315	320	325
cgc ggg atg ggg gcc gag gat ttc tcg tat ttc ctc gaa aag cgc ccg				1123
Arg Gly Met Gly Ala Glu Asp Phe Ser Tyr Phe Leu Glu Lys Arg Pro				
330		335	340	
ggt gcc tac ctg ttc gtc ggt aat ggc gac agc gcg ggc ctt cac aac				1171
Gly Ala Tyr Leu Phe Val Gly Asn Gly Asp Ser Ala Gly Leu His Asn				
345		350	355	
ccc gcc tat aat ttc aac gac gag gcc gcg ccc tac ggc gca tcg ttc				1219
Pro Ala Tyr Asn Phe Asn Asp Glu Ala Ala Pro Tyr Gly Ala Ser Phe				
360		365	370	
ttg gcc cgc atg gca gaa cgc ccc ttg ccg tta aag ggc tgcacatgg				1268
Leu Ala Arg Met Ala Glu Arg Pro Leu Pro Leu Lys Gly				
375		380	385	
cgctcgaaga tgc				1281

&lt;210&gt; 364

&lt;211&gt; 386

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 364

Met	Pro	Val	Ile	Asn	Ser	Ile	Ala	Ser	Phe	Ser	Asp	Glu	Met	Thr	Arg
1				5					10					15	

Trp	Arg	Arg	His	Leu	His	Gln	Asn	Pro	Glu	Ile	Ser	Phe	Asp	Cys	Val
			20					25					30		

Glu	Thr	Ala	Ala	Phe	Val	Ala	Glu	Gln	Leu	Arg	Ser	Phe	Gly	Val	Asp
		35					40					45			

Glu	Ile	His	Thr	Gly	Ile	Ala	Lys	Thr	Gly	Ile	Ile	Ala	Leu	Ile	His
	50					55					60				

Gly	Arg	Glu	Ala	Gly	Pro	Val	Val	Gly	Leu	Arg	Ala	Asp	Met	Asp	Ala
65					70					75					80



Leu Pro Leu Thr Glu Ile Thr Gly Val Asp Tyr Ala Ser Thr Thr Pro  
 85 90 95  
 Gly Lys Met His Ala Cys Gly His Asp Gly His Thr Thr Met Leu Leu  
 100 105 110  
 Gly Ala Ala Lys Tyr Leu Ala Glu Thr Arg Asn Phe Ala Gly Thr Val  
 115 120 125  
 Ala Leu Ile Phe Gln Pro Ala Glu Glu Asn Gly Gly Ala Gly Val  
 130 135 140  
 Met Val Asp Glu Gly Val Leu Asp Arg Phe Ala Ile Ala Glu Val Tyr  
 145 150 155 160  
 Ala Leu His Asn Gln Pro Gly Leu Pro Leu Gly His Phe Met Thr Thr  
 165 170 175  
 Ala Gly Pro Ile Met Ala Ala Val Asp Thr Phe Asp Ile Asn Ile Thr  
 180 185 190  
 Gly Arg Gly Gly His Gly Ala Lys Pro His Gln Thr Arg Asp Pro Ile  
 195 200 205  
 Val Ala Ala Val Gly Ile Val Gln Ala Phe Gln Thr Ile Val Ser Arg  
 210 215 220  
 Asn His Asn Pro Val Glu Asp Leu Val Val Ser Val Thr Gln Ile His  
 225 230 235 240  
 Thr Gly Ser Ala Asp Asn Ile Ile Pro Glu Thr Ala Tyr Ile Asn Gly  
 245 250 255  
 Thr Val Arg Thr Phe Asn Lys Asp Val Gln Ala Met Val Ile Thr Arg  
 260 265 270  
 Met Glu Glu Ile Val Ala Gly Gln Ala Ala Ala Tyr Gly Val Glu Ala  
 275 280 285  
 Thr Leu Thr Tyr Asn Arg Asn Tyr Pro Ala Thr Ile Asn Asp Ala Ala  
 290 295 300  
 Lys Ala Ala Ile Ala Ala Glu Val Ala Gly Glu Val Gly Leu Gly Val  
 305 310 315 320  
 Asn Pro Asn Gly Ser Arg Gly Met Gly Ala Glu Asp Phe Ser Tyr Phe  
 325 330 335  
 Leu Glu Lys Arg Pro Gly Ala Tyr Leu Phe Val Gly Asn Gly Asp Ser  
 340 345 350  
 Ala Gly Leu His Asn Pro Ala Tyr Asn Phe Asn Asp Glu Ala Ala Pro  
 355 360 365  
 Tyr Gly Ala Ser Phe Leu Ala Arg Met Ala Glu Arg Pro Leu Pro Leu  
 370 375 380  
 Lys Gly  
 385

<210> 365  
 <211> 1386  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (101)..(1363)  
 <223> RXS02101

<400> 365

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agtttttagtg tcgctgcgca ggtactctac tatctaattcc atg agc cgc att tca 115
                               Met Ser Arg Ile Ser
                               1           5

gaa ctt cta aac aat cat ggt gtt gat ctg tcg tgg caa gag gcc gca 163
Glu Leu Leu Asn Asn His Gly Val Asp Leu Ser Trp Gln Glu Ala Ala
                        10                15                20

tat cag gat ttc cac gaa cat cct gag ctg tcc ggc ttc gaa tca gag 211
Tyr Gln Asp Phe His Glu His Pro Glu Leu Ser Gly Phe Glu Ser Glu
                        25                30                35

acc gca gat cgc att cag aaa tac ctg gag cgt ttt gat tgt gag gtg 259
Thr Ala Asp Arg Ile Gln Lys Tyr Leu Glu Arg Phe Asp Cys Glu Val
                        40                45                50

att cca aat gtt ggc ggt tac ggc att ctg gcc gtg ttc cga aat ggg 307
Ile Pro Asn Val Gly Gly Tyr Gly Ile Leu Ala Val Phe Arg Asn Gly
                        55                60                65

tcg aca gat cct ggt gcc cct gtt gcg tta atg cgc gca gat ttc gat 355
Ser Thr Asp Pro Gly Ala Pro Val Ala Leu Met Arg Ala Asp Phe Asp
                        70                75                80                85

ggc ctt ccc gtc aag gaa atc acc gga gtt ccg ttt gct tcc act cgt 403
Gly Leu Pro Val Lys Glu Ile Thr Gly Val Pro Phe Ala Ser Thr Arg
                        90                95                100

atg cgt ccg cat gat ggg gca aat gtc cat gtc atg cac gca tgc ggc 451
Met Arg Pro His Asp Gly Ala Asn Val His Val Met His Ala Cys Gly
                        105                110                115

cac gat gtc cac gtc acc gcg ctg ctt ggt gcg tgt gcc att tta gat 499
His Asp Val His Val Thr Ala Leu Leu Gly Ala Cys Ala Ile Leu Asp
                        120                125                130

gag cgt cgc gat gca tgg gaa ggc acg ttc atc gcg ttg ttc cag cca 547
Glu Arg Arg Asp Ala Trp Glu Gly Thr Phe Ile Ala Leu Phe Gln Pro
                        135                140                145

tcg gag gaa aac tcc caa ggc gct aac aag atg gtc gcc ggc ggt tta 595
Ser Glu Glu Asn Ser Gln Gly Ala Asn Lys Met Val Ala Gly Gly Leu
                        150                155                160                165

gtt gat ctg atc cca cgc cct gat gtg tgc ttt ggc cag cat gta gtc 643
Val Asp Leu Ile Pro Arg Pro Asp Val Cys Phe Gly Gln His Val Val
                        170                175                180

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ccc ggt gct gca gga acc gtg atg agc atg cct ggc ggt gct ctc gct 691  
 Pro Gly Ala Ala Gly Thr Val Met Ser Met Pro Gly Gly Ala Leu Ala  
 185 190 195

gcc tgc gat tcc att gaa atc cgc att cag ggt cgc agc gcc cat ggt 739  
 Ala Cys Asp Ser Ile Glu Ile Arg Ile Gln Gly Arg Ser Ala His Gly  
 200 205 210

tcc atg cct cat aat tcc atc gat ccc act tat gtt gca gcg atg att 787  
 Ser Met Pro His Asn Ser Ile Asp Pro Thr Tyr Val Ala Ala Met Ile  
 215 220 225

gtc gtg cga ctc caa gga atc gtg ggc cgc gag gtt tct cca gag gat 835  
 Val Val Arg Leu Gln Gly Ile Val Gly Arg Glu Val Ser Pro Glu Asp  
 230 235 240 245

ttc gcc gtt att tct gtg ggc acc ctc cag tgc ggc aac acc aac aac 883  
 Phe Ala Val Ile Ser Val Gly Thr Leu Gln Ser Gly Asn Thr Asn Asn  
 250 255 260

acc att cca gca agt gct cgt ttg gtg ttg aac tgc cgt ttc tac aac 931  
 Thr Ile Pro Ala Ser Ala Arg Leu Val Leu Asn Cys Arg Phe Tyr Asn  
 265 270 275

gac aaa gtc aag cac aag gtc tac cga gcc atc gaa cgt gtt gtc cgt 979  
 Asp Lys Val Lys His Lys Val Tyr Arg Ala Ile Glu Arg Val Val Arg  
 280 285 290

ggt gaa tgc ctt gct tcc ggt att gag gaa gaa cct gtc att gag tac 1027  
 Gly Glu Cys Leu Ala Ser Gly Ile Glu Glu Glu Pro Val Ile Glu Tyr  
 295 300 305

ttc gcc cac ggt gat ctc acc aac aac acc cct gtt gtc ttc gat act 1075  
 Phe Ala His Gly Asp Leu Thr Asn Asn Thr Pro Val Val Phe Asp Thr  
 310 315 320 325

gtg cgc cct gtc ttc gac gat gtt ttc ggc gag gat tct att gac gct 1123  
 Val Arg Pro Val Phe Asp Asp Val Phe Gly Glu Asp Ser Ile Asp Ala  
 330 335 340

tac cgg tgg act gcg tgc gag gat ttc ccc tcc att cct aag gca ttc 1171  
 Tyr Arg Trp Thr Ala Ser Glu Asp Phe Pro Ser Ile Pro Lys Ala Phe  
 345 350 355

aac agc cct tac ctg tac tgg acg att ggt gtc acg ccg cgc gat cag 1219  
 Asn Ser Pro Tyr Leu Tyr Trp Thr Ile Gly Val Thr Pro Arg Asp Gln  
 360 365 370

tgg aca gaa gcc gta gaa aga gac cgc gtg gca tgc gat gtg cca gcc 1267  
 Trp Thr Glu Ala Val Glu Arg Asp Arg Val Ala Ser Asp Val Pro Ala  
 375 380 385

aat cac atg gga gat ttc ctc cct gat tat gcg ccg acg atg tcc gct 1315  
 Asn His Met Gly Asp Phe Leu Pro Asp Tyr Ala Pro Thr Met Ser Ala  
 390 395 400 405

gcc acc cgc gca gcc gca gcc gcg ctg ctg acc tac ttg gga act aac 1363  
 Ala Thr Arg Ala Ala Ala Ala Leu Leu Thr Tyr Leu Gly Thr Asn  
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taatcatcta gttttctgcg acg

1386

<210> 366

<211> 421

<212> PRT

<213> Corynebacterium glutamicum

<400> 366

Met Ser Arg Ile Ser Glu Leu Leu Asn Asn His Gly Val Asp Leu Ser  
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Trp Gln Glu Ala Ala Tyr Gln Asp Phe His Glu His Pro Glu Leu Ser  
20 25 30

Gly Phe Glu Ser Glu Thr Ala Asp Arg Ile Gln Lys Tyr Leu Glu Arg  
35 40 45

Phe Asp Cys Glu Val Ile Pro Asn Val Gly Gly Tyr Gly Ile Leu Ala  
50 55 60

Val Phe Arg Asn Gly Ser Thr Asp Pro Gly Ala Pro Val Ala Leu Met  
65 70 75 80

Arg Ala Asp Phe Asp Gly Leu Pro Val Lys Glu Ile Thr Gly Val Pro  
85 90 95

Phe Ala Ser Thr Arg Met Arg Pro His Asp Gly Ala Asn Val His Val  
100 105 110

Met His Ala Cys Gly His Asp Val His Val Thr Ala Leu Leu Gly Ala  
115 120 125

Cys Ala Ile Leu Asp Glu Arg Arg Asp Ala Trp Glu Gly Thr Phe Ile  
130 135 140

Ala Leu Phe Gln Pro Ser Glu Glu Asn Ser Gln Gly Ala Asn Lys Met  
145 150 155 160

Val Ala Gly Gly Leu Val Asp Leu Ile Pro Arg Pro Asp Val Cys Phe  
165 170 175

Gly Gln His Val Val Pro Gly Ala Ala Gly Thr Val Met Ser Met Pro  
180 185 190

Gly Gly Ala Leu Ala Ala Cys Asp Ser Ile Glu Ile Arg Ile Gln Gly  
195 200 205

Arg Ser Ala His Gly Ser Met Pro His Asn Ser Ile Asp Pro Thr Tyr  
210 215 220

Val Ala Ala Met Ile Val Val Arg Leu Gln Gly Ile Val Gly Arg Glu  
225 230 235 240

Val Ser Pro Glu Asp Phe Ala Val Ile Ser Val Gly Thr Leu Gln Ser  
245 250 255

Gly Asn Thr Asn Asn Thr Ile Pro Ala Ser Ala Arg Leu Val Leu Asn  
260 265 270

Cys Arg Phe Tyr Asn Asp Lys Val Lys His Lys Val Tyr Arg Ala Ile

275					280					285						
Glu	Arg	Val	Val	Arg	Gly	Glu	Cys	Leu	Ala	Ser	Gly	Ile	Glu	Glu	Glu	
290					295					300						
Pro	Val	Ile	Glu	Tyr	Phe	Ala	His	Gly	Asp	Leu	Thr	Asn	Asn	Thr	Pro	
305					310					315					320	
Val	Val	Phe	Asp	Thr	Val	Arg	Pro	Val	Phe	Asp	Asp	Val	Phe	Gly	Glu	
325					330					335						
Asp	Ser	Ile	Asp	Ala	Tyr	Arg	Trp	Thr	Ala	Ser	Glu	Asp	Phe	Pro	Ser	
340					345					350						
Ile	Pro	Lys	Ala	Phe	Asn	Ser	Pro	Tyr	Leu	Tyr	Trp	Thr	Ile	Gly	Val	
355					360					365						
Thr	Pro	Arg	Asp	Gln	Trp	Thr	Glu	Ala	Val	Glu	Arg	Asp	Arg	Val	Ala	
370					375					380						
Ser	Asp	Val	Pro	Ala	Asn	His	Met	Gly	Asp	Phe	Leu	Pro	Asp	Tyr	Ala	
385					390					395					400	
Pro	Thr	Met	Ser	Ala	Ala	Thr	Arg	Ala	Ala	Ala	Ala	Ala	Leu	Leu	Thr	
405					410					415						
Tyr	Leu	Gly	Thr	Asn												
420																

&lt;210&gt; 367

&lt;211&gt; 3462

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(3439)

&lt;223&gt; RXS02234

&lt;400&gt; 367

accagaggc cgctgccggc ccaaattgatg caagccccct gtttgaccag tttgttgagc 60

tgatggatgc	agacgctcag	aagaaaggcg	cataaataac	atg	cca	aag	cgt	tca	115
				Met	Pro	Lys	Arg	Ser	
				1				5	

gat	att	aac	cac	gtc	ctc	gtc	atc	ggc	tcc	ggc	ccc	atc	gtc	att	ggc	163
Asp	Ile	Asn	His	Val	Leu	Val	Ile	Gly	Ser	Gly	Pro	Ile	Val	Ile	Gly	
				10				15						20		

cag	gca	tgt	gaa	ttc	gac	tac	tcc	ggc	acc	cag	gct	tgc	cgc	gtg	ctg	211
Gln	Ala	Cys	Glu	Phe	Asp	Tyr	Ser	Gly	Thr	Gln	Ala	Cys	Arg	Val	Leu	
			25					30					35			

aag	gaa	gag	gga	ctg	cgc	gtc	acc	ctc	atc	aac	tcc	aac	cca	gca	acg	259
Lys	Glu	Glu	Gly	Leu	Arg	Val	Thr	Leu	Ile	Asn	Ser	Asn	Pro	Ala	Thr	
			40				45					50				

atc	atg	acc	gac	cca	gaa	atg	gct	gac	cac	acc	tac	gtg	gag	cca	atc	307
Ile	Met	Thr	Asp	Pro	Glu	Met	Ala	Asp	His	Thr	Tyr	Val	Glu	Pro	Ile	

55	60	65	
gag ccg gaa tac atc gac aag att ttc gct aag gaa atc gag cag ggc			355
Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala Lys Glu Ile Glu Gln Gly			
70	75	80	85
cac cca atc gac gcc gtc ctg gca acc ctt ggt ggc cag act gca ctt			403
His Pro Ile Asp Ala Val Leu Ala Thr Leu Gly Gly Gln Thr Ala Leu			
90	95		100
aac gca gct atc cag ctg gat cgc ctc ggc atc ctg gaa aag tac ggc			451
Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly Ile Leu Glu Lys Tyr Gly			
105	110		115
gtt gaa ctc atc ggt gca gac atc gat gcc att gag cgc ggc gaa gat			499
Val Glu Leu Ile Gly Ala Asp Ile Asp Ala Ile Glu Arg Gly Glu Asp			
120	125		130
cgc cag aag ttc aag gat att gtc acc acc atc ggt ggc gaa tcc gcg			547
Arg Gln Lys Phe Lys Asp Ile Val Thr Thr Ile Gly Gly Glu Ser Ala			
135	140		145
cgt tcc cgc gtc tgc cac aac atg gaa gaa gtc cac gag act gtc gca			595
Arg Ser Arg Val Cys His Asn Met Glu Glu Val His Glu Thr Val Ala			
150	155		160
165			
gaa ctc ggc ctt cca gta gtc gtg cgt cca tcc ttc act atg ggt ggc			643
Glu Leu Gly Leu Pro Val Val Val Arg Pro Ser Phe Thr Met Gly Gly			
170	175		180
ctg ggc tcc ggt ctt gca tac aac acc gaa gac ctt gag cgc atc gct			691
Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu Asp Leu Glu Arg Ile Ala			
185	190		195
ggt ggc gga ctt gct gca tct cct gaa gca aac gtc ttg atc gaa gaa			739
Gly Gly Gly Leu Ala Ala Ser Pro Glu Ala Asn Val Leu Ile Glu Glu			
200	205		210
tcc atc ctt ggt tgg aag gaa ttc gag ctc gag ctc atg cgc gat acc			787
Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu Glu Leu Met Arg Asp Thr			
215	220		225
gca gac aac gtt gtg gtt atc tgc tcc att gaa aac gtc gac gca ctg			835
Ala Asp Asn Val Val Val Ile Cys Ser Ile Glu Asn Val Asp Ala Leu			
230	235		240
245			
ggc gtg cac acc ggc gac tct gtc acc gtg gca cct gcc ctg acc ctg			883
Gly Val His Thr Gly Asp Ser Val Thr Val Ala Pro Ala Leu Thr Leu			
250	255		260
act gac cgt gaa ttc cag aag atg cgc gat cag ggt atc gcc atc atc			931
Thr Asp Arg Glu Phe Gln Lys Met Arg Asp Gln Gly Ile Ala Ile Ile			
265	270		275
cgc gag gtc ggc gtg gac acc ggt gga tgt aac atc cag ttc gcc atc			979
Arg Glu Val Gly Val Asp Thr Gly Gly Cys Asn Ile Gln Phe Ala Ile			
280	285		290
aac cca gtt gat ggc cgc atc atc acc att gag atg aac cca cgt gtg			1027
Asn Pro Val Asp Gly Arg Ile Ile Thr Ile Glu Met Asn Pro Arg Val			
295	300		305

tct cgt tcc tcc gct ctg gca tcc aag gca acg ggc ttc cca att gcc	1075
Ser Arg Ser Ser Ala Leu Ala Ser Lys Ala Thr Gly Phe Pro Ile Ala	
310 315 320 325	
aag atg gct gcc aag ctg gct atc gga tac acc ctg gat gag atc acc	1123
Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr Thr Leu Asp Glu Ile Thr	
330 335 340	
aac gac atc act ggt gaa acc cca gct gcg ttt gag ccc acc atc gac	1171
Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala Phe Glu Pro Thr Ile Asp	
345 350 355	
tac gtc gtg gtc aag gcc cca cgc ttt gct ttc gag aag ttt gtc ggc	1219
Tyr Val Val Val Lys Ala Pro Arg Phe Ala Phe Glu Lys Phe Val Gly	
360 365 370	
gct gat gac act ttg acc acc acc atg aag tcc gtc ggt gag gtc atg	1267
Ala Asp Asp Thr Leu Thr Thr Thr Met Lys Ser Val Gly Glu Val Met	
375 380 385	
tcc ctg ggc cgc aac tac att gca gca ctg aac aag gca ctg cgt tcc	1315
Ser Leu Gly Arg Asn Tyr Ile Ala Ala Leu Asn Lys Ala Leu Arg Ser	
390 395 400 405	
ctg gaa acc aag cag cag ggt ttc tgg acc aag cct gat gag ttc ttc	1363
Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr Lys Pro Asp Glu Phe Phe	
410 415 420	
gca ggg gag cgc gct acc gat aag gca gct gtt ctg gaa gat ctc aag	1411
Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala Val Leu Glu Asp Leu Lys	
425 430 435	
cgc cca acc gaa ggc cgc ctc tac gac gtt gag ctg gca atg cgc ctt	1459
Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val Glu Leu Ala Met Arg Leu	
440 445 450	
ggc gca agc gtg gaa gaa ctc tac gaa gca tct tct att gat cct tgg	1507
Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala Ser Ser Ile Asp Pro Trp	
455 460 465	
ttc ctc gcc gag ctt gaa gct ctc gtg cag ttc cgc cag aag ctc gtt	1555
Phe Leu Ala Glu Leu Glu Ala Leu Val Gln Phe Arg Gln Lys Leu Val	
470 475 480 485	
gac gca cca ttc cta aac gaa gat ctc ctg cgc gaa gca aag ttc atg	1603
Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu Arg Glu Ala Lys Phe Met	
490 495 500	
ggt ctg tcc gac ctg cag atc gca gcc ctt cgc cca gag ttc gct ggc	1651
Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu Arg Pro Glu Phe Ala Gly	
505 510 515	
gaa gac ggc gta cgc acc ttg cgt ctg tcc cta ggc atc cgc cca gta	1699
Glu Asp Gly Val Arg Thr Leu Arg Leu Ser Leu Gly Ile Arg Pro Val	
520 525 530	
ttc aag act gtg gat acc tgt gca gca gag ttt gaa gct aag act ccg	1747
Phe Lys Thr Val Asp Thr Cys Ala Ala Glu Phe Glu Ala Lys Thr Pro	
535 540 545	

tac	cac	tac	tcc	gca	tac	gag	ctg	gat	cca	gca	gct	gag	tct	gag	gtc	1795
Tyr	His	Tyr	Ser	Ala	Tyr	Glu	Leu	Asp	Pro	Ala	Ala	Glu	Ser	Glu	Val	
550					555					560					565	
gca	cca	cag	act	gag	cgt	gaa	aag	gtc	ctg	atc	ttg	ggc	tcc	ggg	cca	1843
Ala	Pro	Gln	Thr	Glu	Arg	Glu	Lys	Val	Leu	Ile	Leu	Gly	Ser	Gly	Pro	
				570					575					580		
aac	cgc	atc	ggc	cag	ggc	atc	gag	ttc	gac	tac	tcc	tgt	gtt	cac	gca	1891
Asn	Arg	Ile	Gly	Gln	Gly	Ile	Glu	Phe	Asp	Tyr	Ser	Cys	Val	His	Ala	
			585					590					595			
gct	ctt	gag	ctc	tcc	cgc	gtc	ggc	tac	gaa	act	gtc	atg	gtc	aac	tgc	1939
Ala	Leu	Glu	Leu	Ser	Arg	Val	Gly	Tyr	Glu	Thr	Val	Met	Val	Asn	Cys	
		600					605					610				
aac	cca	gag	acc	gtg	tcc	acc	gac	tac	gac	acc	gct	gac	cgc	ctg	tac	1987
Asn	Pro	Glu	Thr	Val	Ser	Thr	Asp	Tyr	Asp	Thr	Ala	Asp	Arg	Leu	Tyr	
	615					620					625					
ttc	gag	cca	ctg	acc	ttc	gaa	gac	gtc	atg	gag	gtc	tac	cac	gct	gag	2035
Phe	Glu	Pro	Leu	Thr	Phe	Glu	Asp	Val	Met	Glu	Val	Tyr	His	Ala	Glu	
630					635					640					645	
gcg	cag	tcc	ggc	acc	gtc	gca	ggt	gtt	atc	gtc	cag	ctt	ggg	ggc	cag	2083
Ala	Gln	Ser	Gly	Thr	Val	Ala	Gly	Val	Ile	Val	Gln	Leu	Gly	Gly	Gln	
				650					655					660		
act	cct	ctg	ggc	ttg	gca	gat	cgt	ttg	aag	aag	gct	ggc	gtc	cct	gtc	2131
Thr	Pro	Leu	Gly	Leu	Ala	Asp	Arg	Leu	Lys	Lys	Ala	Gly	Val	Pro	Val	
			665					670					675			
att	ggt	acc	tcc	cca	gag	gca	atc	gac	atg	gct	gag	gac	cgt	ggc	gag	2179
Ile	Gly	Thr	Ser	Pro	Glu	Ala	Ile	Asp	Met	Ala	Glu	Asp	Arg	Gly	Glu	
		680					685					690				
ttc	ggt	gca	ctg	ctg	aac	cgc	gag	cag	ctt	cct	gct	cca	gca	ttc	ggc	2227
Phe	Gly	Ala	Leu	Leu	Asn	Arg	Glu	Gln	Leu	Pro	Ala	Pro	Ala	Phe	Gly	
	695					700					705					
acc	gca	acc	tct	ttc	gaa	gag	gct	cgc	aca	gta	gcc	gat	gag	atc	agc	2275
Thr	Ala	Thr	Ser	Phe	Glu	Glu	Ala	Arg	Thr	Val	Ala	Asp	Glu	Ile	Ser	
710					715					720					725	
tac	cca	gtg	ctg	gtt	cgc	cct	tcc	tac	gtc	ttg	ggt	ggc	cgt	ggc	atg	2323
Tyr	Pro	Val	Leu	Val	Arg	Pro	Ser	Tyr	Val	Leu	Gly	Gly	Arg	Gly	Met	
				730					735					740		
gag	att	gtc	tac	gat	gag	gct	tcc	ctc	gag	gat	tac	atc	aac	cgc	gca	2371
Glu	Ile	Val	Tyr	Asp	Glu	Ala	Ser	Leu	Glu	Asp	Tyr	Ile	Asn	Arg	Ala	
			745					750					755			
act	gag	ttg	tct	tct	gac	cac	cca	gtg	ctg	gtt	gac	cgc	ttc	cta	gac	2419
Thr	Glu	Leu	Ser	Ser	Asp	His	Pro	Val	Leu	Val	Asp	Arg	Phe	Leu	Asp	
		760					765					770				
aac	gct	att	gag	atc	gac	gtc	gac	gca	ctg	tgc	gac	ggc	gac	gag	gtc	2467
Asn	Ala	Ile	Glu	Ile	Asp	Val	Asp	Ala	Leu	Cys	Asp	Gly	Asp	Glu	Val	
	775					780					785					
tac	ctg	gca	ggc	gtc	atg	gag	cac	atc	gag	gaa	gcc	ggc	att	cac	tcc	2515



Tyr 790	Leu	Ala	Gly	Val	Met 795	Glu	His	Ile	Glu	Glu 800	Ala	Gly	Ile	His	Ser 805	
ggt	gac	tcc	gca	tgt	gca	ctt	cct	cca	atg	act	ttg	ggc	gca	cag	gac	2563
Gly	Asp	Ser	Ala	Cys 810	Ala	Leu	Pro	Pro	Met 815	Thr	Leu	Gly	Ala	Gln 820	Asp	
atc	gag	aag	gtc	cgc	gaa	gca	acc	aag	aag	ctg	gct	ctg	ggc	atc	ggt	2611
Ile	Glu	Lys	Val 825	Arg	Glu	Ala	Thr	Lys 830	Lys	Leu	Ala	Leu	Gly 835	Ile	Gly	
gta	cag	ggc	ctg	atg	aac	gtc	cag	tac	gca	ctc	aag	gac	gac	atc	ctc	2659
Val	Gln	Gly	Leu	Met	Asn	Val	Gln	Tyr	Ala	Leu	Lys	Asp	Asp	Ile	Leu	
			840				845					850				
tac	gtc	atc	gag	gca	aac	cca	cgt	gca	tcc	cgc	acc	gtg	ccg	ttc	gtc	2707
Tyr	Val	Ile	Glu	Ala	Asn	Pro	Arg	Ala	Ser	Arg	Thr	Val	Pro	Phe	Val	
	855					860					865					
tcc	aag	gca	acg	ggc	gtc	aac	ctg	gcc	aag	gca	gca	tcc	cgt	atc	gca	2755
Ser	Lys	Ala	Thr	Gly	Val	Asn	Leu	Ala	Lys	Ala	Ala	Ser	Arg	Ile	Ala	
	870				875					880					885	
gtg	ggc	gcc	acc	atc	aag	gat	ctc	caa	gat	gag	ggc	atg	att	cct	acc	2803
Val	Gly	Ala	Thr	Ile	Lys	Asp	Leu	Gln	Asp	Glu	Gly	Met	Ile	Pro	Thr	
				890					895					900		
gag	tac	gac	ggc	ggc	tcc	ttg	cca	ctg	gac	gct	cca	atc	gct	gtg	aag	2851
Glu	Tyr	Asp	Gly	Gly	Ser	Leu	Pro	Leu	Asp	Ala	Pro	Ile	Ala	Val	Lys	
			905					910					915			
gaa	gca	gtg	ttg	ccg	ttc	aac	cgc	ttc	cgt	cgc	cca	gat	gga	aag	acc	2899
Glu	Ala	Val	Leu	Pro	Phe	Asn	Arg	Phe	Arg	Arg	Pro	Asp	Gly	Lys	Thr	
		920					925					930				
ctg	gac	acc	ctg	ctt	tcc	cca	gag	atg	aag	tcc	act	ggc	gag	gtc	atg	2947
Leu	Asp	Thr	Leu	Leu	Ser	Pro	Glu	Met	Lys	Ser	Thr	Gly	Glu	Val	Met	
	935					940					945					
ggc	ttg	gcc	aac	aac	ttc	ggc	gct	gca	tat	gca	aag	gct	gaa	gct	ggc	2995
Gly	Leu	Ala	Asn	Asn	Phe	Gly	Ala	Ala	Tyr	Ala	Lys	Ala	Glu	Ala	Gly	
	950				955					960					965	
gcg	ttt	ggt	gca	ttg	cca	acc	gaa	ggc	acc	gtc	ttc	gtg	acc	gtg	gct	3043
Ala	Phe	Gly	Ala	Leu	Pro	Thr	Glu	Gly	Thr	Val	Phe	Val	Thr	Val	Ala	
				970					975					980		
aac	cgc	gac	aag	cgc	acc	ctg	atc	ctg	cca	atc	cag	cgc	ctg	gcg	ttg	3091
Asn	Arg	Asp	Lys	Arg	Thr	Leu	Ile	Leu	Pro	Ile	Gln	Arg	Leu	Ala	Leu	
			985					990					995			
atg	ggc	tac	aag	atc	ctc	gcc	acc	gaa	ggc	acc	gca	ggc	atg	ctg	cgc	3139
Met	Gly	Tyr	Lys	Ile	Leu	Ala	Thr	Glu	Gly	Thr	Ala	Gly	Met	Leu	Arg	
		1000					1005					1010				
cgc	aac	ggc	att	gag	tgt	gaa	gtt	gtg	ctc	aag	gct	tcc	gac	atc	cgc	3187
Arg	Asn	Gly	Ile	Glu	Cys	Glu	Val	Val	Leu	Lys	Ala	Ser	Asp	Ile	Arg	
	1015					1020					1025					
gaa	ggt	gta	gag	ggc	aag	tcc	atc	gtg	gat	cgt	atc	cgc	gaa	ggc	gaa	3235
Glu	Gly	Val	Glu	Gly	Lys	Ser	Ile	Val	Asp	Arg	Ile	Arg	Glu	Gly	Glu	

1030	1035	1040	1045
ggt gac ctc atc ctc aac acc cca gct ggt tct gct ggc gct cgc cac			3283
Val Asp Leu Ile Leu Asn Thr Pro Ala Gly Ser Ala Gly Ala Arg His			
1050	1055	1060	
gat ggc tac gat atc cgc gca gca gca gtg acc gtg ggt gtt ccg ctg			3331
Asp Gly Tyr Asp Ile Arg Ala Ala Val Thr Val Gly Val Pro Leu			
1065	1070	1075	
atc acc act gtt cag ggt gtc acc gca gct gtc cag ggc ata gag gcc			3379
Ile Thr Thr Val Gln Gly Val Thr Ala Ala Val Gln Gly Ile Glu Ala			
1080	1085	1090	
ctg cgt gag ggc gtt gtc agc gtc cgc gcg ctg cag gaa ctc gac cac			3427
Leu Arg Glu Gly Val Val Ser Val Arg Ala Leu Gln Glu Leu Asp His			
1095	1100	1105	
gca gtc aag gct taagccctat gacattcggc gag			3462
Ala Val Lys Ala			
1110			

&lt;210&gt; 368

&lt;211&gt; 1113

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 368

Met	Pro	Lys	Arg	Ser	Asp	Ile	Asn	His	Val	Leu	Val	Ile	Gly	Ser	Gly
1				5					10					15	

Pro	Ile	Val	Ile	Gly	Gln	Ala	Cys	Glu	Phe	Asp	Tyr	Ser	Gly	Thr	Gln
		20						25					30		

Ala	Cys	Arg	Val	Leu	Lys	Glu	Glu	Gly	Leu	Arg	Val	Thr	Leu	Ile	Asn
		35					40					45			

Ser	Asn	Pro	Ala	Thr	Ile	Met	Thr	Asp	Pro	Glu	Met	Ala	Asp	His	Thr
	50					55					60				

Tyr	Val	Glu	Pro	Ile	Glu	Pro	Glu	Tyr	Ile	Asp	Lys	Ile	Phe	Ala	Lys
	65				70				75						80

Glu	Ile	Glu	Gln	Gly	His	Pro	Ile	Asp	Ala	Val	Leu	Ala	Thr	Leu	Gly
			85						90					95	

Gly	Gln	Thr	Ala	Leu	Asn	Ala	Ala	Ile	Gln	Leu	Asp	Arg	Leu	Gly	Ile
		100						105					110		

Leu	Glu	Lys	Tyr	Gly	Val	Glu	Leu	Ile	Gly	Ala	Asp	Ile	Asp	Ala	Ile
		115					120					125			

Glu	Arg	Gly	Glu	Asp	Arg	Gln	Lys	Phe	Lys	Asp	Ile	Val	Thr	Thr	Ile
	130					135					140				

Gly	Gly	Glu	Ser	Ala	Arg	Ser	Arg	Val	Cys	His	Asn	Met	Glu	Glu	Val
145					150					155					160

His	Glu	Thr	Val	Ala	Glu	Leu	Gly	Leu	Pro	Val	Val	Val	Arg	Pro	Ser
				165					170					175	

Phe	Thr	Met	Gly	Gly	Leu	Gly	Ser	Gly	Leu	Ala	Tyr	Asn	Thr	Glu	Asp	
			180					185					190			
Leu	Glu	Arg	Ile	Ala	Gly	Gly	Gly	Leu	Ala	Ala	Ser	Pro	Glu	Ala	Asn	
		195					200					205				
Val	Leu	Ile	Glu	Glu	Ser	Ile	Leu	Gly	Trp	Lys	Glu	Phe	Glu	Leu	Glu	
	210					215					220					
Leu	Met	Arg	Asp	Thr	Ala	Asp	Asn	Val	Val	Val	Ile	Cys	Ser	Ile	Glu	
225					230					235					240	
Asn	Val	Asp	Ala	Leu	Gly	Val	His	Thr	Gly	Asp	Ser	Val	Thr	Val	Ala	
				245					250					255		
Pro	Ala	Leu	Thr	Leu	Thr	Asp	Arg	Glu	Phe	Gln	Lys	Met	Arg	Asp	Gln	
			260					265						270		
Gly	Ile	Ala	Ile	Ile	Arg	Glu	Val	Gly	Val	Asp	Thr	Gly	Gly	Cys	Asn	
		275					280						285			
Ile	Gln	Phe	Ala	Ile	Asn	Pro	Val	Asp	Gly	Arg	Ile	Ile	Thr	Ile	Glu	
	290					295					300					
Met	Asn	Pro	Arg	Val	Ser	Arg	Ser	Ser	Ala	Leu	Ala	Ser	Lys	Ala	Thr	
305					310					315					320	
Gly	Phe	Pro	Ile	Ala	Lys	Met	Ala	Ala	Lys	Leu	Ala	Ile	Gly	Tyr	Thr	
				325					330					335		
Leu	Asp	Glu	Ile	Thr	Asn	Asp	Ile	Thr	Gly	Glu	Thr	Pro	Ala	Ala	Phe	
			340					345					350			
Glu	Pro	Thr	Ile	Asp	Tyr	Val	Val	Val	Lys	Ala	Pro	Arg	Phe	Ala	Phe	
		355					360					365				
Glu	Lys	Phe	Val	Gly	Ala	Asp	Asp	Thr	Leu	Thr	Thr	Thr	Met	Lys	Ser	
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Val	Gly	Glu	Val	Met	Ser	Leu	Gly	Arg	Asn	Tyr	Ile	Ala	Ala	Leu	Asn	
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Lys	Ala	Leu	Arg	Ser	Leu	Glu	Thr	Lys	Gln	Gln	Gly	Phe	Trp	Thr	Lys	
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Pro	Asp	Glu	Phe	Phe	Ala	Gly	Glu	Arg	Ala	Thr	Asp	Lys	Ala	Ala	Val	
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Leu	Glu	Asp	Leu	Lys	Arg	Pro	Thr	Glu	Gly	Arg	Leu	Tyr	Asp	Val	Glu	
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Leu	Ala	Met	Arg	Leu	Gly	Ala	Ser	Val	Glu	Glu	Leu	Tyr	Glu	Ala	Ser	
		450				455						460				
Ser	Ile	Asp	Pro	Trp	Phe	Leu	Ala	Glu	Leu	Glu	Ala	Leu	Val	Gln	Phe	
465					470					475					480	
Arg	Gln	Lys	Leu	Val	Asp	Ala	Pro	Phe	Leu	Asn	Glu	Asp	Leu	Leu	Arg	
				485					490						495	

Glu Ala Lys Phe Met Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu Arg  
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 Pro Glu Phe Ala Gly Glu Asp Gly Val Arg Thr Leu Arg Leu Ser Leu  
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 Gly Ile Arg Pro Val Phe Lys Thr Val Asp Thr Cys Ala Ala Glu Phe  
 530 535 540  
 Glu Ala Lys Thr Pro Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro Ala  
 545 550 555 560  
 Ala Glu Ser Glu Val Ala Pro Gln Thr Glu Arg Glu Lys Val Leu Ile  
 565 570 575  
 Leu Gly Ser Gly Pro Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp Tyr  
 580 585 590  
 Ser Cys Val His Ala Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu Thr  
 595 600 605  
 Val Met Val Asn Cys Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp Thr  
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 Ala Asp Arg Leu Tyr Phe Glu Pro Leu Thr Phe Glu Asp Val Met Glu  
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 Val Tyr His Ala Glu Ala Gln Ser Gly Thr Val Ala Gly Val Ile Val  
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 Ala Gly Val Pro Val Ile Gly Thr Ser Pro Glu Ala Ile Asp Met Ala  
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 Glu Asp Arg Gly Glu Phe Gly Ala Leu Leu Asn Arg Glu Gln Leu Pro  
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 Gly Gly Arg Gly Met Glu Ile Val Tyr Asp Glu Ala Ser Leu Glu Asp  
 740 745 750  
 Tyr Ile Asn Arg Ala Thr Glu Leu Ser Ser Asp His Pro Val Leu Val  
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 Asp Arg Phe Leu Asp Asn Ala Ile Glu Ile Asp Val Asp Ala Leu Cys  
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 Ala Gly Ile His Ser Gly Asp Ser Ala Cys Ala Leu Pro Pro Met Thr  
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 Leu Gly Ala Gln Asp Ile Glu Lys Val Arg Glu Ala Thr Lys Lys Leu

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Lys	Asp	Asp	Ile	Leu	Tyr	Val	Ile	Glu	Ala	Asn	Pro	Arg	Ala	Ser	Arg
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Thr	Val	Pro	Phe	Val	Ser	Lys	Ala	Thr	Gly	Val	Asn	Leu	Ala	Lys	Ala
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Ala	Ser	Arg	Ile	Ala	Val	Gly	Ala	Thr	Ile	Lys	Asp	Leu	Gln	Asp	Glu
			885						890					895	
Gly	Met	Ile	Pro	Thr	Glu	Tyr	Asp	Gly	Gly	Ser	Leu	Pro	Leu	Asp	Ala
			900					905					910		
Pro	Ile	Ala	Val	Lys	Glu	Ala	Val	Leu	Pro	Phe	Asn	Arg	Phe	Arg	Arg
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Pro	Asp	Gly	Lys	Thr	Leu	Asp	Thr	Leu	Leu	Ser	Pro	Glu	Met	Lys	Ser
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Thr	Gly	Glu	Val	Met	Gly	Leu	Ala	Asn	Asn	Phe	Gly	Ala	Ala	Tyr	Ala
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Lys	Ala	Glu	Ala	Gly	Ala	Phe	Gly	Ala	Leu	Pro	Thr	Glu	Gly	Thr	Val
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Phe	Val	Thr	Val	Ala	Asn	Arg	Asp	Lys	Arg	Thr	Leu	Ile	Leu	Pro	Ile
			980					985					990		
Gln	Arg	Leu	Ala	Leu	Met	Gly	Tyr	Lys	Ile	Leu	Ala	Thr	Glu	Gly	Thr
		995					1000						1005		
Ala	Gly	Met	Leu	Arg	Arg	Asn	Gly	Ile	Glu	Cys	Glu	Val	Val	Leu	Lys
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Ile	Arg	Glu	Gly	Glu	Val	Asp	Leu	Ile	Leu	Asn	Thr	Pro	Ala	Gly	Ser
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Ala	Gly	Ala	Arg	His	Asp	Gly	Tyr	Asp	Ile	Arg	Ala	Ala	Ala	Val	Thr
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Val	Gly	Val	Pro	Leu	Ile	Thr	Thr	Val	Gln	Gly	Val	Thr	Ala	Ala	Val
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Gln	Gly	Ile	Glu	Ala	Leu	Arg	Glu	Gly	Val	Val	Ser	Val	Arg	Ala	Leu
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Gln	Glu	Leu	Asp	His	Ala	Val	Lys	Ala							
1105						1110									

&lt;210&gt; 369

&lt;211&gt; 3221

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(3198)

&lt;223&gt; FRXA02234

&lt;400&gt; 369

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acc tac gtg gag cca atc gag ccg gaa tac atc gac aag att ttc gct      96
Thr Tyr Val Glu Pro Ile Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala
      20              25              30

aag gaa atc gag cag ggc cac cca atc gac gcc gtc ctg gca acc ctt      144
Lys Glu Ile Glu Gln Gly His Pro Ile Asp Ala Val Leu Ala Thr Leu
      35              40              45

ggt ggc cag act gca ctt aac gca gct atc cag ctg gat cgc ctc ggc      192
Gly Gly Gln Thr Ala Leu Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly
      50              55              60

atc ctg gaa aag tac ggc gtt gaa ctc atc ggt gca gac atc gat gcc      240
Ile Leu Glu Lys Tyr Gly Val Glu Leu Ile Gly Ala Asp Ile Asp Ala
      65              70              75              80

att gag cgc ggc gaa gat cgc cag aag ttc aag gat att gtc acc acc      288
Ile Glu Arg Gly Glu Asp Arg Gln Lys Phe Lys Asp Ile Val Thr Thr
      85              90              95

atc ggt ggc gaa tcc gcg cgt tcc cgc gtc tgc cac aac atg gaa gaa      336
Ile Gly Gly Glu Ser Ala Arg Ser Arg Val Cys His Asn Met Glu Glu
      100              105              110

gtc cac gag act gtc gca gaa ctc ggc ctt cca gta gtc gtg cgt cca      384
Val His Glu Thr Val Ala Glu Leu Gly Leu Pro Val Val Val Arg Pro
      115              120              125

tcc ttc act atg ggt ggc ctg ggc tcc ggt ctt gca tac aac acc gaa      432
Ser Phe Thr Met Gly Gly Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu
      130              135              140

gac ctt gag cgc atc gct ggt ggc gga ctt gct gca tct cct gaa gca      480
Asp Leu Glu Arg Ile Ala Gly Gly Gly Leu Ala Ala Ser Pro Glu Ala
      145              150              155              160

aac gtc ttg atc gaa gaa tcc atc ctt ggt tgg aag gaa ttc gag ctc      528
Asn Val Leu Ile Glu Glu Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu
      165              170              175

gag ctc atg cgc gat acc gca gac aac gtt gtg gtt atc tgc tcc att      576
Glu Leu Met Arg Asp Thr Ala Asp Asn Val Val Val Ile Cys Ser Ile
      180              185              190

gaa aac gtc gac gca ctg ggc gtg cac acc ggc gac tct gtc acc gtg      624
Glu Asn Val Asp Ala Leu Gly Val His Thr Gly Asp Ser Val Thr Val
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gca cct gcc ctg acc ctg act gac cgt gaa ttc cag aag atg cgc gat      672
Ala Pro Ala Leu Thr Leu Thr Asp Arg Glu Phe Gln Lys Met Arg Asp

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aac atc cag ttc gcc atc aac cca gtt gat ggc cgc atc atc acc att Asn Ile Gln Phe Ala Ile Asn Pro Val Asp Gly Arg Ile Ile Thr Ile 245 250 255			768
gag atg aac cca cgt gtg tct cgt tcc tcc gct ctg gca tcc aag gca Glu Met Asn Pro Arg Val Ser Arg Ser Ser Ala Leu Ala Ser Lys Ala 260 265 270			816
acg ggc ttc cca att gcc aag atg gct gcc aag ctg gct atc gga tac Thr Gly Phe Pro Ile Ala Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr 275 280 285			864
acc ctg gat gag atc acc aac gac atc act ggt gaa acc cca gct gcg Thr Leu Asp Glu Ile Thr Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala 290 295 300			912
ttt gag ccc acc atc gac tac gtc gtg gtc aag gcc cca cgc ttt gct Phe Glu Pro Thr Ile Asp Tyr Val Val Val Lys Ala Pro Arg Phe Ala 305 310 315 320			960
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gtt ctg gaa gat ctc aag cgc cca acc gaa ggc cgc ctc tac gac gtt Val Leu Glu Asp Leu Lys Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val 385 390 395 400			1200
gag ctg gca atg cgc ctt ggc gca agc gtg gaa gaa ctc tac gaa gca Glu Leu Ala Met Arg Leu Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala 405 410 415			1248
tct tct att gat cct tgg ttc ctc gcc gag ctt gaa gct ctc gtg cag Ser Ser Ile Asp Pro Trp Phe Leu Ala Glu Leu Glu Ala Leu Val Gln 420 425 430			1296
ttc cgc cag aag ctc gtt gac gca cca ttc cta aac gaa gat ctc ctg Phe Arg Gln Lys Leu Val Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu 435 440 445			1344
cgc gaa gca aag ttc atg ggt ctg tcc gac ctg cag atc gca gcc ctt Arg Glu Ala Lys Phe Met Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu 450 455 460			1392

cgc cca gag ttc gct ggc gaa gac ggc gta cgc acc ttg cgt ctg tcc	1440
Arg Pro Glu Phe Ala Gly Glu Asp Gly Val Arg Thr Leu Arg Leu Ser	
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Leu Gly Ile Arg Pro Val Phe Lys Thr Val Asp Thr Cys Ala Ala Glu	
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Phe Glu Ala Lys Thr Pro Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro	
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Ala Ala Glu Ser Glu Val Ala Pro Gln Thr Glu Arg Glu Lys Val Leu	
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Ile Leu Gly Ser Gly Pro Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp	
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Tyr Ser Cys Val His Ala Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu	
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Thr Ala Asp Arg Leu Tyr Phe Glu Pro Leu Thr Phe Glu Asp Val Met	
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Val Gln Leu Gly Gly Gln Thr Pro Leu Gly Leu Ala Asp Arg Leu Lys	
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Ala Glu Asp Arg Gly Glu Phe Gly Ala Leu Leu Asn Arg Glu Gln Leu	
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gta gcc gat gag atc agc tac cca gtg ctg gtt cgc cct tcc tac gtc	2064
Val Ala Asp Glu Ile Ser Tyr Pro Val Leu Val Arg Pro Ser Tyr Val	
675 680 685	
ttg ggt ggc cgt ggc atg gag att gtc tac gat gag gct tcc ctc gag	2112
Leu Gly Gly Arg Gly Met Glu Ile Val Tyr Asp Glu Ala Ser Leu Glu	
690 695 700	



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Asp	Tyr	Ile	Asn	Arg	Ala	Thr	Glu	Leu	Ser	Ser	Asp	His	Pro	Val	Leu	
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gtt	gac	cgc	ttc	cta	gac	aac	gct	att	gag	atc	gac	gtc	gac	gca	ctg	2208
Val	Asp	Arg	Phe	Leu	Asp	Asn	Ala	Ile	Glu	Ile	Asp	Val	Asp	Ala	Leu	
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tgc	gac	ggc	gac	gag	gtc	tac	ctg	gca	ggc	gtc	atg	gag	cac	atc	gag	2256
Cys	Asp	Gly	Asp	Glu	Val	Tyr	Leu	Ala	Gly	Val	Met	Glu	His	Ile	Glu	
			740					745					750			
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Glu	Ala	Gly	Ile	His	Ser	Gly	Asp	Ser	Ala	Cys	Ala	Leu	Pro	Pro	Met	
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act	ttg	ggc	gca	cag	gac	atc	gag	aag	gtc	cgc	gaa	gca	acc	aag	aag	2352
Thr	Leu	Gly	Ala	Gln	Asp	Ile	Glu	Lys	Val	Arg	Glu	Ala	Thr	Lys	Lys	
	770					775					780					
ctg	gct	ctg	ggc	atc	ggt	gta	cag	ggc	ctg	atg	aac	gtc	cag	tac	gca	2400
Leu	Ala	Leu	Gly	Ile	Gly	Val	Gln	Gly	Leu	Met	Asn	Val	Gln	Tyr	Ala	
785					790					795					800	
ctc	aag	gac	gac	atc	ctc	tac	gtc	atc	gag	gca	aac	cca	cgt	gca	tcc	2448
Leu	Lys	Asp	Asp	Ile	Leu	Tyr	Val	Ile	Glu	Ala	Asn	Pro	Arg	Ala	Ser	
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cgc	acc	gtg	ccg	ttc	gtc	tcc	aag	gca	acg	ggc	gtc	aac	ctg	gcc	aag	2496
Arg	Thr	Val	Pro	Phe	Val	Ser	Lys	Ala	Thr	Gly	Val	Asn	Leu	Ala	Lys	
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gca	gca	tcc	cgt	atc	gca	gtg	ggc	gcc	acc	atc	aag	gat	ctc	caa	gat	2544
Ala	Ala	Ser	Arg	Ile	Ala	Val	Gly	Ala	Thr	Ile	Lys	Asp	Leu	Gln	Asp	
		835					840					845				
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Glu	Gly	Met	Ile	Pro	Thr	Glu	Tyr	Asp	Gly	Gly	Ser	Leu	Pro	Leu	Asp	
	850					855					860					
gct	cca	atc	gct	gtg	aag	gaa	gca	gtg	ttg	ccg	ttc	aac	cgc	ttc	cgt	2640
Ala	Pro	Ile	Ala	Val	Lys	Glu	Ala	Val	Leu	Pro	Phe	Asn	Arg	Phe	Arg	
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cgc	cca	gat	gga	aag	acc	ctg	gac	acc	ctg	ctt	tcc	cca	gag	atg	aag	2688
Arg	Pro	Asp	Gly	Lys	Thr	Leu	Asp	Thr	Leu	Leu	Ser	Pro	Glu	Met	Lys	
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tcc	act	ggc	gag	gtc	atg	ggc	ttg	gcc	aac	aac	ttc	ggc	gct	gca	tat	2736
Ser	Thr	Gly	Glu	Val	Met	Gly	Leu	Ala	Asn	Asn	Phe	Gly	Ala	Ala	Tyr	
			900					905					910			
gca	aag	gct	gaa	gct	ggc	gcg	ttt	ggt	gca	ttg	cca	acc	gaa	ggc	acc	2784
Ala	Lys	Ala	Glu	Ala	Gly	Ala	Phe	Gly	Ala	Leu	Pro	Thr	Glu	Gly	Thr	
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gtc	ttc	gtg	acc	gtg	gct	aac	cgc	gac	aag	cgc	acc	ctg	atc	ctg	cca	2832
Val	Phe	Val	Thr	Val	Ala	Asn	Arg	Asp	Lys	Arg	Thr	Leu	Ile	Leu	Pro	
	930					935					940					
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Ile Gln Arg Leu Ala Leu Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly
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Thr Ala Gly Met Leu Arg Arg Asn Gly Ile Glu Cys Glu Val Val Leu
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Lys Ala Ser Asp Ile Arg Glu Gly Val Glu Gly Lys Ser Ile Val Asp
                      980                      985                      990

cgt atc cgc gaa ggc gaa gtt gac ctc atc ctc aac acc cca gct ggt 3024
Arg Ile Arg Glu Gly Glu Val Asp Leu Ile Leu Asn Thr Pro Ala Gly
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Ser Ala Gly Ala Arg His Asp Gly Tyr Asp Ile Arg Ala Ala Val
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Val Gln Gly Ile Glu Ala Leu Arg Glu Gly Val Val Ser Val Arg Ala
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ctg cag gaa ctc gac cac gca gtc aag gct taagccctat gacattcggc 3218
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gag 3221

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Gly Gly Gln Thr Ala Leu Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly
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Ile Leu Glu Lys Tyr Gly Val Glu Leu Ile Gly Ala Asp Ile Asp Ala
65                      70                      75                      80

Ile Glu Arg Gly Glu Asp Arg Gln Lys Phe Lys Asp Ile Val Thr Thr
85                      90                      95

Ile Gly Gly Glu Ser Ala Arg Ser Arg Val Cys His Asn Met Glu Glu
100                      105                      110

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Val His Glu Thr Val Ala Glu Leu Gly Leu Pro Val Val Val Arg Pro  
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 Ser Phe Thr Met Gly Gly Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu  
 130 135 140  
 Asp Leu Glu Arg Ile Ala Gly Gly Gly Leu Ala Ala Ser Pro Glu Ala  
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 Glu Leu Met Arg Asp Thr Ala Asp Asn Val Val Val Ile Cys Ser Ile  
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 Glu Asn Val Asp Ala Leu Gly Val His Thr Gly Asp Ser Val Thr Val  
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 Ala Pro Ala Leu Thr Leu Thr Asp Arg Glu Phe Gln Lys Met Arg Asp  
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 Gln Gly Ile Ala Ile Ile Arg Glu Val Gly Val Asp Thr Gly Gly Cys  
 225 230 235 240  
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 Glu Met Asn Pro Arg Val Ser Arg Ser Ser Ala Leu Ala Ser Lys Ala  
 260 265 270  
 Thr Gly Phe Pro Ile Ala Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr  
 275 280 285  
 Thr Leu Asp Glu Ile Thr Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala  
 290 295 300  
 Phe Glu Pro Thr Ile Asp Tyr Val Val Val Lys Ala Pro Arg Phe Ala  
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 Lys Pro Asp Glu Phe Phe Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala  
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 Ser Ser Ile Asp Pro Trp Phe Leu Ala Glu Leu Glu Ala Leu Val Gln  
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Leu	Gly	Ile	Arg	Pro	Val	Phe	Lys	Thr	Val	Asp	Thr	Cys	Ala	Ala	Glu
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Phe	Glu	Ala	Lys	Thr	Pro	Tyr	His	Tyr	Ser	Ala	Tyr	Glu	Leu	Asp	Pro
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Ala	Ala	Glu	Ser	Glu	Val	Ala	Pro	Gln	Thr	Glu	Arg	Glu	Lys	Val	Leu
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Ile	Leu	Gly	Ser	Gly	Pro	Asn	Arg	Ile	Gly	Gln	Gly	Ile	Glu	Phe	Asp
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Tyr	Ser	Cys	Val	His	Ala	Ala	Leu	Glu	Leu	Ser	Arg	Val	Gly	Tyr	Glu
545					550					555					560
Thr	Val	Met	Val	Asn	Cys	Asn	Pro	Glu	Thr	Val	Ser	Thr	Asp	Tyr	Asp
				565					570					575	
Thr	Ala	Asp	Arg	Leu	Tyr	Phe	Glu	Pro	Leu	Thr	Phe	Glu	Asp	Val	Met
			580					585						590	
Glu	Val	Tyr	His	Ala	Glu	Ala	Gln	Ser	Gly	Thr	Val	Ala	Gly	Val	Ile
		595					600					605			
Val	Gln	Leu	Gly	Gly	Gln	Thr	Pro	Leu	Gly	Leu	Ala	Asp	Arg	Leu	Lys
	610					615					620				
Lys	Ala	Gly	Val	Pro	Val	Ile	Gly	Thr	Ser	Pro	Glu	Ala	Ile	Asp	Met
625					630					635					640
Ala	Glu	Asp	Arg	Gly	Glu	Phe	Gly	Ala	Leu	Leu	Asn	Arg	Glu	Gln	Leu
				645					650					655	
Pro	Ala	Pro	Ala	Phe	Gly	Thr	Ala	Thr	Ser	Phe	Glu	Glu	Ala	Arg	Thr
			660					665						670	
Val	Ala	Asp	Glu	Ile	Ser	Tyr	Pro	Val	Leu	Val	Arg	Pro	Ser	Tyr	Val
		675					680					685			
Leu	Gly	Gly	Arg	Gly	Met	Glu	Ile	Val	Tyr	Asp	Glu	Ala	Ser	Leu	Glu
	690					695					700				
Asp	Tyr	Ile	Asn	Arg	Ala	Thr	Glu	Leu	Ser	Ser	Asp	His	Pro	Val	Leu
705					710					715					720
Val	Asp	Arg	Phe	Leu	Asp	Asn	Ala	Ile	Glu	Ile	Asp	Val	Asp	Ala	Leu
				725					730					735	
Cys	Asp	Gly	Asp	Glu	Val	Tyr	Leu	Ala	Gly	Val	Met	Glu	His	Ile	Glu
			740					745					750		
Glu	Ala	Gly	Ile	His	Ser	Gly	Asp	Ser	Ala	Cys	Ala	Leu	Pro	Pro	Met
		755					760					765			

Thr Leu Gly Ala Gln Asp Ile Glu Lys Val Arg Glu Ala Thr Lys Lys  
 770 775 780  
 Leu Ala Leu Gly Ile Gly Val Gln Gly Leu Met Asn Val Gln Tyr Ala  
 785 790 795 800  
 Leu Lys Asp Asp Ile Leu Tyr Val Ile Glu Ala Asn Pro Arg Ala Ser  
 805 810 815  
 Arg Thr Val Pro Phe Val Ser Lys Ala Thr Gly Val Asn Leu Ala Lys  
 820 825 830  
 Ala Ala Ser Arg Ile Ala Val Gly Ala Thr Ile Lys Asp Leu Gln Asp  
 835 840 845  
 Glu Gly Met Ile Pro Thr Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp  
 850 855 860  
 Ala Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Asn Arg Phe Arg  
 865 870 875 880  
 Arg Pro Asp Gly Lys Thr Leu Asp Thr Leu Leu Ser Pro Glu Met Lys  
 885 890 895  
 Ser Thr Gly Glu Val Met Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr  
 900 905 910  
 Ala Lys Ala Glu Ala Gly Ala Phe Gly Ala Leu Pro Thr Glu Gly Thr  
 915 920 925  
 Val Phe Val Thr Val Ala Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro  
 930 935 940  
 Ile Gln Arg Leu Ala Leu Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly  
 945 950 955 960  
 Thr Ala Gly Met Leu Arg Arg Asn Gly Ile Glu Cys Glu Val Val Leu  
 965 970 975  
 Lys Ala Ser Asp Ile Arg Glu Gly Val Glu Gly Lys Ser Ile Val Asp  
 980 985 990  
 Arg Ile Arg Glu Gly Glu Val Asp Leu Ile Leu Asn Thr Pro Ala Gly  
 995 1000 1005  
 Ser Ala Gly Ala Arg His Asp Gly Tyr Asp Ile Arg Ala Ala Ala Val  
 1010 1015 1020  
 Thr Val Gly Val Pro Leu Ile Thr Thr Val Gln Gly Val Thr Ala Ala  
 1025 1030 1035 1040  
 Val Gln Gly Ile Glu Ala Leu Arg Glu Gly Val Val Ser Val Arg Ala  
 1045 1050 1055  
 Leu Gln Glu Leu Asp His Ala Val Lys Ala  
 1060 1065

&lt;210&gt; 371

&lt;211&gt; 1389

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1366)

&lt;223&gt; RXS02565

&lt;400&gt; 371

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ggaaattcga tacagtgcga tgacgcgata ttagaaagaa aaagatgcgc tttacgacga 60
aaccctcacc ctcttcagg aacttatccg caacgcctgc gtg aat gat cta acc 115
                               Val Asn Asp Leu Thr
                               1 5
cca gat tca ggt cag gaa att aga aac gcg gaa agc cta gaa cgt ttc 163
Pro Asp Ser Gly Gln Glu Ile Arg Asn Ala Glu Ser Leu Glu Arg Phe
                               10 15 20
ttt gaa gga acc ccc aac gtt aaa atc acc aag ctg gaa ccg cat ccg 211
Phe Glu Gly Thr Pro Asn Val Lys Ile Thr Lys Leu Glu Pro His Pro
                               25 30 35
ggc cgg acc tca att atc gtg act gtt cca ggc agc gat cca gat gct 259
Gly Arg Thr Ser Ile Ile Val Thr Val Pro Gly Ser Asp Pro Asp Ala
                               40 45 50
gag cct tta aca ctg ctt gga cat act gat gtt gtg cct gtt gat ctg 307
Glu Pro Leu Thr Leu Leu Gly His Thr Asp Val Val Pro Val Asp Leu
                               55 60 65
cct aaa tgg act aaa gat cca ttc ggt gcg gag att tcg gat gga cag 355
Pro Lys Trp Thr Lys Asp Pro Phe Gly Ala Glu Ile Ser Asp Gly Gln
                               70 75 80 85
att tgg ggt aga ggg tcc gtc gat atg ctc ttt att acc gca acc caa 403
Ile Trp Gly Arg Gly Ser Val Asp Met Leu Phe Ile Thr Ala Thr Gln
                               90 95 100
gcg gcc gtc acc cgt caa gta gcc cgt gaa ggc ggc ctg cgt ggc acg 451
Ala Ala Val Thr Arg Gln Val Ala Arg Glu Gly Gly Leu Arg Gly Thr
                               105 110 115
ctg aca ttc gtt ggc gtt gct gat gag gaa gcc cgc ggc gga ctc gga 499
Leu Thr Phe Val Gly Val Ala Asp Glu Glu Ala Arg Gly Gly Leu Gly
                               120 125 130
gcg aag tgg ctt tcc gaa gaa cac caa aac ctc ttc agc tgg aaa aac 547
Ala Lys Trp Leu Ser Glu Glu His Gln Asn Leu Phe Ser Trp Lys Asn
                               135 140 145
tgc ctc tcc gaa tcc ggt gga tcg cac ctt cca gtc cac gac ggc agc 595
Cys Leu Ser Glu Ser Gly Gly Ser His Leu Pro Val His Asp Gly Ser
                               150 155 160 165
gac gca gta gta att aac gtt gga gaa aaa ggt gca gct caa cgt cgt 643
Asp Ala Val Val Ile Asn Val Gly Glu Lys Gly Ala Ala Gln Arg Arg
                               170 175 180
att cac gtc aat ggc gat gct ggt cat ggt tcc att cct ttc gac cgt 691
Ile His Val Asn Gly Asp Ala Gly His Gly Ser Ile Pro Phe Asp Arg

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				185				190				195							
gac	agc	gct	att	gtc	aag	atc	ggt	gaa	gtc	gcc	cgc	cga	atc	gct	gcc	739			
Asp	Ser	Ala	Ile	Val	Lys	Ile	Gly	Glu	Val	Ala	Arg	Arg	Ile	Ala	Ala				
		200				205				210									
gcc	gat	ctg	aag	gta	gcc	aag	gac	gat	atc	tgg	caa	ggc	ttc	gtc	caa	787			
Ala	Asp	Leu	Lys	Val	Ala	Lys	Asp	Asp	Ile	Trp	Gln	Gly	Phe	Val	Gln				
		215				220				225									
gcg	cac	cgt	ttc	gac	cca	gaa	acg	gag	cag	gcg	ctt	ctt	agc	ggg	acc	835			
Ala	His	Arg	Phe	Asp	Pro	Glu	Thr	Glu	Gln	Ala	Leu	Leu	Ser	Gly	Thr				
				235				240						245					
tcc	cct	gag	gcc	tac	gca	gag	ttc	ggc	gga	ctc	tcc	cgc	ttc	gcc	cac	883			
Ser	Pro	Glu	Ala	Tyr	Ala	Glu	Phe	Gly	Gly	Leu	Ser	Arg	Phe	Ala	His				
				250				255						260					
gcg	gtg	tct	cat	ctc	acg	atc	gcc	caa	act	gtg	gtt	cgt	gca	ggg	caa	931			
Ala	Val	Ser	His	Leu	Thr	Ile	Ala	Gln	Thr	Val	Val	Arg	Ala	Gly	Gln				
		265				270				275									
gcc	atc	aat	gta	ttg	cca	tcg	cat	gcg	tac	ttg	gaa	ctg	gat	atc	cgt	979			
Ala	Ile	Asn	Val	Leu	Pro	Ser	His	Ala	Tyr	Leu	Glu	Leu	Asp	Ile	Arg				
		280				285				290									
acc	ctt	cca	ggc	caa	acc	aat	gac	tat	gtt	gat	gac	acc	ctg	cgt	gct	1027			
Thr	Leu	Pro	Gly	Gln	Thr	Asn	Asp	Tyr	Val	Asp	Asp	Thr	Leu	Arg	Ala				
		295				300				305									
gct	ctg	ggc	gat	ctt	gcc	gat	gaa	gta	gaa	atc	gaa	cac	ctc	atc	tct	1075			
Ala	Leu	Gly	Asp	Leu	Ala	Asp	Glu	Val	Glu	Ile	Glu	His	Leu	Ile	Ser				
		310		315				320						325					
gaa	gaa	gca	acg	gtg	agc	cca	act	gat	tcc	agg	ttg	tat	aac	acc	ttg	1123			
Glu	Glu	Ala	Thr	Val	Ser	Pro	Thr	Asp	Ser	Arg	Leu	Tyr	Asn	Thr	Leu				
				330				335						340					
gaa	aaa	gtt	ctt	ggg	gat	ttc	ttc	ccc	gat	gcg	cct	gtg	gtc	cca	att	1171			
Glu	Lys	Val	Leu	Gly	Asp	Phe	Phe	Pro	Asp	Ala	Pro	Val	Val	Pro	Ile				
		345				350				355									
att	tcc	tct	ggg	ggc	tct	gac	ctg	cgc	ttt	ggg	cgt	cga	cta	ggc	ggg	1219			
Ile	Ser	Ser	Gly	Gly	Ser	Asp	Leu	Arg	Phe	Gly	Arg	Arg	Leu	Gly	Gly				
		360				365				370									
gtt	ggg	tat	ggg	ttt	gca	gtt	cat	gca	cgt	gaa	cga	act	ttg	gcg	gaa	1267			
Val	Gly	Tyr	Gly	Phe	Ala	Val	His	Ala	Arg	Glu	Arg	Thr	Leu	Ala	Glu				
		375				380				385									
gca	atg	ggg	caa	ctt	cac	tcc	cat	gac	gag	gcg	ctg	tac	ctg	gaa	gat	1315			
Ala	Met	Gly	Gln	Leu															

&lt;210&gt; 372

&lt;211&gt; 422

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 372

Val Asn Asp Leu Thr Pro Asp Ser Gly Gln Glu Ile Arg Asn Ala Glu  
 1 5 10 15

Ser Leu Glu Arg Phe Phe Glu Gly Thr Pro Asn Val Lys Ile Thr Lys  
 20 25 30

Leu Glu Pro His Pro Gly Arg Thr Ser Ile Ile Val Thr Val Pro Gly  
 35 40 45

Ser Asp Pro Asp Ala Glu Pro Leu Thr Leu Leu Gly His Thr Asp Val  
 50 55 60

Val Pro Val Asp Leu Pro Lys Trp Thr Lys Asp Pro Phe Gly Ala Glu  
 65 70 75 80

Ile Ser Asp Gly Gln Ile Trp Gly Arg Gly Ser Val Asp Met Leu Phe  
 85 90 95

Ile Thr Ala Thr Gln Ala Ala Val Thr Arg Gln Val Ala Arg Glu Gly  
 100 105 110

Gly Leu Arg Gly Thr Leu Thr Phe Val Gly Val Ala Asp Glu Glu Ala  
 115 120 125

Arg Gly Gly Leu Gly Ala Lys Trp Leu Ser Glu Glu His Gln Asn Leu  
 130 135 140

Phe Ser Trp Lys Asn Cys Leu Ser Glu Ser Gly Gly Ser His Leu Pro  
 145 150 155 160

Val His Asp Gly Ser Asp Ala Val Val Ile Asn Val Gly Glu Lys Gly  
 165 170 175

Ala Ala Gln Arg Arg Ile His Val Asn Gly Asp Ala Gly His Gly Ser  
 180 185 190

Ile Pro Phe Asp Arg Asp Ser Ala Ile Val Lys Ile Gly Glu Val Ala  
 195 200 205

Arg Arg Ile Ala Ala Ala Asp Leu Lys Val Ala Lys Asp Asp Ile Trp  
 210 215 220

Gln Gly Phe Val Gln Ala His Arg Phe Asp Pro Glu Thr Glu Gln Ala  
 225 230 235 240

Leu Leu Ser Gly Thr Ser Pro Glu Ala Tyr Ala Glu Phe Gly Gly Leu  
 245 250 255

Ser Arg Phe Ala His Ala Val Ser His Leu Thr Ile Ala Gln Thr Val  
 260 265 270

Val Arg Ala Gly Gln Ala Ile Asn Val Leu Pro Ser His Ala Tyr Leu  
 275 280 285



Glu Leu Asp Ile Arg Thr Leu Pro Gly Gln Thr Asn Asp Tyr Val Asp  
 290 295 300  
 Asp Thr Leu Arg Ala Ala Leu Gly Asp Leu Ala Asp Glu Val Glu Ile  
 305 310 315 320  
 Glu His Leu Ile Ser Glu Glu Ala Thr Val Ser Pro Thr Asp Ser Arg  
 325 330 335  
 Leu Tyr Asn Thr Leu Glu Lys Val Leu Gly Asp Phe Phe Pro Asp Ala  
 340 345 350  
 Pro Val Val Pro Ile Ile Ser Ser Gly Gly Ser Asp Leu Arg Phe Gly  
 355 360 365  
 Arg Arg Leu Gly Gly Val Gly Tyr Gly Phe Ala Val His Ala Arg Glu  
 370 375 380  
 Arg Thr Leu Ala Glu Ala Met Gly Gln Leu His Ser His Asp Glu Ala  
 385 390 395 400  
 Leu Tyr Leu Glu Asp Leu Glu Leu Thr Val Arg Gly Tyr Asp Ser Val  
 405 410 415  
 Val Arg Glu Phe Leu Gly  
 420

&lt;210&gt; 373

&lt;211&gt; 525

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(502)

&lt;223&gt; RXS02937

&lt;400&gt; 373

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tcgaaacatc caacgcattg gtgacaccgg tgttgctcgcg gtg atc agc aat ggg 115  
 Val Ile Ser Asn Gly  
 1 5

gaa ggt ccg gtt gtt gcg ctt cgt ggc gac att gat gcg ttg ccc atg 163  
 Glu Gly Pro Val Val Ala Leu Arg Gly Asp Ile Asp Ala Leu Pro Met  
 10 15 20

gcg gag cga tcc ggc aaa gaa tac gca gca acc gga gtg aca cag gtg 211  
 Ala Glu Arg Ser Gly Lys Glu Tyr Ala Ala Thr Gly Val Thr Gln Val  
 25 30 35

gat aac acc acc ggt caa gaa act ccg gtg gcg cat acc tgt ggc cac 259  
 Asp Asn Thr Thr Gly Gln Glu Thr Pro Val Ala His Thr Cys Gly His  
 40 45 50

gat gtg cat att tca tca ctg ttg ggt gcg gtg cag gcg ttc aat tct 307  
 Asp Val His Ile Ser Ser Leu Leu Gly Ala Val Gln Ala Phe Asn Ser  
 55 60 65

cat cgg gaa ttg tgg aac gga acg ttg atg gcc gtt ttc cag cca gcg 355  
 His Arg Glu Leu Trp Asn Gly Thr Leu Met Ala Val Phe Gln Pro Ala  
 70 75 80 85

gaa gag acg gca gct ggt gcg agg atg atg gcg gat cag gac aac gcg 403  
 Glu Glu Thr Ala Ala Gly Ala Arg Met Met Ala Asp Gln Asp Asn Ala  
 90 95 100

ccg gga aat cac tct cca gcg ttc gcg cca gat atg cag cca act ctt 451  
 Pro Gly Asn His Ser Pro Ala Phe Ala Pro Asp Met Gln Pro Thr Leu  
 105 110 115

gat cgt ggt gtg gaa gcg ctg gtt gta gct gct tct gcg tgg cta gta 499  
 Asp Arg Gly Val Glu Ala Leu Val Val Ala Ala Ser Ala Trp Leu Val  
 120 125 130

aaa taattggcta atgaatcctt ttc 525  
 Lys

<210> 374  
 <211> 134  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 374  
 Val Ile Ser Asn Gly Glu Gly Pro Val Val Ala Leu Arg Gly Asp Ile  
 1 5 10 15

Asp Ala Leu Pro Met Ala Glu Arg Ser Gly Lys Glu Tyr Ala Ala Thr  
 20 25 30

Gly Val Thr Gln Val Asp Asn Thr Thr Gly Gln Glu Thr Pro Val Ala  
 35 40 45

His Thr Cys Gly His Asp Val His Ile Ser Ser Leu Leu Gly Ala Val  
 50 55 60

Gln Ala Phe Asn Ser His Arg Glu Leu Trp Asn Gly Thr Leu Met Ala  
 65 70 75 80

Val Phe Gln Pro Ala Glu Glu Thr Ala Ala Gly Ala Arg Met Met Ala  
 85 90 95

Asp Gln Asp Asn Ala Pro Gly Asn His Ser Pro Ala Phe Ala Pro Asp  
 100 105 110

Met Gln Pro Thr Leu Asp Arg Gly Val Glu Ala Leu Val Val Ala Ala  
 115 120 125

Ser Ala Trp Leu Val Lys  
 130

<210> 375  
 <211> 966  
 <212> DNA  
 <213> Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(943)

&lt;223&gt; RXA02194

&lt;400&gt; 375

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gaaatctccc agctcattta ttggacccag gtcatcatgg ttgctcgcg cctgaagcca 60

gaagatatct acaagaacct gtaggagttt taaagcaatc atg ttg aaa atc gct 115
                Met Leu Lys Ile Ala
                1 5

gtc cca aac aaa ggc tcg ctg tcc gag cgc gcc atg gaa atc ctc gcc 163
Val Pro Asn Lys Gly Ser Leu Ser Glu Arg Ala Met Glu Ile Leu Ala
                10 15 20

gaa gca ggc tac gca ggc cgt gga gat tcc aaa tcc ctc aac gtt ttt 211
Glu Ala Gly Tyr Ala Gly Arg Gly Asp Ser Lys Ser Leu Asn Val Phe
                25 30 35

gat gaa gca aac aac gtt gaa ttc ttc ttc ctt cgc cct aaa gat atc 259
Asp Glu Ala Asn Asn Val Glu Phe Phe Phe Leu Arg Pro Lys Asp Ile
                40 45 50

gcc atc tac gtt gct ggt ggc cag ctc gat ttg ggt atc acc ggc cgc 307
Ala Ile Tyr Val Ala Gly Gln Leu Asp Leu Gly Ile Thr Gly Arg
                55 60 65

gac ctt gct cgc gat tcc cag gct gat gtc cac gaa gtt ctt tcc ctc 355
Asp Leu Ala Arg Asp Ser Gln Ala Asp Val His Glu Val Leu Ser Leu
                70 75 80 85

ggc ttc ggt tcc tcc act ttc cgt tac gca gca cca gct gat gaa gag 403
Gly Phe Gly Ser Ser Thr Phe Arg Tyr Ala Ala Pro Ala Asp Glu Glu
                90 95 100

tgg agc atc gaa aag ctc gac ggc aag cgc atc gct acc tct tac ccc 451
Trp Ser Ile Glu Lys Leu Asp Gly Lys Arg Ile Ala Thr Ser Tyr Pro
                105 110 115

aac ctt gtt cgc gat gac ctc gca gca cgt ggg ctt tcc gct gag gtg 499
Asn Leu Val Arg Asp Asp Leu Ala Ala Arg Gly Leu Ser Ala Glu Val
                120 125 130

ctc cgc ctc gac ggt gca gta gag gta tcc atc aag ctt ggt gtc gca 547
Leu Arg Leu Asp Gly Ala Val Glu Val Ser Ile Lys Leu Gly Val Ala
                135 140 145

gat gcc atc gcc gat gtt gta tcc acc ggc cgc acg ctg cgt cag caa 595
Asp Ala Ile Ala Asp Val Val Ser Thr Gly Arg Thr Leu Arg Gln Gln
                150 155 160 165

ggt ctt gca cct ttc ggc gag gtt ctg tgc acc tct gag gct gtc att 643
Gly Leu Ala Pro Phe Gly Glu Val Leu Cys Thr Ser Glu Ala Val Ile
                170 175 180

gtt ggc cgc aag gat gaa aag gtc acc cca gag cag cag atc ctg ctt 691
Val Gly Arg Lys Asp Glu Lys Val Thr Pro Glu Gln Gln Ile Leu Leu
                185 190 195

cgc cgc atc cag gga att ttg cac gcg cag aac ttc ctc atg ctg gat 739

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Arg Arg Ile Gln Gly Ile Leu His Ala Gln Asn Phe Leu Met Leu Asp  
 200 205 210

tac aac gtc gac cgc gac aac ctg gac gct gcc act gca gta acc cca 787  
 Tyr Asn Val Asp Arg Asp Asn Leu Asp Ala Ala Thr Ala Val Thr Pro  
 215 220 225

ggc tta tcc ggc cca acg gta tcc cca ctg gca cgc gac aac tgg gtt 835  
 Gly Leu Ser Gly Pro Thr Val Ser Pro Leu Ala Arg Asp Asn Trp Val  
 230 235 240 245

gct gta cgc gcc atg gtg cca cgc agg tca gct aac gcc atc atg gat 883  
 Ala Val Arg Ala Met Val Pro Arg Arg Ser Ala Asn Ala Ile Met Asp  
 250 255 260

aag ctt gct gga ctc ggc gct gaa gcc atc ctg gct tct gaa atc cgc 931  
 Lys Leu Ala Gly Leu Gly Ala Glu Ala Ile Leu Ala Ser Glu Ile Arg  
 265 270 275

atc gcc cgc atc tagttttaac taccctcgaa aat 966  
 Ile Ala Arg Ile  
 280

&lt;210&gt; 376

&lt;211&gt; 281

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 376

Met Leu Lys Ile Ala Val Pro Asn Lys Gly Ser Leu Ser Glu Arg Ala  
 1 5 10 15

Met Glu Ile Leu Ala Glu Ala Gly Tyr Ala Gly Arg Gly Asp Ser Lys  
 20 25 30

Ser Leu Asn Val Phe Asp Glu Ala Asn Asn Val Glu Phe Phe Phe Leu  
 35 40 45

Arg Pro Lys Asp Ile Ala Ile Tyr Val Ala Gly Gly Gln Leu Asp Leu  
 50 55 60

Gly Ile Thr Gly Arg Asp Leu Ala Arg Asp Ser Gln Ala Asp Val His  
 65 70 75 80

Glu Val Leu Ser Leu Gly Phe Gly Ser Ser Thr Phe Arg Tyr Ala Ala  
 85 90 95

Pro Ala Asp Glu Glu Trp Ser Ile Glu Lys Leu Asp Gly Lys Arg Ile  
 100 105 110

Ala Thr Ser Tyr Pro Asn Leu Val Arg Asp Asp Leu Ala Ala Arg Gly  
 115 120 125

Leu Ser Ala Glu Val Leu Arg Leu Asp Gly Ala Val Glu Val Ser Ile  
 130 135 140

Lys Leu Gly Val Ala Asp Ala Ile Ala Asp Val Val Ser Thr Gly Arg  
 145 150 155 160

Thr Leu Arg Gln Gln Gly Leu Ala Pro Phe Gly Glu Val Leu Cys Thr

165										170					175				
Ser	Glu	Ala	Val	Ile	Val	Gly	Arg	Lys	Asp	Glu	Lys	Val	Thr	Pro	Glu				
			180					185							190				
Gln	Gln	Ile	Leu	Leu	Arg	Arg	Ile	Gln	Gly	Ile	Leu	His	Ala	Gln	Asn				
		195					200					205							
Phe	Leu	Met	Leu	Asp	Tyr	Asn	Val	Asp	Arg	Asp	Asn	Leu	Asp	Ala	Ala				
	210					215					220								
Thr	Ala	Val	Thr	Pro	Gly	Leu	Ser	Gly	Pro	Thr	Val	Ser	Pro	Leu	Ala				
225					230					235					240				
Arg	Asp	Asn	Trp	Val	Ala	Val	Arg	Ala	Met	Val	Pro	Arg	Arg	Ser	Ala				
			245						250					255					
Asn	Ala	Ile	Met	Asp	Lys	Leu	Ala	Gly	Leu	Gly	Ala	Glu	Ala	Ile	Leu				
		260						265						270					
Ala	Ser	Glu	Ile	Arg	Ile	Ala	Arg	Ile											
		275					280												

&lt;210&gt; 377

&lt;211&gt; 393

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(370)

&lt;223&gt; RXA02195

&lt;400&gt; 377

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tcctccccc	aacacacatt	gataactgtt		gtgtggaaga		atg	tac	cga	gtg	aag	115
						Met	Tyr	Arg	Val	Lys	
						1				5	

aca	ttt	gac	tcg	ctg	tac	gaa	gaa	ctt	ctt	aac	cgt	gct	cag	acc	cgc	163
Thr	Phe	Asp	Ser	Leu	Tyr	Glu	Glu	Leu	Leu	Asn	Arg	Ala	Gln	Thr	Arg	
				10					15					20		

cct	gaa	ggg	tct	gga	acc	gtg	gcc	gcc	ttg	gat	aaa	ggc	atc	cat	cat	211
Pro	Glu	Gly	Ser	Gly	Thr	Val	Ala	Ala	Leu	Asp	Lys	Gly	Ile	His	His	
			25					30					35			

cta	ggt	aag	aag	gtc	atc	gaa	gaa	gcc	gga	gag	gtc	tgg	att	gca	gcc	259
Leu	Gly	Lys	Lys	Val	Ile	Glu	Glu	Ala	Gly	Glu	Val	Trp	Ile	Ala	Ala	
		40						45				50				

gag	tat	gag	acc	gat	gaa	gag	cta	gcc	gga	gaa	atc	tcc	cag	ctc	att	307
Glu	Tyr	Glu	Thr	Asp	Glu	Glu	Leu	Ala	Gly	Glu	Ile	Ser	Gln	Leu	Ile	
	55					60					65					

tat	tgg	acc	cag	gtc	atc	atg	gtt	gct	cgc	ggc	ctg	aag	cca	gaa	gat	355
Tyr	Trp	Thr	Gln	Val	Ile	Met	Val	Ala	Arg	Gly	Leu	Lys	Pro	Glu	Asp	
	70				75					80					85	

atc tac aag aac ctg taggagtttt aaagcaatca tgt  
 Ile Tyr Lys Asn Leu  
 90

393

<210> 378  
 <211> 90  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 378  
 Met Tyr Arg Val Lys Thr Phe Asp Ser Leu Tyr Glu Glu Leu Leu Asn  
 1 5 10 15  
 Arg Ala Gln Thr Arg Pro Glu Gly Ser Gly Thr Val Ala Ala Leu Asp  
 20 25 30  
 Lys Gly Ile His His Leu Gly Lys Lys Val Ile Glu Glu Ala Gly Glu  
 35 40 45  
 Val Trp Ile Ala Ala Glu Tyr Glu Thr Asp Glu Glu Leu Ala Gly Glu  
 50 55 60  
 Ile Ser Gln Leu Ile Tyr Trp Thr Gln Val Ile Met Val Ala Arg Gly  
 65 70 75 80  
 Leu Lys Pro Glu Asp Ile Tyr Lys Asn Leu  
 85 90

<210> 379  
 <211> 477  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(454)  
 <223> RXA01097

<400> 379  
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 Met Ser Asp Asn Pro  
 1 5  
 caa gag tat gag ctg gat tgg gac gtc gaa aag cga tta aag ctt aac 163  
 Gln Glu Tyr Glu Leu Asp Trp Asp Val Glu Lys Arg Leu Lys Leu Asn  
 10 15 20  
 gac gcc ggc ctg gtg ccg gca atc gtc cag gcc gac ggg acc aac gag 211  
 Asp Ala Gly Leu Val Pro Ala Ile Val Gln Ala Asp Gly Thr Asn Glu  
 25 30 35  
 gtc ctc atg atg gcc tgg atg gat acc cac gcg cta gcc tat act ttg 259  
 Val Leu Met Met Ala Trp Met Asp Thr His Ala Leu Ala Tyr Thr Leu  
 40 45 50  
 gcg acc cgc cgt gga acc tat ttt tct agg tcc cgc aac gag tac tgg 307  
 Ala Thr Arg Arg Gly Thr Tyr Phe Ser Arg Ser Arg Asn Glu Tyr Trp

55	60	65	
atc aag ggc ctg acc tct gga aac gtc caa gaa gtc acc gga ctt gcc			355
Ile Lys Gly Leu Thr Ser Gly Asn Val Gln Glu Val Thr Gly Leu Ala			
70	75	80	85
ctc gac tgc gac ggc gac acc gtc ctt ctg acc gtg aaa caa acc ggc			403
Leu Asp Cys Asp Gly Asp Thr Val Leu Leu Thr Val Lys Gln Thr Gly			
	90	95	100
ggt gcg tgc cac act ggt gcc cac aca tgt ttc gac aat gac gtt ttg			451
Gly Ala Cys His Thr Gly Ala His Thr Cys Phe Asp Asn Asp Val Leu			
	105	110	115
ctg taaaagcaac aacgattaag gaa			477
Leu			

<210> 380  
 <211> 118  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 380  
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 Arg Leu Lys Leu Asn Asp Ala Gly Leu Val Pro Ala Ile Val Gln Ala  
 20 25 30  
 Asp Gly Thr Asn Glu Val Leu Met Met Ala Trp Met Asp Thr His Ala  
 35 40 45  
 Leu Ala Tyr Thr Leu Ala Thr Arg Arg Gly Thr Tyr Phe Ser Arg Ser  
 50 55 60  
 Arg Asn Glu Tyr Trp Ile Lys Gly Leu Thr Ser Gly Asn Val Gln Glu  
 65 70 75 80  
 Val Thr Gly Leu Ala Leu Asp Cys Asp Gly Asp Thr Val Leu Leu Thr  
 85 90 95  
 Val Lys Gln Thr Gly Gly Ala Cys His Thr Gly Ala His Thr Cys Phe  
 100 105 110  
 Asp Asn Asp Val Leu Leu  
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<210> 381  
 <211> 861  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(838)  
 <223> RXA01100

<400> 381

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Met Thr Phe Thr Ile															5	
1																
ctt	cct	gca	gtc	gat	gta	gtt	aac	gga	caa	gca	gtt	cgc	cta	gat	cag	163
Leu	Pro	Ala	Val	Asp	Val	Val	Asn	Gly	Gln	Ala	Val	Arg	Leu	Asp	Gln	
10 15 20																
ggc	gag	gcc	ggc	act	gaa	aag	tct	tat	ggc	acc	cct	ttg	gaa	tcc	gca	211
Gly	Glu	Ala	Gly	Thr	Glu	Lys	Ser	Tyr	Gly	Thr	Pro	Leu	Glu	Ser	Ala	
25 30 35																
ctg	aag	tgg	cag	gag	cag	ggg	gca	aag	tgg	ttg	cac	ttt	gtg	gac	ctg	259
Leu	Lys	Trp	Gln	Glu	Gln	Gly	Ala	Lys	Trp	Leu	His	Phe	Val	Asp	Leu	
40 45 50																
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Asp	Ala	Ala	Phe	Asn	Arg	Gly	Ser	Asn	His	Glu	Met	Met	Ala	Glu	Ile	
55 60 65																
gtc	ggc	aag	ctc	gat	gtt	gat	gtg	gag	ctc	act	ggc	ggg	atc	cgt	gat	355
Val	Gly	Lys	Leu	Asp	Val	Asp	Val	Glu	Leu	Thr	Gly	Gly	Ile	Arg	Asp	
70 75 80 85																
gat	gag	tct	ctg	gag	cgc	gcg	ctg	gca	acc	ggg	gca	cgt	cgt	gta	aac	403
Asp	Glu	Ser	Leu	Glu	Arg	Ala	Leu	Ala	Thr	Gly	Ala	Arg	Arg	Val	Asn	
90 95 100																
att	ggg	acc	gct	gct	ctg	gag	aag	cca	gag	tgg	att	gct	tct	gcg	att	451
Ile	Gly	Thr	Ala	Ala	Leu	Glu	Lys	Pro	Glu	Trp	Ile	Ala	Ser	Ala	Ile	
105 110 115																
caa	cgc	tat	ggc	gag	aag	att	gct	gtc	gat	atc	gct	gtg	cgt	ttg	gaa	499
Gln	Arg	Tyr	Gly	Glu	Lys	Ile	Ala	Val	Asp	Ile	Ala	Val	Arg	Leu	Glu	
120 125 130																
gat	ggg	gaa	tgg	cgc	acc	cgt	gga	aac	ggg	tgg	gtc	tcc	gat	ggg	ggc	547
Asp	Gly	Glu	Trp	Arg	Thr	Arg	Gly	Asn	Gly	Trp	Val	Ser	Asp	Gly	Gly	
135 140 145																
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Asp	Leu	Trp	Glu	Val	Leu	Glu	Arg	Leu	Asp	Ser	Gln	Gly	Cys	Ala	Arg	
150 155 160 165																
ttc	gtg	gtt	acc	gat	gtg	tcc	aag	gac	ggc	acc	ttg	agt	ggg	cca	aat	643
Phe	Val	Val	Thr	Asp	Val	Ser	Lys	Asp	Gly	Thr	Leu	Ser	Gly	Pro	Asn	
170 175 180																
gtt	gag	ctg	ctg	cgt	gag	gtt	gct	gca	gct	aca	gac	gca	cct	atc	gtg	691
Val	Glu	Leu	Leu	Arg	Glu	Val	Ala	Ala	Ala	Thr	Asp	Ala	Pro	Ile	Val	
185 190 195																
gca	tct	ggg	gga	att	tct	gtt	ttg	gaa	gat	gtt	ttg	gaa	cta	gcc	aag	739
Ala	Ser	Gly	Gly	Ile	Ser	Val	Leu	Glu	Asp	Val	Leu	Glu	Leu	Ala	Lys	
200 205 210																
tac	cag	gat	gag	ggc	att	gat	tcc	gtc	atc	att	ggc	aag	gca	ctt	tat	787
Tyr	Gln	Asp	Glu	Gly	Ile	Asp	Ser	Val	Ile	Ile	Gly	Lys	Ala	Leu	Tyr	
215 220 225																



gag cac aag ttc acc ctc gaa gag gct ttg gct gca gta gaa aag ctc 835  
 Glu His Lys Phe Thr Leu Glu Glu Ala Leu Ala Ala Val Glu Lys Leu  
 230 235 240 245

ggt taatacatgg atgctcgtgg gat 861  
 Gly

<210> 382

<211> 246

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 382

Met Thr Phe Thr Ile Leu Pro Ala Val Asp Val Val Asn Gly Gln Ala  
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Val Arg Leu Asp Gln Gly Glu Ala Gly Thr Glu Lys Ser Tyr Gly Thr  
 20 25 30

Pro Leu Glu Ser Ala Leu Lys Trp Gln Glu Gln Gly Ala Lys Trp Leu  
 35 40 45

His Phe Val Asp Leu Asp Ala Ala Phe Asn Arg Gly Ser Asn His Glu  
 50 55 60

Met Met Ala Glu Ile Val Gly Lys Leu Asp Val Asp Val Glu Leu Thr  
 65 70 75 80

Gly Gly Ile Arg Asp Asp Glu Ser Leu Glu Arg Ala Leu Ala Thr Gly  
 85 90 95

Ala Arg Arg Val Asn Ile Gly Thr Ala Ala Leu Glu Lys Pro Glu Trp  
 100 105 110

Ile Ala Ser Ala Ile Gln Arg Tyr Gly Glu Lys Ile Ala Val Asp Ile  
 115 120 125

Ala Val Arg Leu Glu Asp Gly Glu Trp Arg Thr Arg Gly Asn Gly Trp  
 130 135 140

Val Ser Asp Gly Gly Asp Leu Trp Glu Val Leu Glu Arg Leu Asp Ser  
 145 150 155 160

Gln Gly Cys Ala Arg Phe Val Val Thr Asp Val Ser Lys Asp Gly Thr  
 165 170 175

Leu Ser Gly Pro Asn Val Glu Leu Leu Arg Glu Val Ala Ala Ala Thr  
 180 185 190

Asp Ala Pro Ile Val Ala Ser Gly Gly Ile Ser Val Leu Glu Asp Val  
 195 200 205

Leu Glu Leu Ala Lys Tyr Gln Asp Glu Gly Ile Asp Ser Val Ile Ile  
 210 215 220

Gly Lys Ala Leu Tyr Glu His Lys Phe Thr Leu Glu Glu Ala Leu Ala  
 225 230 235 240

Ala Val Glu Lys Leu Gly  
245

<210> 383  
<211> 756  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
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<222> (101)..(733)  
<223> RXA01101

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cggttcttga tcctgaaagc acgtgacata aactatcggc atg acc aaa act gtc 115  
Met Thr Lys Thr Val  
1 5  
gcc ctt ctc gac tac gga tct gga aac ctt cgt tct gct caa cgc gca 163  
Ala Leu Leu Asp Tyr Gly Ser Gly Asn Leu Arg Ser Ala Gln Arg Ala  
10 15 20  
cta gag cgt gcc ggt gca gaa gtt atc gtg agc tcc gat cca gaa gtt 211  
Leu Glu Arg Ala Gly Ala Glu Val Ile Val Ser Ser Asp Pro Glu Val  
25 30 35  
tgc acc aac gct gat ggc ctc cta gtt cct gga gtg ggc gca ttt gat 259  
Cys Thr Asn Ala Asp Gly Leu Leu Val Pro Gly Val Gly Ala Phe Asp  
40 45 50  
gcc tgc atg aag ggt ttg aaa aac gtc ttc gga cat cgc att atc gga 307  
Ala Cys Met Lys Gly Leu Lys Asn Val Phe Gly His Arg Ile Ile Gly  
55 60 65  
cag cgt ctt gct ggt gga cgt cca gtg atg ggt att tgt gtg ggc atg 355  
Gln Arg Leu Ala Gly Gly Arg Pro Val Met Gly Ile Cys Val Gly Met  
70 75 80 85  
cag atc ctg ttc gat gaa ggc gat gag cac ggc att aag tca gct ggt 403  
Gln Ile Leu Phe Asp Glu Gly Asp Glu His Gly Ile Lys Ser Ala Gly  
90 95 100  
tgc ggc gag tgg cct ggc aaa gtg gaa cgc ctc caa gcg gag atc ctg 451  
Cys Gly Glu Trp Pro Gly Lys Val Glu Arg Leu Gln Ala Glu Ile Leu  
105 110 115  
cct cac atg ggg tgg aac aca ctt gaa atg cct acc aac tca cca atg 499  
Pro His Met Gly Trp Asn Thr Leu Glu Met Pro Thr Asn Ser Pro Met  
120 125 130  
ttt gag gga att tca cct gat gag cgt ttc tac ttc gtg cac tcc tat 547  
Phe Glu Gly Ile Ser Pro Asp Glu Arg Phe Tyr Phe Val His Ser Tyr  
135 140 145  
ggt gtg cgc aag tgg acg ttg gaa acc gac gat ctg acc acg cct cca 595  
Gly Val Arg Lys Trp Thr Leu Glu Thr Asp Asp Leu Thr Thr Pro Pro  
150 155 160 165

gag gtt gtg tgg gcg aag cac gaa aat gat cgt ttt gtg gca gct gtg 643  
 Glu Val Val Trp Ala Lys His Glu Asn Asp Arg Phe Val Ala Ala Val  
                   170                  175                  180

gaa aac ggc acg ctg tgg gct act caa ttc cac cca gaa aaa tca ggt 691  
 Glu Asn Gly Thr Leu Trp Ala Thr Gln Phe His Pro Glu Lys Ser Gly  
                   185                  190                  195

gac gca ggc gca cag cta ctg cga aac tgg atc aac tac atc 733  
 Asp Ala Gly Ala Gln Leu Leu Arg Asn Trp Ile Asn Tyr Ile  
                   200                  205                  210

taacagatag gatcaatatt cat 756

&lt;210&gt; 384

&lt;211&gt; 211

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 384

Met Thr Lys Thr Val Ala Leu Leu Asp Tyr Gly Ser Gly Asn Leu Arg  
   1                  5                  10                  15

Ser Ala Gln Arg Ala Leu Glu Arg Ala Gly Ala Glu Val Ile Val Ser  
                   20                  25                  30

Ser Asp Pro Glu Val Cys Thr Asn Ala Asp Gly Leu Leu Val Pro Gly  
                   35                  40                  45

Val Gly Ala Phe Asp Ala Cys Met Lys Gly Leu Lys Asn Val Phe Gly  
   50                  55                  60

His Arg Ile Ile Gly Gln Arg Leu Ala Gly Gly Arg Pro Val Met Gly  
   65                  70                  75                  80

Ile Cys Val Gly Met Gln Ile Leu Phe Asp Glu Gly Asp Glu His Gly  
                   85                  90                  95

Ile Lys Ser Ala Gly Cys Gly Glu Trp Pro Gly Lys Val Glu Arg Leu  
                   100                  105                  110

Gln Ala Glu Ile Leu Pro His Met Gly Trp Asn Thr Leu Glu Met Pro  
   115                  120                  125

Thr Asn Ser Pro Met Phe Glu Gly Ile Ser Pro Asp Glu Arg Phe Tyr  
   130                  135                  140

Phe Val His Ser Tyr Gly Val Arg Lys Trp Thr Leu Glu Thr Asp Asp  
   145                  150                  155                  160

Leu Thr Thr Pro Pro Glu Val Val Trp Ala Lys His Glu Asn Asp Arg  
                   165                  170                  175

Phe Val Ala Ala Val Glu Asn Gly Thr Leu Trp Ala Thr Gln Phe His  
                   180                  185                  190

Pro Glu Lys Ser Gly Asp Ala Gly Ala Gln Leu Leu Arg Asn Trp Ile  
                   195                  200                  205

Asn Tyr Ile

210

&lt;210&gt; 385

&lt;211&gt; 723

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(700)

&lt;223&gt; RXN01657

&lt;400&gt; 385

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ccgacgttcc agcaccacac cgactcgccg agcgcgggctg gtg atc gtt gga gtt 115
                                         Val Ile Val Gly Val
                                         1                               5

tta gct ctc cag ggc ggg gtg gaa gaa cac ctc acc gcc ttg gaa gct 163
Leu Ala Leu Gln Gly Gly Val Glu Glu His Leu Thr Ala Leu Glu Ala
                               10                               15                               20

ctc gga gcg acg acc cga aaa gta cgt gtg cca aag gac ctt gat ggt 211
Leu Gly Ala Thr Arg Lys Val Arg Val Pro Lys Asp Leu Asp Gly
                               25                               30                               35

ctc gaa ggc atc gtc atc ccc ggc ggg gaa tcc acc gtg ttg gac aaa 259
Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser Thr Val Leu Asp Lys
                               40                               45                               50

ctg gct cgg aca ttc gac gtg gta gaa cct cta gcg aat ctc att cgc 307
Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu Ala Asn Leu Ile Arg
                               55                               60                               65

gac ggc cta ccc gtt ttc gct acc tgc gct ggc ctg atc tat ctg gcg 355
Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly Leu Ile Tyr Leu Ala
                               70                               75                               80                               85

aaa cac ctc gac aac cca gca agg gga caa caa acc ttg gcg gta gtg 403
Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln Thr Leu Ala Val Val
                               90                               95                               100

gac gtg gtg gtg cgt cga aac gca ttt ggc gcc caa cgc gaa tcc ttc 451
Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala Gln Arg Glu Ser Phe
                               105                               110                               115

gac acc acc gtg gat gtt tcc ttc gac ggt gca aca ttc ccc gga gtg 499
Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala Thr Phe Pro Gly Val
                               120                               125                               130

cag gcc tcg ttt atc cga gct ccc atc gtc act gct ttt ggt cct acg 547
Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr Ala Phe Gly Pro Thr
                               135                               140                               145

gta gaa gcg atc gct gct ctc aac ggt ggg gag gtg gtt ggt gta cgc 595
Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu Val Val Gly Val Arg
                               150                               155                               160                               165

caa ggc aac atc atc gcg ctg tct ttc cat ccc gaa gaa acc ggc gat 643

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<210> 386
<211> 200
<212> PRT
<213> Corynebacterium glutamicum
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<210>	387
<211>	601
<212>	DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(601)

&lt;223&gt; FRXA01657

&lt;400&gt; 387

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ccgacgttcc agcaccacac cgactcgccg agcgcggctg gtg atc gtt gga gtt 115
                               Val Ile Val Gly Val
                               1 5

tta gct ctc cag ggc ggg gtg gaa gaa cac ctc acc gcc ttg gaa gct 163
Leu Ala Leu Gln Gly Gly Val Glu Glu His Leu Thr Ala Leu Glu Ala
                               10 15 20

ctc gga gcg acg acc cga aaa gta cgt gtg cca aag gac ctt gat ggt 211
Leu Gly Ala Thr Thr Arg Lys Val Arg Val Pro Lys Asp Leu Asp Gly
                               25 30 35

ctc gaa ggc atc gtc atc ccc ggc ggg gaa tcc acc gtg ttg gac aaa 259
Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser Thr Val Leu Asp Lys
                               40 45 50

ctg gct cgg aca ttc gac gtg gta gaa cct cta gcg aat ctc att cgc 307
Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu Ala Asn Leu Ile Arg
                               55 60 65

gac ggc cta ccc gtt ttc gct acc tgc gct ggc ctg atc tat ctg gcg 355
Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly Leu Ile Tyr Leu Ala
                               70 75 80 85

aaa cac ctc gac aac cca gca agg gga caa caa acc ttg gcg gta gtg 403
Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln Thr Leu Ala Val Val
                               90 95 100

gac gtg gtg gtg cgt cga aac gca ttt ggc gcc caa cgc gaa tcc ttc 451
Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala Gln Arg Glu Ser Phe
                               105 110 115

gac acc acc gtg gat gtt tcc ttc gac ggt gca aca ttc ccc gga gtg 499
Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala Thr Phe Pro Gly Val
                               120 125 130

cag gcc tcg ttt atc cga gct ccc atc gtc act gct ttt ggt cct acg 547
Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr Ala Phe Gly Pro Thr
                               135 140 145

gta gaa gcg atc gct gct ctc aac ggt ggg gag gtg gtt ggt gta cgc 595
Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu Val Val Gly Val Arg
                               150 155 160 165

caa ggc
Gln Gly 601

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&lt;210&gt; 388

&lt;211&gt; 167

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 388

Val Ile Val Gly Val Leu Ala Leu Gln Gly Gly Val Glu Glu His Leu  
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Thr Ala Leu Glu Ala Leu Gly Ala Thr Thr Arg Lys Val Arg Val Pro  
 20 25 30

Lys Asp Leu Asp Gly Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser  
 35 40 45

Thr Val Leu Asp Lys Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu  
 50 55 60

Ala Asn Leu Ile Arg Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly  
 65 70 75 80

Leu Ile Tyr Leu Ala Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln  
 85 90 95

Thr Leu Ala Val Val Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala  
 100 105 110

Gln Arg Glu Ser Phe Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala  
 115 120 125

Thr Phe Pro Gly Val Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr  
 130 135 140

Ala Phe Gly Pro Thr Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu  
 145 150 155 160

Val Val Gly Val Arg Gln Gly  
 165

&lt;210&gt; 389

&lt;211&gt; 897

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(874)

&lt;223&gt; RXA01098

&lt;400&gt; 389

aaaagggtc acgatgtgct gttaagtaag attgaaaaag ttcggttgat gcatgcagat 60

gcaggtaatg accagtcgtt aaatgaggag tacaagtaaa atg ggc gtg gca att 115  
 Met Gly Val Ala Ile 5

cga gtt att cct tgc ctg gac gtg gac aac ggc cgg gtt gtt aaa ggc 163  
 Arg Val Ile Pro Cys Leu Asp Val Asp Asn Gly Arg Val Val Lys Gly 20

gtg aac ttt gaa aac ctc cgc gat gct ggc gat cct gtg gag ttg gca 211  
 Val Asn Phe Glu Asn Leu Arg Asp Ala Gly Asp Pro Val Glu Leu Ala

25	30	35	
aag cgc tat gac gag gaa ggg gca gat gag ctg acc ttc ctg gat gtc Lys Arg Tyr Asp Glu Glu Gly Ala Asp Glu Leu Thr Phe Leu Asp Val 40 45 50			259
acc gcc tcg aag cat ggt cgc ggc acc atg ctg gat gtt gtt cga cgc Thr Ala Ser Lys His Gly Arg Gly Thr Met Leu Asp Val Val Arg Arg 55 60 65			307
acc gct gat cag gtg ttc atc cct ctg act gtc ggt ggc ggc gtg cgc Thr Ala Asp Gln Val Phe Ile Pro Leu Thr Val Gly Gly Gly Val Arg 70 75 80 85			355
agc gaa gaa gat gtt gat caa ttg ctg cgc gct ggc gcc gac aag gtt Ser Glu Glu Asp Val Asp Gln Leu Leu Arg Ala Gly Ala Asp Lys Val 90 95 100			403
tcg gtg aac acg tct gcg att gcc cgt cca gaa ctg ctg tca gag ctg Ser Val Asn Thr Ser Ala Ile Ala Arg Pro Glu Leu Leu Ser Glu Leu 105 110 115			451
tcc aag cgt ttt ggt gct cag tgc atc gtg ttg tct gtg gat gcc agg Ser Lys Arg Phe Gly Ala Gln Cys Ile Val Leu Ser Val Asp Ala Arg 120 125 130			499
cgc gtt cct gaa ggt gga act cct cag cca tct ggt ttt gaa gtc acc Arg Val Pro Glu Gly Gly Thr Pro Gln Pro Ser Gly Phe Glu Val Thr 135 140 145			547
acc cac ggc ggt tcc aag tcc gca gaa ctt gat gca atc gag tgg gca Thr His Gly Gly Ser Lys Ser Ala Glu Leu Asp Ala Ile Glu Trp Ala 150 155 160 165			595
aag cgc ggc gaa gag ctg ggc gtt ggc gaa att ctg ctc aac tcc atg Lys Arg Gly Glu Glu Leu Gly Val Gly Glu Ile Leu Leu Asn Ser Met 170 175 180			643
gac ggc gac ggc acc aaa aac ggc ttt gac cta gag ctg ctg gaa aaa Asp Gly Asp Gly Thr Lys Asn Gly Phe Asp Leu Glu Leu Leu Glu Lys 185 190 195			691
gtt cgc gca gcc gta tcc att cct gta atc gcc tcc ggc ggc gct ggc Val Arg Ala Ala Val Ser Ile Pro Val Ile Ala Ser Gly Gly Ala Gly 200 205 210			739
aag gcg gag cat ttc cca cca gct gtt gca gct ggc gcc aac gca gtg Lys Ala Glu His Phe Pro Pro Ala Val Ala Ala Gly Ala Asn Ala Val 215 220 225			787
ctt gcc gcg acc att ttc cac ttc cgc gaa gta acc atc gcc gaa gta Leu Ala Ala Thr Ile Phe His Phe Arg Glu Val Thr Ile Ala Glu Val 230 235 240 245			835
aag gga gcc att aaa gat gca gga ttt gag gtg cgg aaa tgagtgacaa Lys Gly Ala Ile Lys Asp Ala Gly Phe Glu Val Arg Lys 250 255			884
tccacaagag tat			897



&lt;210&gt; 390

&lt;211&gt; 258

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 390

Met Gly Val Ala Ile Arg Val Ile Pro Cys Leu Asp Val Asp Asn Gly  
 1 5 10 15

Arg Val Val Lys Gly Val Asn Phe Glu Asn Leu Arg Asp Ala Gly Asp  
 20 25 30

Pro Val Glu Leu Ala Lys Arg Tyr Asp Glu Glu Gly Ala Asp Glu Leu  
 35 40 45

Thr Phe Leu Asp Val Thr Ala Ser Lys His Gly Arg Gly Thr Met Leu  
 50 55 60

Asp Val Val Arg Arg Thr Ala Asp Gln Val Phe Ile Pro Leu Thr Val  
 65 70 75 80

Gly Gly Gly Val Arg Ser Glu Glu Asp Val Asp Gln Leu Leu Arg Ala  
 85 90 95

Gly Ala Asp Lys Val Ser Val Asn Thr Ser Ala Ile Ala Arg Pro Glu  
 100 105 110

Leu Leu Ser Glu Leu Ser Lys Arg Phe Gly Ala Gln Cys Ile Val Leu  
 115 120 125

Ser Val Asp Ala Arg Arg Val Pro Glu Gly Gly Thr Pro Gln Pro Ser  
 130 135 140

Gly Phe Glu Val Thr Thr His Gly Gly Ser Lys Ser Ala Glu Leu Asp  
 145 150 155 160

Ala Ile Glu Trp Ala Lys Arg Gly Glu Glu Leu Gly Val Gly Glu Ile  
 165 170 175

Leu Leu Asn Ser Met Asp Gly Asp Gly Thr Lys Asn Gly Phe Asp Leu  
 180 185 190

Glu Leu Leu Glu Lys Val Arg Ala Ala Val Ser Ile Pro Val Ile Ala  
 195 200 205

Ser Gly Gly Ala Gly Lys Ala Glu His Phe Pro Pro Ala Val Ala Ala  
 210 215 220

Gly Ala Asn Ala Val Leu Ala Ala Thr Ile Phe His Phe Arg Glu Val  
 225 230 235 240

Thr Ile Ala Glu Val Lys Gly Ala Ile Lys Asp Ala Gly Phe Glu Val  
 245 250 255

Arg Lys

&lt;210&gt; 391

&lt;211&gt; 729

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(706)

&lt;223&gt; RXN01104

&lt;400&gt; 391

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gagatcatca agctgaacct gtaagagaga agaatttttc atg act gtc gca cca 115
                                         Met Thr Val Ala Pro
                                         1           5

aga att ggt acc gca acc cgc acc acc agc gaa tcc gac atc acc gtc 163
Arg Ile Gly Thr Ala Thr Arg Thr Thr Ser Glu Ser Asp Ile Thr Val
                        10                15                20

gag atc aac ctg gac ggc acc ggc aaa gta gat atc gat acc ggc ctg 211
Glu Ile Asn Leu Asp Gly Thr Gly Lys Val Asp Ile Asp Thr Gly Leu
                        25                30                35

cca ttt ttc gac cac atg ctc act gca ttc ggc gtg cac ggc agt ttt 259
Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly Val His Gly Ser Phe
                        40                45                50

gat ctg aaa gtc cat gcc aag ggc gac atc gag atc gac gca cac cac 307
Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu Ile Asp Ala His His
                        55                60                65

acc gtg gaa gat acc gcc atc gtg ctc ggc caa gca ctc ctt gac gct 355
Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln Ala Leu Leu Asp Ala
                        70                75                80                85

att ggc gac aag aaa ggc atc cgc cgt ttc gca tcc tgc cag ctg ccc 403
Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala Ser Cys Gln Leu Pro
                        90                95                100

atg gat gag gca tta gtg gag tcc gtg gtg gat atc tcc ggt cgc cca 451
Met Asp Glu Ala Leu Val Glu Ser Val Val Asp Ile Ser Gly Arg Pro
                        105                110                115

tac ttc gtg atc tcc ggc gaa cca gac cac atg atc acc tcc gtg atc 499
Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met Ile Thr Ser Val Ile
                        120                125                130

ggt gga cac tac gca acc gtg atc aac gag cac ttc ttt gaa acc ctc 547
Gly Gly His Tyr Ala Thr Val Ile Asn Glu His Phe Phe Glu Thr Leu
                        135                140                145

gcg ctc aac tcc cga atc acc ctc cac gtg atc tgc cac tac ggc cgc 595
Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile Cys His Tyr Gly Arg
                        150                155                160                165

gac cct cac cac atc acc gaa gca gag tac aag gct gtt gcc cgt gcg 643
Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys Ala Val Ala Arg Ala
                        170                175                180

ctg cgc ggt gcc gta gag atg gat cct cgt caa aca gga atc cca tcc 691
Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln Thr Gly Ile Pro Ser
                        185                190                195

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act aag gga gcg ctc tagacatgaa ctcttctccc atc  
 Thr Lys Gly Ala Leu  
 200

729

&lt;210&gt; 392

&lt;211&gt; 202

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 392

Met Thr Val Ala Pro Arg Ile Gly Thr Ala Thr Arg Thr Thr Ser Glu  
 1 5 10 15

Ser Asp Ile Thr Val Glu Ile Asn Leu Asp Gly Thr Gly Lys Val Asp  
 20 25 30

Ile Asp Thr Gly Leu Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly  
 35 40 45

Val His Gly Ser Phe Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu  
 50 55 60

Ile Asp Ala His His Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln  
 65 70 75 80

Ala Leu Leu Asp Ala Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala  
 85 90 95

Ser Cys Gln Leu Pro Met Asp Glu Ala Leu Val Glu Ser Val Val Asp  
 100 105 110

Ile Ser Gly Arg Pro Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met  
 115 120 125

Ile Thr Ser Val Ile Gly Gly His Tyr Ala Thr Val Ile Asn Glu His  
 130 135 140

Phe Phe Glu Thr Leu Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile  
 145 150 155 160

Cys His Tyr Gly Arg Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys  
 165 170 175

Ala Val Ala Arg Ala Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln  
 180 185 190

Thr Gly Ile Pro Ser Thr Lys Gly Ala Leu  
 195 200

&lt;210&gt; 393

&lt;211&gt; 729

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(706)

&lt;223&gt; FRXA01104



<400> 394

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<210> 395
<211> 987
<212> DNA
<213> Corynebacterium glutamicum
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 $\langle 220 \rangle$ 

<221> CDS

$\langle 222 \rangle$  (10

<223> RXN00446

<400> 395

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ggtgacggag gctacttggg gggctaatacg gtaccgcat atg ggt gcg gtt gag 115  
Met Gly Ala Val Glu

																1	5
ctc	cgt	gag	gct	ctt	gca	gag	cat	tta	gag	gtt	gag	ttt	gac	cag	gtc	163	
Leu	Arg	Glu	Ala	Leu	Ala	Glu	His	Leu	Glu	Val	Glu	Phe	Asp	Gln	Val		
				10					15					20			
acg	gta	ggg	tgc	ggc	tcg	tct	gcg	ctg	tgt	caa	cag	ctg	gtt	cag	gca	211	
Thr	Val	Gly	Cys	Gly	Ser	Ser	Ala	Leu	Cys	Gln	Gln	Leu	Val	Gln	Ala		
				25					30					35			
acg	tgc	gct	cag	ggc	gat	gag	gtc	att	ttt	cca	tgg	cgc	agc	ttt	gag	259	
Thr	Cys	Ala	Gln	Gly	Asp	Glu	Val	Ile	Phe	Pro	Trp	Arg	Ser	Phe	Glu		
				40					45					50			
gct	tat	cca	att	ttc	gcg	cag	gtc	gcg	ggc	gcc	act	cct	gtt	gcc	att	307	
Ala	Tyr	Pro	Ile	Phe	Ala	Gln	Val	Ala	Gly	Ala	Thr	Pro	Val	Ala	Ile		
				55					60					65			
ccg	ctg	act	gct	gat	cag	aat	cat	gat	ctt	gat	gcg	atg	gca	gcc	gcg	355	
Pro	Leu	Thr	Ala	Asp	Gln	Asn	His	Asp	Leu	Asp	Ala	Met	Ala	Ala	Ala		
				70					75					80			
atc	act	gat	aag	acc	cgc	ctc	att	ttc	atc	tgc	aac	ccc	aac	aat	cct	403	
Ile	Thr	Asp	Lys	Thr	Arg	Leu	Ile	Phe	Ile	Cys	Asn	Pro	Asn	Asn	Pro		
				90					95					100			
tcg	ggc	acc	acc	atc	acc	cag	gcg	cag	ttt	gat	aat	ttc	atg	gaa	aag	451	
Ser	Gly	Thr	Thr	Ile	Thr	Gln	Ala	Gln	Phe	Asp	Asn	Phe	Met	Glu	Lys		
				105					110					115			
gtt	cca	aac	gat	gtc	gtt	gtt	ggg	ctg	gat	gag	gct	tat	ttt	gag	ttc	499	
Val	Pro	Asn	Asp	Val	Val	Val	Gly	Leu	Asp	Glu	Ala	Tyr	Phe	Glu	Phe		
				120					125					130			
aac	cgc	gcg	gac	gac	acc	cca	gtt	gcc	act	gag	gaa	atc	cac	cgc	cac	547	
Asn	Arg	Ala	Asp	Asp	Thr	Pro	Val	Ala	Thr	Glu	Glu	Ile	His	Arg	His		
				135					140					145			
gac	aac	gtg	att	ggg	ttg	cgc	acg	ttc	tcc	aag	gcg	tat	ggc	ctg	gcg	595	
Asp	Asn	Val	Ile	Gly	Leu	Arg	Thr	Phe	Ser	Lys	Ala	Tyr	Gly	Leu	Ala		
				150					155					160			
ggc	ttg	cgt	gtt	ggg	tac	gcc	ttc	gga	aac	gca	gag	atc	atc	gca	gcg	643	
Gly	Leu	Arg	Val	Gly	Tyr	Ala	Phe	Gly	Asn	Ala	Glu	Ile	Ile	Ala	Ala		
				170					175					180			
atg	aat	aag	gtg	gct	att	cct	ttc	gcg	gtg	aat	tca	gca	gct	cag	gcg	691	
Met	Asn	Lys	Val	Ala	Ile	Pro	Phe	Ala	Val	Asn	Ser	Ala	Ala	Gln	Ala		
				185					190					195			
gca	gcg	ctt	gcg	agt	ttg	aat	tct	gcc	gat	gag	ttg	atg	gaa	cgg	gtg	739	
Ala	Ala	Leu	Ala	Ser	Leu	Asn	Ser	Ala	Asp	Glu	Leu	Met	Glu	Arg	Val		
				200					205					210			
gag	gaa	acc	gtc	gaa	aag	cgt	gat	gct	gtg	gtg	tca	gcg	ctt	ggg	gct	787	
Glu	Glu	Thr	Val	Glu	Lys	Arg	Asp	Ala	Val	Val	Ser	Ala	Leu	Gly	Ala		
				215					220					225			
gcg	ccg	acg	cag	gcc	aat	ttc	gtc	tgg	ctg	ccg	ggc	gag	ggc	gcc	gct	835	
Ala	Pro	Thr	Gln	Ala	Asn	Phe	Val	Trp	Leu	Pro	Gly	Glu	Gly	Ala	Ala		
				230					235					240			
														245			

gag ttg gcg gct aaa ttg gcc gag cac ggc atc gtg att cgc gcg ttc 883  
 Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile Arg Ala Phe  
                   250                  255                  260

ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa act gac aag 931  
 Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu Thr Asp Lys  
                   265                  270                  275

ctg ctg cgc gcg tgg gag gcc atc aat gct ggg tagtcctttgg cgttttgagg 984  
 Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly  
                   280                  285

tgc 987

<210> 396

<211> 288

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 396

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Glu Phe Asp Gln Val Thr Val Gly Cys Gly Ser Ser Ala Leu Cys Gln  
                   20                  25                  30

Gln Leu Val Gln Ala Thr Cys Ala Gln Gly Asp Glu Val Ile Phe Pro  
                   35                  40                  45

Trp Arg Ser Phe Glu Ala Tyr Pro Ile Phe Ala Gln Val Ala Gly Ala  
                   50                  55                  60

Thr Pro Val Ala Ile Pro Leu Thr Ala Asp Gln Asn His Asp Leu Asp  
                   65                  70                  75                  80

Ala Met Ala Ala Ala Ile Thr Asp Lys Thr Arg Leu Ile Phe Ile Cys  
                   85                  90                  95

Asn Pro Asn Asn Pro Ser Gly Thr Thr Ile Thr Gln Ala Gln Phe Asp  
                   100                  105                  110

Asn Phe Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu  
                   115                  120                  125

Ala Tyr Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu  
                   130                  135                  140

Glu Ile His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys  
                   145                  150                  155                  160

Ala Tyr Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala  
                   165                  170                  175

Glu Ile Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn  
                   180                  185                  190

Ser Ala Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu  
                   195                  200                  205

Leu Met Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val  
 210 215 220  
 Ser Ala Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro  
 225 230 235 240  
 Gly Glu Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile  
 245 250 255  
 Val Ile Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala  
 260 265 270  
 Glu Glu Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly  
 275 280 285

<210> 397  
 <211> 545  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1) .. (522)  
 <223> FRXA00446

<400> 397  
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 ttt gag ttc aac cgc gcg gac gac acc cca gtt gcc act gag gaa atc 96  
 Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile  
 20 25 30  
 cac cgc cac gac aac gtg att ggt ttg cgc acg ttc tcc aag gcg tat 144  
 His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr  
 35 40 45  
 ggc ctg gcg ggc ttg cgt gtt ggt tac gcc ttc gga aac gca gag atc 192  
 Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile  
 50 55 60  
 atc gca gcg atg aat aag gtg gct att cct ttc gcg gtg aat tca gca 240  
 Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala  
 65 70 75 80  
 gct cag gcg gca gcg ctt gcg agt ttg aat tct gcc gat gag ttg atg 288  
 Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met  
 85 90 95  
 gaa cgg gtg gag gaa acc gtc gaa aag cgt gat gct gtg gtg tca gcg 336  
 Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala  
 100 105 110  
 ctt ggt gct gcg ccg acg cag gcc aat ttc gtc tgg ctg ccg ggc gag 384  
 Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu  
 115 120 125



ggc gcc gct gag ttg gcg gct aaa ttg gcc gag cac ggc atc gtg att 432  
 Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile  
 130 135 140

cgc gcg ttc ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa 480  
 Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu  
 145 150 155 160

act gac aag ctg ctg cgc gcg tgg gag gcc atc aat gct ggg 522  
 Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly  
 165 170

tagtcctttgg cgttttgcgg tgc 545

<210> 398

<211> 174

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 398

Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu Ala Tyr  
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Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile  
 20 25 30

His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr  
 35 40 45

Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile  
 50 55 60

Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala  
 65 70 75 80

Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met  
 85 90 95

Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala  
 100 105 110

Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu  
 115 120 125

Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile  
 130 135 140

Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu  
 145 150 155 160

Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly  
 165 170

<210> 399

<211> 1221

<212> DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1198)

&lt;223&gt; RXA01105

&lt;400&gt; 399

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gctttgaaaa cctccccacc accgacgagg cctaagaaaa atg acc aaa att act 115
                Met Thr Lys Ile Thr
                1                5

ttg agc gat ttg cca ttg cgt gaa gaa ctg cgc ggt gag cac gct tac 163
Leu Ser Asp Leu Pro Leu Arg Glu Glu Leu Arg Gly Glu His Ala Tyr
                10                15                20

ggc gca ccc cag ctc aac gtt gat att cgc ctc aac acc aac gaa aac 211
Gly Ala Pro Gln Leu Asn Val Asp Ile Arg Leu Asn Thr Asn Glu Asn
                25                30                35

cct tac cca ccg tca gag gca ttg gtc gct gac ttg gtt gcc acc gtg 259
Pro Tyr Pro Pro Ser Glu Ala Leu Val Ala Asp Leu Val Ala Thr Val
                40                45                50

gat aag atc gcc acc gag ctg aac cgc tac cca gag cgc gat gct gtg 307
Asp Lys Ile Ala Thr Glu Leu Asn Arg Tyr Pro Glu Arg Asp Ala Val
                55                60                65

gaa ctg cgt gat gag ttg gct gcg tac atc acc aag caa acc ggc gtg 355
Glu Leu Arg Asp Glu Leu Ala Ala Tyr Ile Thr Lys Gln Thr Gly Val
                70                75                80                85

gct gtc acc agg gat aac ctg tgg gct gcc aat ggt tcc aat gaa att 403
Ala Val Thr Arg Asp Asn Leu Trp Ala Ala Asn Gly Ser Asn Glu Ile
                90                95                100

ctg cag cag ctg ctg cag gct ttt ggt gga cct gga cgc acc gcg ttg 451
Leu Gln Gln Leu Leu Gln Ala Phe Gly Gly Pro Gly Arg Thr Ala Leu
                105                110                115

gga ttc caa ccc agc tat tcc atg cac cca att ttg gct aaa ggc acc 499
Gly Phe Gln Pro Ser Tyr Ser Met His Pro Ile Leu Ala Lys Gly Thr
                120                125                130

cac act gaa ttc att gcg gtg tcc cga ggt gct gat ttc cgc atc gat 547
His Thr Glu Phe Ile Ala Val Ser Arg Gly Ala Asp Phe Arg Ile Asp
                135                140                145

atg gat gtg gcg ctg gaa gaa att cgt gca aag cag cct gac att gtt 595
Met Asp Val Ala Leu Glu Glu Ile Arg Ala Lys Gln Pro Asp Ile Val
                150                155                160                165

ttt gtc acc acc ccg aac aac ccg acc ggt gat gtg acc tcg ctg gac 643
Phe Val Thr Thr Pro Asn Asn Pro Thr Gly Asp Val Thr Ser Leu Asp
                170                175                180

gat gtt gag cgc atc atc aac gtt gcc cca ggc atc gtg atc gtg gat 691
Asp Val Glu Arg Ile Ile Asn Val Ala Pro Gly Ile Val Ile Val Asp
                185                190                195

gaa gct tat gcg gaa ttc tcc cca tca cct tca gca acc act ctt ctg 739

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Glu	Ala	Tyr	Ala	Glu	Phe	Ser	Pro	Ser	Pro	Ser	Ala	Thr	Thr	Leu	Leu		
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gag	aag	tac	cca	acc	aag	ctg	gtg	gtg	tcc	cgc	acc	atg	agt	aag	gct	787	
Glu	Lys	Tyr	Pro	Thr	Lys	Leu	Val	Val	Ser	Arg	Thr	Met	Ser	Lys	Ala		
	215					220					225						
ttt	gat	ttc	gca	ggt	gga	cgc	ctc	ggc	tac	ttc	gtg	gcc	aac	cca	gcg	835	
Phe	Asp	Phe	Ala	Gly	Gly	Arg	Leu	Gly	Tyr	Phe	Val	Ala	Asn	Pro	Ala		
230					235					240					245		
ttt	atc	gac	gcc	gtg	atg	cta	gtc	cgc	ctt	cgc	tat	cat	ctt	tca	gcg	883	
Phe	Ile	Asp	Ala	Val	Met	Leu	Val	Arg	Leu	Pro	Tyr	His	Leu	Ser	Ala		
				250					255					260			
ctg	agc	caa	gca	gcc	gca	atc	gta	gcg	ctg	cgt	cac	tcc	gct	gac	acg	931	
Leu	Ser	Gln	Ala	Ala	Ala	Ile	Val	Ala	Leu	Arg	His	Ser	Ala	Asp	Thr		
		265					270						275				
ctg	gga	acc	gtc	gaa	aag	ctc	tct	gta	gag	cgt	gtt	cgc	gtg	gca	gca	979	
Leu	Gly	Thr	Val	Glu	Lys	Leu	Ser	Val	Glu	Arg	Val	Arg	Val	Ala	Ala		
		280					285					290					
cgc	ttg	gag	gaa	ctg	ggc	tac	gct	gtg	gtt	cca	agt	gag	tcc	aac	ttt	1027	
Arg	Leu	Glu	Glu	Leu	Gly	Tyr	Ala	Val	Val	Pro	Ser	Glu	Ser	Asn	Phe		
	295					300					305						
gtg	ttc	ttt	gga	gat	ttc	tcc	gat	cag	cac	gcg	gca	tgg	cag	gca	ttt	1075	
Val	Phe	Phe	Gly	Asp	Phe	Ser	Asp	Gln	His	Ala	Ala	Trp	Gln	Ala	Phe		
310					315					320					325		
ttg	gat	agg	gga	gtg	ctc	atc	cgc	gat	gtg	gga	atc	gct	ggg	cac	ttg	1123	
Leu	Asp	Arg	Gly	Val	Leu	Ile	Arg	Asp	Val	Gly	Ile	Ala	Gly	His	Leu		
				330					335					340			
cgc	act	acc	att	ggt	gtg	cct	gag	gaa	aat	gat	gcg	ttt	ttg	gac	gca	1171	
Arg	Thr	Thr	Ile	Gly	Val	Pro	Glu	Glu	Asn	Asp	Ala	Phe	Leu	Asp	Ala		
			345					350					355				
gct	gca	gag	atc	atc	aag	ctg	aac	ctg	taagagagaa	gaatttttca						1218	
Ala	Ala	Glu	Ile	Ile	Lys	Leu	Asn	Leu									
		360				365											
tga																	1221

&lt;210&gt; 400

&lt;211&gt; 366

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 400

Met	Thr	Lys	Ile	Thr	Leu	Ser	Asp	Leu	Pro	Leu	Arg	Glu	Glu	Leu	Arg
1				5					10					15	

Gly	Glu	His	Ala	Tyr	Gly	Ala	Pro	Gln	Leu	Asn	Val	Asp	Ile	Arg	Leu
			20					25					30		

Asn	Thr	Asn	Glu	Asn	Pro	Tyr	Pro	Pro	Ser	Glu	Ala	Leu	Val	Ala	Asp
		35					40					45			

Leu Val Ala Thr Val Asp Lys Ile Ala Thr Glu Leu Asn Arg Tyr Pro  
 50 55 60  
 Glu Arg Asp Ala Val Glu Leu Arg Asp Glu Leu Ala Ala Tyr Ile Thr  
 65 70 75 80  
 Lys Gln Thr Gly Val Ala Val Thr Arg Asp Asn Leu Trp Ala Ala Asn  
 85 90 95  
 Gly Ser Asn Glu Ile Leu Gln Gln Leu Leu Gln Ala Phe Gly Gly Pro  
 100 105 110  
 Gly Arg Thr Ala Leu Gly Phe Gln Pro Ser Tyr Ser Met His Pro Ile  
 115 120 125  
 Leu Ala Lys Gly Thr His Thr Glu Phe Ile Ala Val Ser Arg Gly Ala  
 130 135 140  
 Asp Phe Arg Ile Asp Met Asp Val Ala Leu Glu Glu Ile Arg Ala Lys  
 145 150 155 160  
 Gln Pro Asp Ile Val Phe Val Thr Thr Pro Asn Asn Pro Thr Gly Asp  
 165 170 175  
 Val Thr Ser Leu Asp Asp Val Glu Arg Ile Ile Asn Val Ala Pro Gly  
 180 185 190  
 Ile Val Ile Val Asp Glu Ala Tyr Ala Glu Phe Ser Pro Ser Pro Ser  
 195 200 205  
 Ala Thr Thr Leu Leu Glu Lys Tyr Pro Thr Lys Leu Val Val Ser Arg  
 210 215 220  
 Thr Met Ser Lys Ala Phe Asp Phe Ala Gly Gly Arg Leu Gly Tyr Phe  
 225 230 235 240  
 Val Ala Asn Pro Ala Phe Ile Asp Ala Val Met Leu Val Arg Leu Pro  
 245 250 255  
 Tyr His Leu Ser Ala Leu Ser Gln Ala Ala Ala Ile Val Ala Leu Arg  
 260 265 270  
 His Ser Ala Asp Thr Leu Gly Thr Val Glu Lys Leu Ser Val Glu Arg  
 275 280 285  
 Val Arg Val Ala Ala Arg Leu Glu Glu Leu Gly Tyr Ala Val Val Pro  
 290 295 300  
 Ser Glu Ser Asn Phe Val Phe Phe Gly Asp Phe Ser Asp Gln His Ala  
 305 310 315 320  
 Ala Trp Gln Ala Phe Leu Asp Arg Gly Val Leu Ile Arg Asp Val Gly  
 325 330 335  
 Ile Ala Gly His Leu Arg Thr Thr Ile Gly Val Pro Glu Glu Asn Asp  
 340 345 350  
 Ala Phe Leu Asp Ala Ala Ala Glu Ile Ile Lys Leu Asn Leu  
 355 360 365

<400> 401															
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aagaatttcg attcaacctt ttaagggaga acttttcgcc atg ttg aat gtc act 115															
Met Leu Asn Val Thr 1 5															
gac ctg cga ggt caa aca cca tcc aag agc gac atc cga cgt gct ttg 163															
Asp Leu Arg Gly Gln Thr Pro Ser Lys Ser Asp Ile Arg Arg Ala Leu 10 15 20															
cca cgt ggt ggc act gac gtg tgg tct gtg ctt ccc ata gtg cag cct 211															
Pro Arg Gly Gly Thr Asp Val Trp Ser Val Leu Pro Ile Val Gln Pro 25 30 35															
gtt gta gaa gat gtc caa aac cgc ggc gct gaa gct gct ttg gat tac 259															
Val Val Glu Asp Val Gln Asn Arg Gly Ala Glu Ala Ala Leu Asp Tyr 40 45 50															
ggc gag aag ttc gac cat att cgc ccc gcc tcg gtg cgg gtg cca gct 307															
Gly Glu Lys Phe Asp His Ile Arg Pro Ala Ser Val Arg Val Pro Ala 55 60 65															
gag gtt att gct gca gca gaa aac acc tta gat ccg ttg gtg cgt gaa 355															
Glu Val Ile Ala Ala Ala Glu Asn Thr Leu Asp Pro Leu Val Arg Glu 70 75 80 85															
tcg att gaa gag tcg att cgt cgc gtc cgc aag gtt cac gct gag caa 403															
Ser Ile Glu Glu Ser Ile Arg Arg Val Arg Lys Val His Ala Glu Gln 90 95 100															
aag cca tcc gag cac acc act gaa ctt tca cca ggt ggc acc gtc act 451															
Lys Pro Ser Glu His Thr Thr Glu Leu Ser Pro Gly Gly Thr Val Thr 105 110 115															
gag cgt ttc atg ccg att gat cgc gtg gga ctg tac gtt cca ggc ggc 499															
Glu Arg Phe Met Pro Ile Asp Arg Val Gly Leu Tyr Val Pro Gly Gly 120 125 130															
aat gcg gtg tac cca tca agc gtg att atg aat act gtc cca gct caa 547															
Asn Ala Val Tyr Pro Ser Ser Val Ile Met Asn Thr Val Pro Ala Gln 135 140 145															
gag gct ggt gtg aac tcc ctt gtg gtt gcg tcg cct cct cag gct gag 595															
Glu Ala Gly Val Asn Ser Leu Val Val Ala Ser Pro Pro Gln Ala Glu 150 155 160 165															
cac ggt ggc tgg cct cac ccc acc att ttg gcg gcg tgt tcc atc ttg 643															
His Gly Gly Trp Pro His Pro Thr Ile Leu Ala Ala Cys Ser Ile Leu 170 175 180															

ggt gtt gat gag gtg tgg gct gtc ggc ggc ggt cag gcc gtg gcg ttg	691
Gly Val Asp Glu Val Trp Ala Val Gly Gly Gly Gln Ala Val Ala Leu	
185 190 195	
ctg gct tat ggt gat gac gct gca ggt ctc gag cct gtg gat atg atc	739
Leu Ala Tyr Gly Asp Asp Ala Ala Gly Leu Glu Pro Val Asp Met Ile	
200 205 210	
act gga cct ggc aat atc ttt gtc acc gct gcg aag cgc ctg gtc agg	787
Thr Gly Pro Gly Asn Ile Phe Val Thr Ala Ala Lys Arg Leu Val Arg	
215 220 225	
gga gtg gta ggt act gat tct gag gct ggc cct aca gaa atc gct gtg	835
Gly Val Val Gly Thr Asp Ser Glu Ala Gly Pro Thr Glu Ile Ala Val	
230 235 240 245	
ctt gct gat gcc tct gcc aac gcc gtc aac gtt gcc tac gat ctg atc	883
Leu Ala Asp Ala Ser Ala Asn Ala Val Asn Val Ala Tyr Asp Leu Ile	
250 255 260	
agc caa gca gaa cac gat gtc atg gct gcg tcc gtg ctc atc act gac	931
Ser Gln Ala Glu His Asp Val Met Ala Ala Ser Val Leu Ile Thr Asp	
265 270 275	
tcc gag cag ctt gcc aag gac gta aac agg gaa atc gag gcg cgt tac	979
Ser Glu Gln Leu Ala Lys Asp Val Asn Arg Glu Ile Glu Ala Arg Tyr	
280 285 290	
tca atc acg cgc aac gcc gag cgc gtc gca gaa gct ttg cgc ggg gcc	1027
Ser Ile Thr Arg Asn Ala Glu Arg Val Ala Glu Ala Leu Arg Gly Ala	
295 300 305	
cag agt ggc atc gtg ctt gtc gac gac att tcc gtg ggt atc caa gta	1075
Gln Ser Gly Ile Val Leu Val Asp Asp Ile Ser Val Gly Ile Gln Val	
310 315 320 325	
gcc gat caa tac gca gcg gaa cac ctg gaa atc cac act gag aac gcg	1123
Ala Asp Gln Tyr Ala Ala Glu His Leu Glu Ile His Thr Glu Asn Ala	
330 335 340	
cgc gcc gta gca gag cag atc acc aac gcg ggt gcg atc ttc gtg ggc	1171
Arg Ala Val Ala Glu Gln Ile Thr Asn Ala Gly Ala Ile Phe Val Gly	
345 350 355	
gat ttc tca cca gta cca ctg ggt gat tac tcc gca gga tcc aac cac	1219
Asp Phe Ser Pro Val Pro Leu Gly Asp Tyr Ser Ala Gly Ser Asn His	
360 365 370	
gtg ctg cca acc tct gga tcc gct cgt ttc tcc gca ggt cta tcc acg	1267
Val Leu Pro Thr Ser Gly Ser Ala Arg Phe Ser Ala Gly Leu Ser Thr	
375 380 385	
cac acg ttc ctt cgc cca gtc aac ctc att gaa tac gat gag gct gct	1315
His Thr Phe Leu Arg Pro Val Asn Leu Ile Glu Tyr Asp Glu Ala Ala	
390 395 400 405	
ctg aag gac gtc tcg cag gtt gtc atc aac ttt gcc aac gcc gaa gat	1363
Leu Lys Asp Val Ser Gln Val Val Ile Asn Phe Ala Asn Ala Glu Asp	
410 415 420	
ctt cca gcg cac ggc gaa gca atc cgt gca cgc ttt gaa aac ctc ccc	1411

Leu Pro Ala His Gly Glu Ala Ile Arg Ala Arg Phe Glu Asn Leu Pro  
 425 430 435

acc acc gac gag gcc taagaaaaat gaccaaatt act  
 Thr Thr Asp Glu Ala  
 440

1449

&lt;210&gt; 402

&lt;211&gt; 442

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 402

Met Leu Asn Val Thr Asp Leu Arg Gly Gln Thr Pro Ser Lys Ser Asp  
 1 5 10 15

Ile Arg Arg Ala Leu Pro Arg Gly Gly Thr Asp Val Trp Ser Val Leu  
 20 25 30

Pro Ile Val Gln Pro Val Val Glu Asp Val Gln Asn Arg Gly Ala Glu  
 35 40 45

Ala Ala Leu Asp Tyr Gly Glu Lys Phe Asp His Ile Arg Pro Ala Ser  
 50 55 60

Val Arg Val Pro Ala Glu Val Ile Ala Ala Ala Glu Asn Thr Leu Asp  
 65 70 75 80

Pro Leu Val Arg Glu Ser Ile Glu Glu Ser Ile Arg Arg Val Arg Lys  
 85 90 95

Val His Ala Glu Gln Lys Pro Ser Glu His Thr Thr Glu Leu Ser Pro  
 100 105 110

Gly Gly Thr Val Thr Glu Arg Phe Met Pro Ile Asp Arg Val Gly Leu  
 115 120 125

Tyr Val Pro Gly Gly Asn Ala Val Tyr Pro Ser Ser Val Ile Met Asn  
 130 135 140

Thr Val Pro Ala Gln Glu Ala Gly Val Asn Ser Leu Val Val Ala Ser  
 145 150 155 160

Pro Pro Gln Ala Glu His Gly Gly Trp Pro His Pro Thr Ile Leu Ala  
 165 170 175

Ala Cys Ser Ile Leu Gly Val Asp Glu Val Trp Ala Val Gly Gly Gly  
 180 185 190

Gln Ala Val Ala Leu Leu Ala Tyr Gly Asp Asp Ala Ala Gly Leu Glu  
 195 200 205

Pro Val Asp Met Ile Thr Gly Pro Gly Asn Ile Phe Val Thr Ala Ala  
 210 215 220

Lys Arg Leu Val Arg Gly Val Val Gly Thr Asp Ser Glu Ala Gly Pro  
 225 230 235 240

Thr Glu Ile Ala Val Leu Ala Asp Ala Ser Ala Asn Ala Val Asn Val  
 245 250 255

Ala Tyr Asp Leu Ile Ser Gln Ala Glu His Asp Val Met Ala Ala Ser  
 260 265 270

Val Leu Ile Thr Asp Ser Glu Gln Leu Ala Lys Asp Val Asn Arg Glu  
 275 280 285

Ile Glu Ala Arg Tyr Ser Ile Thr Arg Asn Ala Glu Arg Val Ala Glu  
 290 295 300

Ala Leu Arg Gly Ala Gln Ser Gly Ile Val Leu Val Asp Asp Ile Ser  
 305 310 315 320

Val Gly Ile Gln Val Ala Asp Gln Tyr Ala Ala Glu His Leu Glu Ile  
 325 330 335

His Thr Glu Asn Ala Arg Ala Val Ala Glu Gln Ile Thr Asn Ala Gly  
 340 345 350

Ala Ile Phe Val Gly Asp Phe Ser Pro Val Pro Leu Gly Asp Tyr Ser  
 355 360 365

Ala Gly Ser Asn His Val Leu Pro Thr Ser Gly Ser Ala Arg Phe Ser  
 370 375 380

Ala Gly Leu Ser Thr His Thr Phe Leu Arg Pro Val Asn Leu Ile Glu  
 385 390 395 400

Tyr Asp Glu Ala Ala Leu Lys Asp Val Ser Gln Val Val Ile Asn Phe  
 405 410 415

Ala Asn Ala Glu Asp Leu Pro Ala His Gly Glu Ala Ile Arg Ala Arg  
 420 425 430

Phe Glu Asn Leu Pro Thr Thr Asp Glu Ala  
 435 440

&lt;210&gt; 403

&lt;211&gt; 876

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(853)

&lt;223&gt; RXC00930

&lt;400&gt; 403

acggcgccacc acacatttgg tggtgtattg agctatctct gggctgcgtg agaaaccatt 60

ttccggtgga tgatggaagc tagacgacga aagggagcat atg tct ggc cac tca 115  
 Met Ser Gly His Ser  
 1 5

aaa tgg gcg act acc aag cac aag aag gct gct aac gac gcc aag cga 163  
 Lys Trp Ala Thr Thr Lys His Lys Lys Ala Ala Asn Asp Ala Lys Arg  
 10 15 20

ggc aag gaa ttt gcc aag ctg atc aag aac atc gaa gtt gcg gca cgt 211  
 Gly Lys Glu Phe Ala Lys Leu Ile Lys Asn Ile Glu Val Ala Ala Arg



25	30	35	
aca ggc ggt gga gat ccg tct gcg aac cca acg ctt gat gac atg atc			259
Thr Gly Gly Gly Asp Pro Ser Ala Asn Pro Thr Leu Asp Asp Met Ile			
40	45	50	
aag aaa gcc aag aag gct tct gtg ccg aac gat aac atc gaa cgt gca			307
Lys Lys Ala Lys Lys Ala Ser Val Pro Asn Asp Asn Ile Glu Arg Ala			
55	60	65	
cgc aag cgt ggc tcc ggc gaa gaa gct ggt ggc gct gac tgg atg aac			355
Arg Lys Arg Gly Ser Gly Glu Glu Ala Gly Gly Ala Asp Trp Met Asn			
70	75	80	85
atc atg tac gag gga tac ggc ccc aac ggc gtt gcc atg ctt atc gag			403
Ile Met Tyr Glu Gly Tyr Gly Pro Asn Gly Val Ala Met Leu Ile Glu			
90	95	100	
tgt ctg acc gac aac cgt aac cgc gca gct acc gaa gtt cgc acc gca			451
Cys Leu Thr Asp Asn Arg Asn Arg Ala Ala Thr Glu Val Arg Thr Ala			
105	110	115	
atg acc aaa aac ggt ggc aac ttg ggc gag tcc ggt tcc gtg tcc tac			499
Met Thr Lys Asn Gly Gly Asn Leu Gly Glu Ser Gly Ser Val Ser Tyr			
120	125	130	
atg ttc acc cgc acc ggt gtc gtc acc gta caa aag ggc gat ctt agt			547
Met Phe Thr Arg Thr Gly Val Val Thr Val Gln Lys Gly Asp Leu Ser			
135	140	145	
gaa gat gac gtg ctc atg gct gtt ctt gaa gct ggt gct gaa gaa gtc			595
Glu Asp Asp Val Leu Met Ala Val Leu Glu Ala Gly Ala Glu Glu Val			
150	155	160	165
aac gac aac ggc gat ctg ttc gag gtt acc tgc gca cca act gac att			643
Asn Asp Asn Gly Asp Leu Phe Glu Val Thr Cys Ala Pro Thr Asp Ile			
170	175	180	
cag gct gtt cgc gac gca ctc gtg gaa gct ggc att gaa gta gaa gat			691
Gln Ala Val Arg Asp Ala Leu Val Glu Ala Gly Ile Glu Val Glu Asp			
185	190	195	
tct gaa tca gac ttc cgg gca tct gtt cag gtc ccc ctg gac gct gac			739
Ser Glu Ser Asp Phe Arg Ala Ser Val Gln Val Pro Leu Asp Ala Asp			
200	205	210	
ggt gca cgc aag atc ttc aag ctt gtg gac gcg ttg gaa gat tcc gac			787
Gly Ala Arg Lys Ile Phe Lys Leu Val Asp Ala Leu Glu Asp Ser Asp			
215	220	225	
gat gtg caa aac gtc tac acc aac atc gac ttg agc gat gag gtt ttg			835
Asp Val Gln Asn Val Tyr Thr Asn Ile Asp Leu Ser Asp Glu Val Leu			
230	235	240	245
aca gag ctg gaa aac gac tagttcgtat ttccgcact ccg			876
Thr Glu Leu Glu Asn Asp			
250			

&lt;210&gt; 404

&lt;211&gt; 251

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 404

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Met Ser Gly His Ser Lys Trp Ala Thr Thr Lys His Lys Lys Ala Ala
  1              5              10              15

Asn Asp Ala Lys Arg Gly Lys Glu Phe Ala Lys Leu Ile Lys Asn Ile
      20              25              30

Glu Val Ala Ala Arg Thr Gly Gly Gly Asp Pro Ser Ala Asn Pro Thr
      35              40              45

Leu Asp Asp Met Ile Lys Lys Ala Lys Lys Ala Ser Val Pro Asn Asp
      50              55              60

Asn Ile Glu Arg Ala Arg Lys Arg Gly Ser Gly Glu Glu Ala Gly Gly
      65              70              75              80

Ala Asp Trp Met Asn Ile Met Tyr Glu Gly Tyr Gly Pro Asn Gly Val
      85              90              95

Ala Met Leu Ile Glu Cys Leu Thr Asp Asn Arg Asn Arg Ala Ala Thr
      100              105              110

Glu Val Arg Thr Ala Met Thr Lys Asn Gly Gly Asn Leu Gly Glu Ser
      115              120              125

Gly Ser Val Ser Tyr Met Phe Thr Arg Thr Gly Val Val Thr Val Gln
      130              135              140

Lys Gly Asp Leu Ser Glu Asp Asp Val Leu Met Ala Val Leu Glu Ala
      145              150              155              160

Gly Ala Glu Glu Val Asn Asp Asn Gly Asp Leu Phe Glu Val Thr Cys
      165              170              175

Ala Pro Thr Asp Ile Gln Ala Val Arg Asp Ala Leu Val Glu Ala Gly
      180              185              190

Ile Glu Val Glu Asp Ser Glu Ser Asp Phe Arg Ala Ser Val Gln Val
      195              200              205

Pro Leu Asp Ala Asp Gly Ala Arg Lys Ile Phe Lys Leu Val Asp Ala
      210              215              220

Leu Glu Asp Ser Asp Asp Val Gln Asn Val Tyr Thr Asn Ile Asp Leu
      225              230              235              240

Ser Asp Glu Val Leu Thr Glu Leu Glu Asn Asp
      245              250

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&lt;210&gt; 405

&lt;211&gt; 547

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(547)

&lt;223&gt; RXC01096

&lt;400&gt; 405

accgtgaaac aaaccggcgg tgcgtgccac actggtgccc acacatgttt cgacaatgac 60

gttttgcctgt aaaagcaaca acgattaagg aagaaatctt atg aag cca cgc gtg 115  
Met Lys Pro Arg Val  
1 5

ctg tca gca tta ggc att gga gct ggc gcc ctg gtt gtc tgg atc agc 163  
Leu Ser Ala Leu Gly Ile Gly Ala Gly Ala Leu Val Val Trp Ile Ser  
10 15 20

tca cgc atg aac tgg gta acc atc gag gct ttc gac gat aaa tca ggt 211  
Ser Arg Met Asn Trp Val Thr Ile Glu Ala Phe Asp Asp Lys Ser Gly  
25 30 35

agt gtc acc caa tct att gtg ggt gca acc tgg tct aca gaa atc atg 259  
Ser Val Thr Gln Ser Ile Val Gly Ala Thr Trp Ser Thr Glu Ile Met  
40 45 50

gcg ctt gca ctt gct ttg ctc gct gcc ttc gcc gcc gcg ttg gtg ctc 307  
Ala Leu Ala Leu Ala Leu Leu Ala Ala Phe Ala Ala Ala Leu Val Leu  
55 60 65

aag cgc atg ggt cgg cgc atc att ggt ggt att tcg gcg ctg atc gcg 355  
Lys Arg Met Gly Arg Arg Ile Ile Gly Gly Ile Ser Ala Leu Ile Ala  
70 75 80 85

gtg ggt gcc agc ctg tct cca ctc gcg ctt ctc acc caa gac cca gac 403  
Val Gly Ala Ser Leu Ser Pro Leu Ala Leu Leu Thr Gln Asp Pro Asp  
90 95 100

gca gaa cgg gcc cga acc ctg ctg acc tcc ggt gtg gcc tca cag aag 451  
Ala Glu Arg Ala Arg Thr Leu Leu Thr Ser Gly Val Ala Ser Gln Lys  
105 110 115

gct aat tcc gga acc ctg ctg tct gat tgg gcg gag atc atc aat acc 499  
Ala Asn Ser Gly Thr Leu Leu Ser Asp Trp Ala Glu Ile Ile Asn Thr  
120 125 130

acc acc cat cca ctg gcg gca gtg gta gcc atg att ggc tgc gcg cta 547  
Thr Thr His Pro Leu Ala Ala Val Val Ala Met Ile Gly Cys Ala Leu  
135 140 145

&lt;210&gt; 406

&lt;211&gt; 149

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 406

Met Lys Pro Arg Val Leu Ser Ala Leu Gly Ile Gly Ala Gly Ala Leu  
1 5 10 15

Val Val Trp Ile Ser Ser Arg Met Asn Trp Val Thr Ile Glu Ala Phe  
20 25 30

Asp Asp Lys Ser Gly Ser Val Thr Gln Ser Ile Val Gly Ala Thr Trp  
35 40 45

Ser Thr Glu Ile Met Ala Leu Ala Leu Ala Leu Ala Ala Phe Ala  
 50 55 60

Ala Ala Leu Val Leu Lys Arg Met Gly Arg Arg Ile Ile Gly Gly Ile  
 65 70 75 80

Ser Ala Leu Ile Ala Val Gly Ala Ser Leu Ser Pro Leu Ala Leu Leu  
 85 90 95

Thr Gln Asp Pro Asp Ala Glu Arg Ala Arg Thr Leu Leu Thr Ser Gly  
 100 105 110

Val Ala Ser Gln Lys Ala Asn Ser Gly Thr Leu Leu Ser Asp Trp Ala  
 115 120 125

Glu Ile Ile Asn Thr Thr Thr His Pro Leu Ala Ala Val Val Ala Met  
 130 135 140

Ile Gly Cys Ala Leu  
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<210> 407  
 <211> 1020  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(997)  
 <223> RXC01656

<400> 407  
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atctaccgct agtccacttt gtggcggttg atcatctgtc atg acc gaa act caa 115  
 Met Thr Glu Thr Gln  
 1 5

gaa act tac caa gca acc act cgt gtg aag cgc ggc ctt gcc gac atg 163  
 Glu Thr Tyr Gln Ala Thr Thr Arg Val Lys Arg Gly Leu Ala Asp Met  
 10 15 20

ctc aag ggt ggt gtg atc atg gat gtg gtc acc cct gaa caa gcg cgc 211  
 Leu Lys Gly Gly Val Ile Met Asp Val Val Thr Pro Glu Gln Ala Arg  
 25 30 35

atc gcc gaa gat gca ggt gcc agc gca gtt atg gca ctc gag cgc gtt 259  
 Ile Ala Glu Asp Ala Gly Ala Ser Ala Val Met Ala Leu Glu Arg Val  
 40 45 50

ccc gcc gat atc cgt tct cag ggc ggc gtt gct cgc atg agt gat cct 307  
 Pro Ala Asp Ile Arg Ser Gln Gly Gly Val Ala Arg Met Ser Asp Pro  
 55 60 65

gac ctg atc gaa gga atc gtc aat gcg gtc tcc atc ccg gtc atg gcg 355  
 Asp Leu Ile Glu Gly Ile Val Asn Ala Val Ser Ile Pro Val Met Ala  
 70 75 80 85

aaa gct cgc atc ggt cac ttc gtg gaa gct cag gtt ctg gaa gct ctc 403  
 Lys Ala Arg Ile Gly His Phe Val Glu Ala Gln Val Leu Glu Ala Leu

90					95					100					
ggt gtt gat ttc atc gac gag tcc gaa gtt ctc agc cct gcc gac tac	451														
Gly Val Asp Phe Ile Asp Glu Ser Glu Val Leu Ser Pro Ala Asp Tyr															
105 110 115															
acg cac cac atc aac aag tgg aag ttc gac gtt cct ttc gtc tgt ggc	499														
Thr His His Ile Asn Lys Trp Lys Phe Asp Val Pro Phe Val Cys Gly															
120 125 130															
gcg acc aac ctc ggc gaa gct ttg cga cgc atc acc gaa ggc gct gca	547														
Ala Thr Asn Leu Gly Glu Ala Leu Arg Arg Ile Thr Glu Gly Ala Ala															
135 140 145															
atg atc cgt tcc aag ggc gaa gcc ggc acc ggc gat gtc tct gaa gct	595														
Met Ile Arg Ser Lys Gly Glu Ala Gly Thr Gly Asp Val Ser Glu Ala															
150 155 160 165															
gtc cgt cac ctg cgc acc atc cgc ggc gac atc aat cgc ctg cgc tcc	643														
Val Arg His Leu Arg Thr Ile Arg Gly Asp Ile Asn Arg Leu Arg Ser															
170 175 180															
ctg gat gag gat gaa ctc ttc gtc gcc gcc aag gaa ttc cag gca cca	691														
Leu Asp Glu Asp Glu Leu Phe Val Ala Ala Lys Glu Phe Gln Ala Pro															
185 190 195															
tac gac ctg gtc cgc gaa gtc gcc tcc acc ggc aag ctc cct gtg gtc	739														
Tyr Asp Leu Val Arg Glu Val Ala Ser Thr Gly Lys Leu Pro Val Val															
200 205 210															
acc ttc gtt gca ggt ggc gtc gca acc cca gcc gac gct gca ctc gtg	787														
Thr Phe Val Ala Gly Gly Val Ala Thr Pro Ala Asp Ala Ala Leu Val															
215 220 225															
cgc caa atg ggc gcc gaa ggc gtc ttt gtc ggc tcc ggc atc ttc aaa	835														
Arg Gln Met Gly Ala Glu Gly Val Phe Val Gly Ser Gly Ile Phe Lys															
230 235 240 245															
tcc ggc aat cca gcc gcc cgc gcc gca gcg atc gtc aag gct gca acg	883														
Ser Gly Asn Pro Ala Ala Arg Ala Ala Ala Ile Val Lys Ala Ala Thr															
250 255 260															
ctt ttc gac gac ccc tcc gtc att gcc gac gta tcc cgc ggc ctg ggt	931														
Leu Phe Asp Asp Pro Ser Val Ile Ala Asp Val Ser Arg Gly Leu Gly															
265 270 275															
gaa gcc atg gtg ggc atc aac gta tcc gac gtt cca gca cca cac cga	979														
Glu Ala Met Val Gly Ile Asn Val Ser Asp Val Pro Ala Pro His Arg															
280 285 290															
ctc gcc gag cgc ggc tgg tgatcggttg agtttttagct ctc	1020														
Leu Ala Glu Arg Gly Trp															
295															

&lt;210&gt; 408

&lt;211&gt; 299

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 408

<210> 409  
<211> 1065  
<212> DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1042)

&lt;223&gt; RXC01158

&lt;400&gt; 409

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agttatctca aaaaagaaga agaagtctcc tacgggagag atg tcc att gtt gag 115
                                         Met Ser Ile Val Glu
                                         1 5

cac atc aaa gag ttt cga cgc cga ctt ctt atc gct ctg gcg ggc atc 163
His Ile Lys Glu Phe Arg Arg Arg Leu Leu Ile Ala Leu Ala Gly Ile
                        10 15 20

ctc gtg ggc acc att atc ggc ttt att tgg tac gat ttc tca ttt tgg 211
Leu Val Gly Thr Ile Ile Gly Phe Ile Trp Tyr Asp Phe Ser Phe Trp
                        25 30 35

cag atc ccc act ttg ggc gag ctg ctg agg gat ccg tac tgt tct ctg 259
Gln Ile Pro Thr Leu Gly Glu Leu Leu Arg Asp Pro Tyr Cys Ser Leu
                        40 45 50

cct gct gaa tcc cgc tgg gcc atg agc gac tca gag gaa tgt cga ctg 307
Pro Ala Glu Ser Arg Trp Ala Met Ser Asp Ser Glu Glu Cys Arg Leu
                        55 60 65

ctc gca acc ggc ccg ttt gat cca ttc atg ctt cgc ctt aaa gta gcg 355
Leu Ala Thr Gly Pro Phe Asp Pro Phe Met Leu Arg Leu Lys Val Ala
                        70 75 80 85

gcg ttg gtg ggt atg gtt ctt ggc tca ccc gtg tgg ctg agc cag ctg 403
Ala Leu Val Gly Met Val Leu Gly Ser Pro Val Trp Leu Ser Gln Leu
                        90 95 100

tgg ggc ttt atc acc cca ggt ttg atg aag aat gag cgc cgt tac acc 451
Trp Gly Phe Ile Thr Pro Gly Leu Met Lys Asn Glu Arg Arg Tyr Thr
                        105 110 115

gca atc ttc gtc acg att gct gtt gtg ctg ttt gtc ggc ggt gct gtt 499
Ala Ile Phe Val Thr Ile Ala Val Val Leu Phe Val Gly Gly Ala Val
                        120 125 130

ctt gcg tac ttc gtc gtt gca tat ggt ttg gag ttc ctc ctt acc att 547
Leu Ala Tyr Phe Val Val Ala Tyr Gly Leu Glu Phe Leu Leu Thr Ile
                        135 140 145

ggt gga gac acc cag gca gcg gcc ctg act ggt gat aag tac ttc gga 595
Gly Gly Asp Thr Gln Ala Ala Ala Leu Thr Gly Asp Lys Tyr Phe Gly
                        150 155 160 165

ttc ttg ctc gcg ttg ttg gcg att ttc ggc gtg agc ttc gaa gtt cca 643
Phe Leu Leu Ala Leu Leu Ala Ile Phe Gly Val Ser Phe Glu Val Pro
                        170 175 180

ctg gtg atc ggc atg ctc aac att gtg ggt atc ttg cct tac gat gcc 691
Leu Val Ile Gly Met Leu Asn Ile Val Gly Ile Leu Pro Tyr Asp Ala
                        185 190 195

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att aaa gat aag cga cgc atg atc atc atg att ttg ttc gtg ttc gct 739  
 Ile Lys Asp Lys Arg Arg Met Ile Ile Met Ile Leu Phe Val Phe Ala  
 200 205 210

gct ttc atg aca ccc ggc cag gat cct ttc acc atg ttg gtg ttg gcg 787  
 Ala Phe Met Thr Pro Gly Gln Asp Pro Phe Thr Met Leu Val Leu Ala  
 215 220 225

ctt tca ctc acc gtt ctg gta gag ctt gcc ctg cag ttc tgt cgc ttc 835  
 Leu Ser Leu Thr Val Leu Val Glu Leu Ala Leu Gln Phe Cys Arg Phe  
 230 235 240 245

aac gac aaa cgc cgg gac aag aag cgc cca gaa tgg ctt gat ggc gat 883  
 Asn Asp Lys Arg Arg Asp Lys Lys Arg Pro Glu Trp Leu Asp Gly Asp  
 250 255 260

gac ctc tct gca tca cca ctg gat act tct gct ggt gga gaa gat gct 931  
 Asp Leu Ser Ala Ser Pro Leu Asp Thr Ser Ala Gly Gly Glu Asp Ala  
 265 270 275

cca agc cca gtc gaa acc cca gag gcg gtg gag cct tcg cgg atg ctg 979  
 Pro Ser Pro Val Glu Thr Pro Glu Ala Val Glu Pro Ser Arg Met Leu  
 280 285 290

aac cca agt ggg gag gcg tcg ata agc tat aaa ccc ggg cgc gcc gac 1027  
 Asn Pro Ser Gly Glu Ala Ser Ile Ser Tyr Lys Pro Gly Arg Ala Asp  
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ttc ggt gac gtg ctc tagggcctag ccaggtaccc tta 1065  
 Phe Gly Asp Val Leu  
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<210> 410  
 <211> 314  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 410  
 Met Ser Ile Val Glu His Ile Lys Glu Phe Arg Arg Arg Leu Leu Ile  
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Ala Leu Ala Gly Ile Leu Val Gly Thr Ile Ile Gly Phe Ile Trp Tyr  
 20 25 30

Asp Phe Ser Phe Trp Gln Ile Pro Thr Leu Gly Glu Leu Leu Arg Asp  
 35 40 45

Pro Tyr Cys Ser Leu Pro Ala Glu Ser Arg Trp Ala Met Ser Asp Ser  
 50 55 60

Glu Glu Cys Arg Leu Leu Ala Thr Gly Pro Phe Asp Pro Phe Met Leu  
 65 70 75 80

Arg Leu Lys Val Ala Ala Leu Val Gly Met Val Leu Gly Ser Pro Val  
 85 90 95

Trp Leu Ser Gln Leu Trp Gly Phe Ile Thr Pro Gly Leu Met Lys Asn  
 100 105 110



Glu Arg Arg Tyr Thr Ala Ile Phe Val Thr Ile Ala Val Val Leu Phe  
 115 120 125  
 Val Gly Gly Ala Val Leu Ala Tyr Phe Val Val Ala Tyr Gly Leu Glu  
 130 135 140  
 Phe Leu Leu Thr Ile Gly Gly Asp Thr Gln Ala Ala Leu Thr Gly  
 145 150 155 160  
 Asp Lys Tyr Phe Gly Phe Leu Leu Ala Leu Leu Ala Ile Phe Gly Val  
 165 170 175  
 Ser Phe Glu Val Pro Leu Val Ile Gly Met Leu Asn Ile Val Gly Ile  
 180 185 190  
 Leu Pro Tyr Asp Ala Ile Lys Asp Lys Arg Arg Met Ile Ile Met Ile  
 195 200 205  
 Leu Phe Val Phe Ala Ala Phe Met Thr Pro Gly Gln Asp Pro Phe Thr  
 210 215 220  
 Met Leu Val Leu Ala Leu Ser Leu Thr Val Leu Val Glu Leu Ala Leu  
 225 230 235 240  
 Gln Phe Cys Arg Phe Asn Asp Lys Arg Arg Asp Lys Lys Arg Pro Glu  
 245 250 255  
 Trp Leu Asp Gly Asp Asp Leu Ser Ala Ser Pro Leu Asp Thr Ser Ala  
 260 265 270  
 Gly Gly Glu Asp Ala Pro Ser Pro Val Glu Thr Pro Glu Ala Val Glu  
 275 280 285  
 Pro Ser Arg Met Leu Asn Pro Ser Gly Glu Ala Ser Ile Ser Tyr Lys  
 290 295 300  
 Pro Gly Arg Ala Asp Phe Gly Asp Val Leu  
 305 310

&lt;210&gt; 411

&lt;211&gt; 1413

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1390)

&lt;223&gt; RXA02458

&lt;400&gt; 411

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 ggtggtgaac aaaacaaatc ttccacacat aacatctatt atg gtc ttt gtg tct 115  
 Met Val Phe Val Ser  
 1 5

 gat tcg tct atc tct ttg ccc att tgg gat gct ccg cgc gct cgc ggc 163  
 Asp Ser Ser Ile Ser Leu Pro Ile Trp Asp Ala Pro Arg Ala Arg Gly  
 10 15 20

ccc	ata	gtc	tcg	gac	ctg	gct	atc	cct	ggg	tcc	aag	tcg	atc	acc	aac	211
Pro	Ile	Val	Ser	Asp	Leu	Ala	Ile	Pro	Gly	Ser	Lys	Ser	Ile	Thr	Asn	
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cgc	gcc	ctc	atc	ttg	gct	gcg	ctc	gca	tca	act	cca	tcc	acc	atc	att	259
Arg	Ala	Leu	Ile	Leu	Ala	Ala	Leu	Ala	Ser	Thr	Pro	Ser	Thr	Ile	Ile	
		40					45					50				
gat	gtc	ctt	cgt	agt	cgt	gat	acc	gat	ctc	atg	act	gat	ggg	cta	cgc	307
Asp	Val	Leu	Arg	Ser	Arg	Asp	Thr	Asp	Leu	Met	Thr	Asp	Gly	Leu	Arg	
		55				60					65					
agc	ctc	gga	atc	acc	att	act	gaa	gag	gca	gtc	gat	cgc	tac	cgc	gtt	355
Ser	Leu	Gly	Ile	Thr	Ile	Thr	Glu	Glu	Ala	Val	Asp	Arg	Tyr	Arg	Val	
	70				75				80						85	
gag	ccc	gga	cag	ttg	tct	gct	ggc	tcc	gtt	gag	tgt	ggg	ctt	gct	ggg	403
Glu	Pro	Gly	Gln	Leu	Ser	Ala	Gly	Ser	Val	Glu	Cys	Gly	Leu	Ala	Gly	
			90					95						100		
acg	gtc	atg	cgc	ttt	ttg	cct	cct	gtt	gct	gct	ttc	gct	gat	ggg	cct	451
Thr	Val	Met	Arg	Phe	Leu	Pro	Pro	Val	Ala	Ala	Phe	Ala	Asp	Gly	Pro	
			105					110					115			
gtt	cat	ttt	gat	ggc	gat	cct	caa	gct	cgt	gtt	cgt	ccg	atg	acc	agc	499
Val	His	Phe	Asp	Gly	Asp	Pro	Gln	Ala	Arg	Val	Arg	Pro	Met	Thr	Ser	
		120					125					130				
att	ttg	gat	gcg	ctg	cgt	tcg	ctt	ggg	gtg	gag	gta	gac	aac	aac	aat	547
Ile	Leu	Asp	Ala	Leu	Arg	Ser	Leu	Gly	Val	Glu	Val	Asp	Asn	Asn	Asn	
		135				140					145					
ctg	cct	ttc	act	gtt	aat	gct	ggg	gag	gtc	cct	gag	ggg	ggc	gtg	gtt	595
Leu	Pro	Phe	Thr	Val	Asn	Ala	Gly	Glu	Val	Pro	Glu	Gly	Gly	Val	Val	
	150				155				160					165		
gag	att	gat	gct	tcc	ggc	tca	tct	cag	ttt	gtt	tct	ggg	ctt	ttg	ctt	643
Glu	Ile	Asp	Ala	Ser	Gly	Ser	Ser	Gln	Phe	Val	Ser	Gly	Leu	Leu	Leu	
			170					175						180		
tca	gcg	cct	cgt	ttt	aaa	aat	ggc	gtc	acc	gtt	aag	cac	gtc	ggg	ggg	691
Ser	Ala	Pro	Arg	Phe	Lys	Asn	Gly	Val	Thr	Val	Lys	His	Val	Gly	Gly	
			185					190					195			
cgt	ctg	ccg	agc	atg	ccg	cat	att	gag	atg	acc	gtc	gat	atg	ctt	cgt	739
Arg	Leu	Pro	Ser	Met	Pro	His	Ile	Glu	Met	Thr	Val	Asp	Met	Leu	Arg	
		200					205					210				
tcc	gca	ggc	att	gag	atc	gaa	gag	tca	gaa	aat	cag	tgg	gtt	gtt	cat	787
Ser	Ala	Gly	Ile	Glu	Ile	Glu	Glu	Ser	Glu	Asn	Gln	Trp	Val	Val	His	
	215					220					225					
cct	ggg	gag	atc	ttg	ggg	cgg	acc	tgg	cgc	att	gag	ccg	gat	ctt	tct	835
Pro	Gly	Glu	Ile	Leu	Gly	Arg	Thr	Trp	Arg	Ile	Glu	Pro	Asp	Leu	Ser	
	230				235					240				245		
aat	gcg	act	ccg	ttc	cta	gct	gcc	gct	gcg	gtc	act	ggg	gga	acc	atc	883
Asn	Ala	Thr	Pro	Phe	Leu	Ala	Ala	Ala	Ala	Val	Thr	Gly	Gly	Thr	Ile	
			250					255						260		
aag	att	aac	cac	tgg	cca	atc	aaa	act	act	cag	cct	ggc	gat	gct	att	931

Lys Ile Asn His Trp Pro Ile Lys Thr Thr Gln Pro Gly Asp Ala Ile  
 265 270 275  
 cgt tcg att ctt gag cgc atg ggc tgc gaa gtt gag ctg gtt gct cag 979  
 Arg Ser Ile Leu Glu Arg Met Gly Cys Glu Val Glu Leu Val Ala Gln  
 280 285 290  
 ggt gaa ggt tac gat ctg tcg gtg act ggt ccg gtt gct ctc aag ggc 1027  
 Gly Glu Gly Tyr Asp Leu Ser Val Thr Gly Pro Val Ala Leu Lys Gly  
 295 300 305  
 att gag atc gat atg tcc gat atc ggt gag ttg acc cct acc gtg gcg 1075  
 Ile Glu Ile Asp Met Ser Asp Ile Gly Glu Leu Thr Pro Thr Val Ala  
 310 315 320 325  
 gcg ttg gct gcg ttg gcg tcg aca gag tct cgt ttg acc ggt att gct 1123  
 Ala Leu Ala Ala Leu Ala Ser Thr Glu Ser Arg Leu Thr Gly Ile Ala  
 330 335 340  
 cat ctt cgt ggc cat gag acg gat cgt ttg gct gcg ttg act gcg gag 1171  
 His Leu Arg Gly His Glu Thr Asp Arg Leu Ala Ala Leu Thr Ala Glu  
 345 350 355  
 atc aac aaa ctt ggt gga aag tgc act gag ctt aag gat ggt ctg ttg 1219  
 Ile Asn Lys Leu Gly Gly Lys Cys Thr Glu Leu Lys Asp Gly Leu Leu  
 360 365 370  
 att gag cct gcg tcg ctg cac ggt ggt gtg tgg cat tca tat gct gat 1267  
 Ile Glu Pro Ala Ser Leu His Gly Gly Val Trp His Ser Tyr Ala Asp  
 375 380 385  
 cac cgt atg gct act gct ggt gcg atc att ggc ctc gcg gtt gat ggc 1315  
 His Arg Met Ala Thr Ala Gly Ala Ile Ile Gly Leu Ala Val Asp Gly  
 390 395 400 405  
 gtt cag gtt gaa gac att aag acc act tcc aaa act ttc cct ggt ttt 1363  
 Val Gln Val Glu Asp Ile Lys Thr Thr Ser Lys Thr Phe Pro Gly Phe  
 410 415 420  
 gaa aat gtt tgg gag gag atg gtt ggc tagacgcagc tatgacgaat 1410  
 Glu Asn Val Trp Glu Glu Met Val Gly 430  
 ccg 1413

&lt;210&gt; 412

&lt;211&gt; 430

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 412

Met Val Phe Val Ser Asp Ser Ser Ile Ser Leu Pro Ile Trp Asp Ala  
 1 5 10 15

Pro Arg Ala Arg Gly Pro Ile Val Ser Asp Leu Ala Ile Pro Gly Ser  
 20 25 30

Lys Ser Ile Thr Asn Arg Ala Leu Ile Leu Ala Ala Leu Ala Ser Thr  
 35 40 45

Pro Ser Thr Ile Ile Asp Val Leu Arg Ser Arg Asp Thr Asp Leu Met  
 50 55 60  
 Thr Asp Gly Leu Arg Ser Leu Gly Ile Thr Ile Thr Glu Glu Ala Val  
 65 70 75 80  
 Asp Arg Tyr Arg Val Glu Pro Gly Gln Leu Ser Ala Gly Ser Val Glu  
 85 90 95  
 Cys Gly Leu Ala Gly Thr Val Met Arg Phe Leu Pro Pro Val Ala Ala  
 100 105 110  
 Phe Ala Asp Gly Pro Val His Phe Asp Gly Asp Pro Gln Ala Arg Val  
 115 120 125  
 Arg Pro Met Thr Ser Ile Leu Asp Ala Leu Arg Ser Leu Gly Val Glu  
 130 135 140  
 Val Asp Asn Asn Asn Leu Pro Phe Thr Val Asn Ala Gly Glu Val Pro  
 145 150 155 160  
 Glu Gly Gly Val Val Glu Ile Asp Ala Ser Gly Ser Ser Gln Phe Val  
 165 170 175  
 Ser Gly Leu Leu Leu Ser Ala Pro Arg Phe Lys Asn Gly Val Thr Val  
 180 185 190  
 Lys His Val Gly Gly Arg Leu Pro Ser Met Pro His Ile Glu Met Thr  
 195 200 205  
 Val Asp Met Leu Arg Ser Ala Gly Ile Glu Ile Glu Glu Ser Glu Asn  
 210 215 220  
 Gln Trp Val Val His Pro Gly Glu Ile Leu Gly Arg Thr Trp Arg Ile  
 225 230 235 240  
 Glu Pro Asp Leu Ser Asn Ala Thr Pro Phe Leu Ala Ala Ala Val  
 245 250 255  
 Thr Gly Gly Thr Ile Lys Ile Asn His Trp Pro Ile Lys Thr Thr Gln  
 260 265 270  
 Pro Gly Asp Ala Ile Arg Ser Ile Leu Glu Arg Met Gly Cys Glu Val  
 275 280 285  
 Glu Leu Val Ala Gln Gly Glu Gly Tyr Asp Leu Ser Val Thr Gly Pro  
 290 295 300  
 Val Ala Leu Lys Gly Ile Glu Ile Asp Met Ser Asp Ile Gly Glu Leu  
 305 310 315 320  
 Thr Pro Thr Val Ala Ala Leu Ala Ala Leu Ala Ser Thr Glu Ser Arg  
 325 330 335  
 Leu Thr Gly Ile Ala His Leu Arg Gly His Glu Thr Asp Arg Leu Ala  
 340 345 350  
 Ala Leu Thr Ala Glu Ile Asn Lys Leu Gly Gly Lys Cys Thr Glu Leu  
 355 360 365  
 Lys Asp Gly Leu Leu Ile Glu Pro Ala Ser Leu His Gly Gly Val Trp

370 375 380

His Ser Tyr Ala Asp His Arg Met Ala Thr Ala Gly Ala Ile Ile Gly  
385 390 395 400

Leu Ala Val Asp Gly Val Gln Val Glu Asp Ile Lys Thr Thr Ser Lys  
405 410 415

Thr Phe Pro Gly Phe Glu Asn Val Trp Glu Glu Met Val Gly  
420 425 430

<210> 413  
<211> 1266  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(1243)  
<223> RXA02790

<400> 413

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agggaaattt cccaggatga accaaatccg aaaccgcgcg atg gag ccc gtc tac 115  
Met Glu Pro Val Tyr  
1 5

gta aag cgc cgc caa cgg ttt att gcc gtg acg atc gct tca ctc atc 163  
Val Lys Arg Arg Gln Arg Phe Ile Ala Val Thr Ile Ala Ser Leu Ile  
10 15 20

ctc att atc ggt gcc atc atc tat atc ggt gta gcc acc tca aac cgg 211  
Leu Ile Ile Gly Ala Ile Ile Tyr Ile Gly Val Ala Thr Ser Asn Arg  
25 30 35

acg cca cat gac tat gaa ggc tcc gga aac ggt gtg gtt cag ctg gtc 259  
Thr Pro His Asp Tyr Glu Gly Ser Gly Asn Gly Val Val Gln Leu Val  
40 45 50

gaa atc cct gaa ggt tcc tcc ata tca gag ctc ggc cca gag ttg gaa 307  
Glu Ile Pro Glu Gly Ser Ser Ile Ser Glu Leu Gly Pro Glu Leu Glu  
55 60 65

gaa cga gat atc gtg gcc acc aac tca gcg ttc caa aca gcg gcc agc 355  
Glu Arg Asp Ile Val Ala Thr Asn Ser Ala Phe Gln Thr Ala Ala Ser  
70 75 80 85

aac aac ccc aac gcg ggt agt gta cag cca ggt ttc tac cgt ctg cag 403  
Asn Asn Pro Asn Ala Gly Ser Val Gln Pro Gly Phe Tyr Arg Leu Gln  
90 95 100

gaa caa atg aac gca gca gct gca gtg tcg gct ctg ctt gat cca gac 451  
Glu Gln Met Asn Ala Ala Ala Val Ser Ala Leu Leu Asp Pro Asp  
105 110 115

aac cag gtt gat ctc ctc gac att cac ggc ggc gcc acc ttg atg gac 499  
Asn Gln Val Asp Leu Leu Asp Ile His Gly Gly Ala Thr Leu Met Asp  
120 125 130

gtc	act	gtt	gtc	ggc	gga	aac	acc	cgc	gcg	gga	atc	tac	tcc	cag	atc	547
Val	Thr	Val	Val	Gly	Gly	Asn	Thr	Arg	Ala	Gly	Ile	Tyr	Ser	Gln	Ile	
	135					140					145					
gca	gcc	gtg	acc	tgc	acc	gaa	ggc	tcc	gcc	aac	tgc	atc	acc	gct	gag	595
Ala	Ala	Val	Thr	Cys	Thr	Glu	Gly	Ser	Ala	Asn	Cys	Ile	Thr	Ala	Glu	
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Asp	Leu	Gln	Gln	Val	Ala	Ser	Thr	Val	Ser	Pro	Ala	Glu	Leu	Gly	Val	
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Pro	Asp	Trp	Ala	Ile	Ala	Ala	Val	Glu	Ala	Arg	Gly	Thr	Asp	Pro	Lys	
			185					190					195			
cgc	ctc	gaa	ggc	ctg	atc	atg	cct	ggc	caa	tac	gtg	gtg	gat	cca	tcc	739
Arg	Leu	Glu	Gly	Leu	Ile	Met	Pro	Gly	Gln	Tyr	Val	Val	Asp	Pro	Ser	
	200						205					210				
aac	gac	gcc	cag	gga	atc	ctc	acc	gat	ctg	atc	acg	cga	tca	gca	aac	787
Asn	Asp	Ala	Gln	Gly	Ile	Leu	Thr	Asp	Leu	Ile	Thr	Arg	Ser	Ala	Asn	
	215					220					225					
cat	ttc	caa	gaa	acc	gac	atc	acg	ggc	cgt	gca	gat	gcc	atc	gga	ctt	835
His	Phe	Gln	Glu	Thr	Asp	Ile	Thr	Gly	Arg	Ala	Asp	Ala	Ile	Gly	Leu	
	230				235				240						245	
act	cca	tat	gag	ctg	gtc	acc	gca	gca	tct	tta	atc	gag	cgc	gaa	gca	883
Thr	Pro	Tyr	Glu	Leu	Val	Thr	Ala	Ala	Ser	Leu	Ile	Glu	Arg	Glu	Ala	
			250						255					260		
cca	gca	gga	gat	ttt	gat	aag	gtc	gcc	cgc	gtc	atc	ttg	aac	cgt	ctc	931
Pro	Ala	Gly	Asp	Phe	Asp	Lys	Val	Ala	Arg	Val	Ile	Leu	Asn	Arg	Leu	
			265				270						275			
gcc	gag	cca	atg	cag	ctg	caa	ttc	gac	tcc	acc	gtc	aac	tac	ggt	ctg	979
Ala	Glu	Pro	Met	Gln	Leu	Gln	Phe	Asp	Ser	Thr	Val	Asn	Tyr	Gly	Leu	
	280					285						290				
tct	gaa	caa	gaa	gta	gca	acc	acc	gac	gaa	gac	cgt	cag	acc	gtc	acc	1027
Ser	Glu	Gln	Glu	Val	Ala	Thr	Thr	Asp	Glu	Asp	Arg	Gln	Thr	Val	Thr	
	295					300					305					
cca	tgg	aac	act	tac	gcc	atg	gac	ggc	ctg	cca	caa	acc	ccc	atc	gcc	1075
Pro	Trp	Asn	Thr	Tyr	Ala	Met	Asp	Gly	Leu	Pro	Gln	Thr	Pro	Ile	Ala	
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gca	gta	tcc	acc	gaa	gca	ctc	caa	gcc	atg	gaa	aac	cct	gca	gaa	gga	1123
Ala	Val	Ser	Thr	Glu	Ala	Leu	Gln	Ala	Met	Glu	Asn	Pro	Ala	Glu	Gly	
				330					335					340		
aac	tgg	ctg	tac	ttt	gtc	acc	atc	gac	acc	gat	gga	acc	acc	gtg	ttc	1171
Asn	Trp	Leu	Tyr	Phe	Val	Thr	Ile	Asp	Thr	Asp	Gly	Thr	Thr	Val	Phe	
			345					350					355			
aac	gac	acc	ttc	gaa	gag	cac	gaa	gcc	gac	att	gag	caa	gct	ttg	aac	1219
Asn	Asp	Thr	Phe	Glu	Glu	His	Glu	Ala	Asp	Ile	Glu	Gln	Ala	Leu	Asn	
	360						365					370				
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Ser Gly Val Leu Asp Ser Asn Arg  
375 380

<210> 414

<211> 381

<212> PRT

<213> Corynebacterium glutamicum

<400> 414

Met Glu Pro Val Tyr Val Lys Arg Arg Gln Arg Phe Ile Ala Val Thr  
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Ile Ala Ser Leu Ile Leu Ile Ile Gly Ala Ile Ile Tyr Ile Gly Val  
20 25 30

Ala Thr Ser Asn Arg Thr Pro His Asp Tyr Glu Gly Ser Gly Asn Gly  
35 40 45

Val Val Gln Leu Val Glu Ile Pro Glu Gly Ser Ser Ile Ser Glu Leu  
50 55 60

Gly Pro Glu Leu Glu Glu Arg Asp Ile Val Ala Thr Asn Ser Ala Phe  
65 70 75 80

Gln Thr Ala Ala Ser Asn Asn Pro Asn Ala Gly Ser Val Gln Pro Gly  
85 90 95

Phe Tyr Arg Leu Gln Glu Gln Met Asn Ala Ala Ala Ala Val Ser Ala  
100 105 110

Leu Leu Asp Pro Asp Asn Gln Val Asp Leu Leu Asp Ile His Gly Gly  
115 120 125

Ala Thr Leu Met Asp Val Thr Val Val Gly Gly Asn Thr Arg Ala Gly  
130 135 140

Ile Tyr Ser Gln Ile Ala Ala Val Thr Cys Thr Glu Gly Ser Ala Asn  
145 150 155 160

Cys Ile Thr Ala Glu Asp Leu Gln Gln Val Ala Ser Thr Val Ser Pro  
165 170 175

Ala Glu Leu Gly Val Pro Asp Trp Ala Ile Ala Ala Val Glu Ala Arg  
180 185 190

Gly Thr Asp Pro Lys Arg Leu Glu Gly Leu Ile Met Pro Gly Gln Tyr  
195 200 205

Val Val Asp Pro Ser Asn Asp Ala Gln Gly Ile Leu Thr Asp Leu Ile  
210 215 220

Thr Arg Ser Ala Asn His Phe Gln Glu Thr Asp Ile Thr Gly Arg Ala  
225 230 235 240

Asp Ala Ile Gly Leu Thr Pro Tyr Glu Leu Val Thr Ala Ala Ser Leu  
245 250 255

Ile Glu Arg Glu Ala Pro Ala Gly Asp Phe Asp Lys Val Ala Arg Val  
260 265 270

Ile Leu Asn Arg Leu Ala Glu Pro Met Gln Leu Gln Phe Asp Ser Thr  
 275 280 285

Val Asn Tyr Gly Leu Ser Glu Gln Glu Val Ala Thr Thr Asp Glu Asp  
 290 295 300

Arg Gln Thr Val Thr Pro Trp Asn Thr Tyr Ala Met Asp Gly Leu Pro  
 305 310 315 320

Gln Thr Pro Ile Ala Ala Val Ser Thr Glu Ala Leu Gln Ala Met Glu  
 325 330 335

Asn Pro Ala Glu Gly Asn Trp Leu Tyr Phe Val Thr Ile Asp Thr Asp  
 340 345 350

Gly Thr Thr Val Phe Asn Asp Thr Phe Glu Glu His Glu Ala Asp Ile  
 355 360 365

Glu Gln Ala Leu Asn Ser Gly Val Leu Asp Ser Asn Arg  
 370 375 380

&lt;210&gt; 415

&lt;211&gt; 644

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (621)

&lt;223&gt; RXN00954

&lt;400&gt; 415

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1				5				10						15		
gcg	tac	aac	cct	gcg	att	gcg	cat	gtg	cag	ccg	gtt	cgc	cag	gcg	ctg	96
Ala	Tyr	Asn	Pro	Ala	Ile	Ala	His	Val	Gln	Pro	Val	Arg	Gln	Ala	Leu	
			20					25					30			
aaa	ttc	ccc	acc	atc	ttc	aac	acg	ctt	gga	cca	ttg	ctg	tcc	ccg	gcg	144
Lys	Phe	Pro	Thr	Ile	Phe	Asn	Thr	Leu	Gly	Pro	Leu	Leu	Ser	Pro	Ala	
		35					40					45				
cgc	ccg	gag	cgt	cag	atc	atg	ggc	gtg	gcc	aat	gcc	aat	cat	gga	cag	192
Arg	Pro	Glu	Arg	Gln	Ile	Met	Gly	Val	Ala	Asn	Ala	Asn	His	Gly	Gln	
	50					55				60						
ctc	atc	gcc	gag	gtc	ttc	cgc	gag	ttg	ggc	cgt	aca	cgc	gcg	ctt	gtt	240
Leu	Ile	Ala	Glu	Val	Phe	Arg	Glu	Leu	Gly	Arg	Thr	Arg	Ala	Leu	Val	
65				70				75						80		
gtg	cat	ggc	gca	ggc	acc	gat	gag	atc	gca	gtc	cac	ggc	acc	acc	ttg	288
Val	His	Gly	Ala	Gly	Thr	Asp	Glu	Ile	Ala	Val	His	Gly	Thr	Thr	Leu	
			85					90						95		
gtg	tgg	gag	ctt	aaa	gaa	gac	ggc	acc	atc	gag	cat	tac	acc	atc	gag	336
Val	Trp	Glu	Leu	Lys	Glu	Asp	Gly	Thr	Ile	Glu	His	Tyr	Thr	Ile	Glu	
		100					105					110				



cct gag gac ctt ggc ctt ggc cgc tac acc ctt gag gat ctc gta ggt 384  
 Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu Glu Asp Leu Val Gly  
           115                                  120                                  125

ggc ctc ggc act gag aac gcc gaa gct atg cgc gct act ttc gcg ggc 432  
 Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg Ala Thr Phe Ala Gly  
           130                                  135                                  140

acc ggc cct gat gca cac cgt gat gcg ttg gct gcg tcc gca ggt gcg 480  
 Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala Ala Ser Ala Gly Ala  
           145                                  150                                  155                                  160

atg ttc tac ctc aac ggc gat gtc gac tcc ttg aaa gat ggt gca caa 528  
 Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu Lys Asp Gly Ala Gln  
                                   165                                  170                                  175

aag gcg ctt tcc ttg ctt gcc gac ggc acc acc cag gca tgg ttg gcc 576  
 Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr Gln Ala Trp Leu Ala  
                                   180                                  185                                  190

aag cac gaa gag atc gat tac tca gaa aag gag tct tcc aat gac 621  
 Lys His Glu Glu Ile Asp Tyr Ser Glu Lys Glu Ser Ser Asn Asp  
                                   195                                  200                                  205

tagtaataat ctgcccacag tgt 644

<210> 416

<211> 207

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 416

Ala Val Lys Trp Phe Glu Ala Ser Asn Phe Thr Phe Leu Phe Ala Pro  
           1                                  5                                  10                                  15

Ala Tyr Asn Pro Ala Ile Ala His Val Gln Pro Val Arg Gln Ala Leu  
                                   20                                  25                                  30

Lys Phe Pro Thr Ile Phe Asn Thr Leu Gly Pro Leu Leu Ser Pro Ala  
                                   35                                  40                                  45

Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn Ala Asn His Gly Gln  
           50                                  55                                  60

Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg Thr Arg Ala Leu Val  
           65                                  70                                  75                                  80

Val His Gly Ala Gly Thr Asp Glu Ile Ala Val His Gly Thr Thr Leu  
                                   85                                  90                                  95

Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu His Tyr Thr Ile Glu  
                                   100                                  105                                  110

Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu Glu Asp Leu Val Gly  
           115                                  120                                  125

Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg Ala Thr Phe Ala Gly  
           130                                  135                                  140

Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala Ala Ser Ala Gly Ala

145		150		155		160
Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu Lys Asp Gly Ala Gln						
		165		170		175
Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr Gln Ala Trp Leu Ala						
		180		185		190
Lys His Glu Glu Ile Asp Tyr Ser Glu Lys Glu Ser Ser Asn Asp						
		195		200		205

&lt;210&gt; 417

&lt;211&gt; 611

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(588)

&lt;223&gt; FRXA00954

&lt;400&gt; 417

ttc ctg ttc gca cct gcg tac aac cct gcg att gcg cat gtg cag ccg	48
Phe Leu Phe Ala Pro Ala Tyr Asn Pro Ala Ile Ala His Val Gln Pro	
1 5 10 15	
ggt cgc cag gcg ctg aaa ttc ccc acc atc ttc aac acg ctt gga cca	96
Val Arg Gln Ala Leu Lys Phe Pro Thr Ile Phe Asn Thr Leu Gly Pro	
20 25 30	
ttg ctg tcc ccg gcg cgc ccg gag cgt cag atc atg ggc gtg gcc aat	144
Leu Leu Ser Pro Ala Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn	
35 40 45	
gcc aat cat gga cag ctc atc gcc gag gtc ttc cgc gag ttg ggc cgt	192
Ala Asn His Gly Gln Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg	
50 55 60	
aca cgc gcg ctt gtt gtg cat ggc gca ggc acc gat gag atc gca gtc	240
Thr Arg Ala Leu Val Val His Gly Ala Gly Thr Asp Glu Ile Ala Val	
65 70 75 80	
cac ggc acc acc ttg gtg tgg gag ctt aaa gaa gac ggc acc atc gag	288
His Gly Thr Thr Leu Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu	
85 90 95	
cat tac acc atc gag cct gag gac ctt ggc ctt ggc cgc tac acc ctt	336
His Tyr Thr Ile Glu Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu	
100 105 110	
gag gat ctc gta ggt ggc ctc ggc act gag aac gcc gaa gct atg cgc	384
Glu Asp Leu Val Gly Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg	
115 120 125	
gct act ttc gcg ggc acc ggc cct gat gca cac cgt gat gcg ttg gct	432
Ala Thr Phe Ala Gly Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala	
130 135 140	
gcg tcc gca ggt gcg atg ttc tac ctc aac ggc gat gtc gac tcc ttg	480
Ala Ser Ala Gly Ala Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu	

145	150	155	160	
aaa gat ggt gca caa aag gcg ctt tcc ttg ctt gcc gac ggc acc acc	528			
Lys Asp Gly Ala Gln Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr				
165	170	175		
cag gca tgg ttg gcc aag cac gaa gag atc gat tac tca gaa aag gag	576			
Gln Ala Trp Leu Ala Lys His Glu Glu Ile Asp Tyr Ser Glu Lys Glu				
180	185	190		
tct tcc aat gac tagtaataat ctgcccacag tgt	611			
Ser Ser Asn Asp				
195				

&lt;210&gt; 418

&lt;211&gt; 196

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 418

Phe Leu Phe Ala Pro Ala Tyr Asn Pro Ala Ile Ala His Val Gln Pro	
1 5 10 15	
Val Arg Gln Ala Leu Lys Phe Pro Thr Ile Phe Asn Thr Leu Gly Pro	
20 25 30	
Leu Leu Ser Pro Ala Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn	
35 40 45	
Ala Asn His Gly Gln Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg	
50 55 60	
Thr Arg Ala Leu Val Val His Gly Ala Gly Thr Asp Glu Ile Ala Val	
65 70 75 80	
His Gly Thr Thr Leu Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu	
85 90 95	
His Tyr Thr Ile Glu Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu	
100 105 110	
Glu Asp Leu Val Gly Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg	
115 120 125	
Ala Thr Phe Ala Gly Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala	
130 135 140	
Ala Ser Ala Gly Ala Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu	
145 150 155 160	
Lys Asp Gly Ala Gln Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr	
165 170 175	
Gln Ala Trp Leu Ala Lys His Glu Glu Ile Asp Tyr Ser Glu Lys Glu	
180 185 190	
Ser Ser Asn Asp	
195	

<210> 419  
 <211> 1677  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (101)..(1654)  
 <223> RXN00957

<400> 419

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aaccggcaag ccctggatcg aatgaagctc gcagcgagta attatttgat gtttcccaga 60

aaggcttcag ccccaaatg atttcctcgg taggtgcccc atg agc acg aat ccc 115
                                   Met Ser Thr Asn Pro
                                   1 5

cat gtt ttc tcc cta gat gtc cgc tat cac gag gat gct tct gca ttg 163
His Val Phe Ser Leu Asp Val Arg Tyr His Glu Asp Ala Ser Ala Leu
                                   10 15 20

ttt gcc cac ttg ggt ggc aca acc gca gat gat gca gcc ctg ttg gaa 211
Phe Ala His Leu Gly Gly Thr Thr Ala Asp Asp Ala Ala Leu Leu Glu
                                   25 30 35

agc gct gat atc acc acc aag aat ggt att tct tcc ctc gcg gtg ttg 259
Ser Ala Asp Ile Thr Thr Lys Asn Gly Ile Ser Ser Leu Ala Val Leu
                                   40 45 50

aag agt tcg gtg cgc att acg tgc acg ggc aac acg gtg gta acg cag 307
Lys Ser Ser Val Arg Ile Thr Cys Thr Gly Asn Thr Val Val Thr Gln
                                   55 60 65

ccg ctg acg gac tcg ggt agg gca gtg gtt gcg cgc cta acg cag cag 355
Pro Leu Thr Asp Ser Gly Arg Ala Val Val Ala Arg Leu Thr Gln Gln
                                   70 75 80 85

ctt ggc cag tac aac acc gca gag aac acc ttt agc ttc ccc gcc tca 403
Leu Gly Gln Tyr Asn Thr Ala Glu Asn Thr Phe Ser Phe Pro Ala Ser
                                   90 95 100

gat gcg gtt gat gag cgc gag cgc ctc acc gca cca agc acc atc gaa 451
Asp Ala Val Asp Glu Arg Glu Arg Leu Thr Ala Pro Ser Thr Ile Glu
                                   105 110 115

gtg ctg cgc aag ttg cag ttc gag tcc ggt tac agc gac gcg tcc ctg 499
Val Leu Arg Lys Leu Gln Phe Glu Ser Gly Tyr Ser Asp Ala Ser Leu
                                   120 125 130

cca ctg ctc atg ggc ggt ttc gcg ttt gat ttc tta gaa acc ttt gaa 547
Pro Leu Leu Met Gly Gly Phe Ala Phe Asp Phe Leu Glu Thr Phe Glu
                                   135 140 145

acg ctc ccc gct gtc gag gag agc gtc aac act tac ccc gat tac cag 595
Thr Leu Pro Ala Val Glu Glu Ser Val Asn Thr Tyr Pro Asp Tyr Gln
                                   150 155 160 165

ttc gtc ctc gcg gaa atc gtc ctg gac atc aat cac cag gac cag acc 643
Phe Val Leu Ala Glu Ile Val Leu Asp Ile Asn His Gln Asp Gln Thr
                                   170 175 180

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gcc	aaa	ctc	gcc	ggc	gtc	tcc	aac	gcc	cca	ggc	gag	ctc	gag	gcc	gag	691
Ala	Lys	Leu	Ala	Gly	Val	Ser	Asn	Ala	Pro	Gly	Glu	Leu	Glu	Ala	Glu	
		185						190					195			
ctc	aac	aag	ctt	tca	ttg	ctt	atc	gac	gcc	gcc	ctc	ccc	gca	acc	gaa	739
Leu	Asn	Lys	Leu	Ser	Leu	Leu	Ile	Asp	Ala	Ala	Leu	Pro	Ala	Thr	Glu	
		200					205					210				
cac	gcc	tac	caa	acc	acc	cct	cac	gac	ggc	gac	act	ctt	cgc	gtt	gtg	787
His	Ala	Tyr	Gln	Thr	Thr	Pro	His	Asp	Gly	Asp	Thr	Leu	Arg	Val	Val	
	215					220					225					
gct	gat	att	ccc	gat	gct	cag	ttc	cgc	acc	cag	atc	aat	gag	ctg	aaa	835
Ala	Asp	Ile	Pro	Asp	Ala	Gln	Phe	Arg	Thr	Gln	Ile	Asn	Glu	Leu	Lys	
230					235				240						245	
gaa	aac	att	tac	aac	ggc	gac	atc	tac	caa	gtt	gtc	ccg	gcg	cgc	act	883
Glu	Asn	Ile	Tyr	Asn	Gly	Asp	Ile	Tyr	Gln	Val	Val	Pro	Ala	Arg	Thr	
				250					255					260		
ttc	acc	gca	cca	tgt	cct	gat	gca	ttc	gct	gct	tat	ctg	cag	ctg	cgt	931
Phe	Thr	Ala	Pro	Cys	Pro	Asp	Ala	Phe	Ala	Ala	Tyr	Leu	Gln	Leu	Arg	
			265				270						275			
gcc	acc	aac	ccg	tcg	ccg	tac	atg	ttc	tat	atc	cgt	ggc	ctc	aac	gaa	979
Ala	Thr	Asn	Pro	Ser	Pro	Tyr	Met	Phe	Tyr	Ile	Arg	Gly	Leu	Asn	Glu	
		280					285					290				
ggc	cgc	tcc	tat	gaa	ctt	ttt	ggc	gca	tcc	cct	gag	tcc	aac	ctc	aag	1027
Gly	Arg	Ser	Tyr	Glu	Leu	Phe	Gly	Ala	Ser	Pro	Glu	Ser	Asn	Leu	Lys	
		295				300					305					
ttc	acc	gct	gct	aac	cgt	gag	ctg	cag	ctg	tac	cca	atc	gca	ggt	acc	1075
Phe	Thr	Ala	Ala	Asn	Arg	Glu	Leu	Gln	Leu	Tyr	Pro	Ile	Ala	Gly	Thr	
310					315					320					325	
cgc	ccc	cgt	gga	ctc	aac	cca	gat	ggc	tcc	atc	aac	gat	gag	cta	gat	1123
Arg	Pro	Arg	Gly	Leu	Asn	Pro	Asp	Gly	Ser	Ile	Asn	Asp	Glu	Leu	Asp	
				330					335					340		
atc	cgc	aat	gag	ttg	gat	atg	cgc	act	gat	gcc	aaa	gag	atc	gcg	gag	1171
Ile	Arg	Asn	Glu	Leu	Asp	Met	Arg	Thr	Asp	Ala	Lys	Glu	Ile	Ala	Glu	
			345					350					355			
cac	acc	atg	ctt	gtc	gat	ctc	gcc	cgc	aac	gac	ctg	gcc	cgc	gtc	tcg	1219
His	Thr	Met	Leu	Val	Asp	Leu	Ala	Arg	Asn	Asp	Leu	Ala	Arg	Val	Ser	
		360					365					370				
gtc	cca	gcg	tcg	cgc	cgg	gtt	gcg	gat	ctt	ttg	cag	gtg	gat	cgc	tat	1267
Val	Pro	Ala	Ser	Arg	Arg	Val	Ala	Asp	Leu	Leu	Gln	Val	Asp	Arg	Tyr	
		375				380					385					
tcc	cgc	gtg	atg	cac	ttg	gtg	tcc	cgt	gtg	acg	gcg	acg	ttg	gac	cca	1315
Ser	Arg	Val	Met	His	Leu	Val	Ser	Arg	Val	Thr	Ala	Thr	Leu	Asp	Pro	
390					395					400					405	
gag	ctt	gat	gct	ttg	gac	gcc	tat	cgg	gcg	tgc	atg	aat	atg	ggc	acg	1363
Glu	Leu	Asp	Ala	Leu	Asp	Ala	Tyr	Arg	Ala	Cys	Met	Asn	Met	Gly	Thr	
				410					415					420		
ttg	acc	ggc	gct	ccg	aag	ttg	cgc	gct	atg	gag	ctg	ttg	cgc	ggc	gtc	1411

Leu Thr Gly Ala Pro Lys Leu Arg Ala Met Glu Leu Leu Arg Gly Val  
 425 430 435  
 gaa aag cgc agg cgt ggt tct tat ggt ggg gca gtg ggg tac ctg cgc 1459  
 Glu Lys Arg Arg Arg Gly Ser Tyr Gly Gly Ala Val Gly Tyr Leu Arg  
 440 445 450  
 ggc aat ggc gat atg gat aat tgc att gtt att cgt tcg gcg ttt gtc 1507  
 Gly Asn Gly Asp Met Asp Asn Cys Ile Val Ile Arg Ser Ala Phe Val  
 455 460 465  
 cag gat ggt gtg gct gct gtg cag gct ggt gct ggt gtg gtc cgc gat 1555  
 Gln Asp Gly Val Ala Ala Val Gln Ala Gly Ala Gly Val Val Arg Asp  
 470 475 480 485  
 tct aat cct caa tct gaa gcc gat gag acg ttg cac aag gcg tat gcc 1603  
 Ser Asn Pro Gln Ser Glu Ala Asp Glu Thr Leu His Lys Ala Tyr Ala  
 490 495 500  
 gtg ttg aat gcc att gcg ctt gct gct ggt tcc act ttg gag gtc atc 1651  
 Val Leu Asn Ala Ile Ala Leu Ala Ala Gly Ser Thr Leu Glu Val Ile  
 505 510 515  
 cga tgacacacgt tggttctcatt gat 1677  
 Arg

&lt;210&gt; 420

&lt;211&gt; 518

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 420

Met Ser Thr Asn Pro His Val Phe Ser Leu Asp Val Arg Tyr His Glu  
 1 5 10 15  
 Asp Ala Ser Ala Leu Phe Ala His Leu Gly Gly Thr Thr Ala Asp Asp  
 20 25 30  
 Ala Ala Leu Leu Glu Ser Ala Asp Ile Thr Thr Lys Asn Gly Ile Ser  
 35 40 45  
 Ser Leu Ala Val Leu Lys Ser Ser Val Arg Ile Thr Cys Thr Gly Asn  
 50 55 60  
 Thr Val Val Thr Gln Pro Leu Thr Asp Ser Gly Arg Ala Val Val Ala  
 65 70 75 80  
 Arg Leu Thr Gln Gln Leu Gly Gln Tyr Asn Thr Ala Glu Asn Thr Phe  
 85 90 95  
 Ser Phe Pro Ala Ser Asp Ala Val Asp Glu Arg Glu Arg Leu Thr Ala  
 100 105 110  
 Pro Ser Thr Ile Glu Val Leu Arg Lys Leu Gln Phe Glu Ser Gly Tyr  
 115 120 125  
 Ser Asp Ala Ser Leu Pro Leu Leu Met Gly Gly Phe Ala Phe Asp Phe  
 130 135 140

Leu Glu Thr Phe Glu Thr Leu Pro Ala Val Glu Glu Ser Val Asn Thr  
 145 150 155 160  
 Tyr Pro Asp Tyr Gln Phe Val Leu Ala Glu Ile Val Leu Asp Ile Asn  
 165 170 175  
 His Gln Asp Gln Thr Ala Lys Leu Ala Gly Val Ser Asn Ala Pro Gly  
 180 185 190  
 Glu Leu Glu Ala Glu Leu Asn Lys Leu Ser Leu Leu Ile Asp Ala Ala  
 195 200 205  
 Leu Pro Ala Thr Glu His Ala Tyr Gln Thr Thr Pro His Asp Gly Asp  
 210 215 220  
 Thr Leu Arg Val Val Ala Asp Ile Pro Asp Ala Gln Phe Arg Thr Gln  
 225 230 235 240  
 Ile Asn Glu Leu Lys Glu Asn Ile Tyr Asn Gly Asp Ile Tyr Gln Val  
 245 250 255  
 Val Pro Ala Arg Thr Phe Thr Ala Pro Cys Pro Asp Ala Phe Ala Ala  
 260 265 270  
 Tyr Leu Gln Leu Arg Ala Thr Asn Pro Ser Pro Tyr Met Phe Tyr Ile  
 275 280 285  
 Arg Gly Leu Asn Glu Gly Arg Ser Tyr Glu Leu Phe Gly Ala Ser Pro  
 290 295 300  
 Glu Ser Asn Leu Lys Phe Thr Ala Ala Asn Arg Glu Leu Gln Leu Tyr  
 305 310 315 320  
 Pro Ile Ala Gly Thr Arg Pro Arg Gly Leu Asn Pro Asp Gly Ser Ile  
 325 330 335  
 Asn Asp Glu Leu Asp Ile Arg Asn Glu Leu Asp Met Arg Thr Asp Ala  
 340 345 350  
 Lys Glu Ile Ala Glu His Thr Met Leu Val Asp Leu Ala Arg Asn Asp  
 355 360 365  
 Leu Ala Arg Val Ser Val Pro Ala Ser Arg Arg Val Ala Asp Leu Leu  
 370 375 380  
 Gln Val Asp Arg Tyr Ser Arg Val Met His Leu Val Ser Arg Val Thr  
 385 390 395 400  
 Ala Thr Leu Asp Pro Glu Leu Asp Ala Leu Asp Ala Tyr Arg Ala Cys  
 405 410 415  
 Met Asn Met Gly Thr Leu Thr Gly Ala Pro Lys Leu Arg Ala Met Glu  
 420 425 430  
 Leu Leu Arg Gly Val Glu Lys Arg Arg Arg Gly Ser Tyr Gly Gly Ala  
 435 440 445  
 Val Gly Tyr Leu Arg Gly Asn Gly Asp Met Asp Asn Cys Ile Val Ile  
 450 455 460  
 Arg Ser Ala Phe Val Gln Asp Gly Val Ala Ala Val Gln Ala Gly Ala

465                      470                      475                      480

Gly Val Val Arg Asp Ser Asn Pro Gln Ser Glu Ala Asp Glu Thr Leu  
                                  485                      490                      495

His Lys Ala Tyr Ala Val Leu Asn Ala Ile Ala Leu Ala Ala Gly Ser  
                                  500                      505                      510

Thr Leu Glu Val Ile Arg  
                                  515

<210> 421  
 <211> 1151  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(1128)  
 <223> FRXA00957

<400> 421

gat	ttc	tta	gaa	acc	ttt	gaa	acg	ctc	ccc	gct	gtc	gag	gag	agc	gtc	48
Asp	Phe	Leu	Glu	Thr	Phe	Glu	Thr	Leu	Pro	Ala	Val	Glu	Glu	Ser	Val	
1				5					10					15		
aac	act	tac	ccc	gat	tac	cag	ttc	gtc	ctc	gcg	gaa	atc	gtc	ctg	gac	96
Asn	Thr	Tyr	Pro	Asp	Tyr	Gln	Phe	Val	Leu	Ala	Glu	Ile	Val	Leu	Asp	
			20					25					30			
atc	aat	cac	cag	gac	cag	acc	gcc	aaa	ctc	gcc	ggc	gtc	tcc	aac	gcc	144
Ile	Asn	His	Gln	Asp	Gln	Thr	Ala	Lys	Leu	Ala	Gly	Val	Ser	Asn	Ala	
			35				40					45				
cca	ggc	gag	ctc	gag	gcc	gag	ctc	aac	aag	ctt	tca	ttg	ctt	atc	gac	192
Pro	Gly	Glu	Leu	Glu	Ala	Glu	Leu	Asn	Lys	Leu	Ser	Leu	Leu	Ile	Asp	
	50					55					60					
gcc	gcc	ctc	ccc	gca	acc	gaa	cac	gcc	tac	caa	acc	acc	cct	cac	gac	240
Ala	Ala	Leu	Pro	Ala	Thr	Glu	His	Ala	Tyr	Gln	Thr	Thr	Pro	His	Asp	
	65				70				75						80	
ggc	gac	act	ctt	cgc	gtt	gtg	gct	gat	att	ccc	gat	gct	cag	ttc	cgc	288
Gly	Asp	Thr	Leu	Arg	Val	Val	Ala	Asp	Ile	Pro	Asp	Ala	Gln	Phe	Arg	
				85					90					95		
acc	cag	atc	aat	gag	ctg	aaa	gaa	aac	att	tac	aac	ggt	gac	atc	tac	336
Thr	Gln	Ile	Asn	Glu	Leu	Lys	Glu	Asn	Ile	Tyr	Asn	Gly	Asp	Ile	Tyr	
			100					105					110			
caa	gtt	gtc	ccg	gcg	cgc	act	ttc	acc	gca	cca	tgt	cct	gat	gca	ttc	384
Gln	Val	Val	Pro	Ala	Arg	Thr	Phe	Thr	Ala	Pro	Cys	Pro	Asp	Ala	Phe	
	115						120					125				
gct	gct	tat	ctg	cag	ctg	cgt	gcc	acc	aac	ccg	tcg	ccg	tac	atg	ttc	432
Ala	Ala	Tyr	Leu	Gln	Leu	Arg	Ala	Thr	Asn	Pro	Ser	Pro	Tyr	Met	Phe	
	130					135					140					
tat	atc	cgt	ggc	ctc	aac	gaa	ggc	cgc	tcc	tat	gaa	ctt	ttt	ggc	gca	480
Tyr	Ile	Arg	Gly	Leu	Asn	Glu	Gly	Arg	Ser	Tyr	Glu	Leu	Phe	Gly	Ala	



145	150	155	160	
tcc cct gag tcc aac ctc aag ttc acc gct gct aac cgt gag ctg cag				528
Ser Pro Glu Ser Asn Leu Lys Phe Thr Ala Ala Asn Arg Glu Leu Gln	165	170	175	
ctg tac cca atc gca ggt acc cgc ccc cgt gga ctc aac cca gat ggc				576
Leu Tyr Pro Ile Ala Gly Thr Arg Pro Arg Gly Leu Asn Pro Asp Gly	180	185	190	
tcc atc aac gat gag cta gat atc cgc aat gag ttg gat atg cgc act				624
Ser Ile Asn Asp Glu Leu Asp Ile Arg Asn Glu Leu Asp Met Arg Thr	195	200	205	
gat gcc aaa gag atc gcg gag cac acc atg ctt gtc gat ctc gcc cgc				672
Asp Ala Lys Glu Ile Ala Glu His Thr Met Leu Val Asp Leu Ala Arg	210	215	220	
aac gac ctg gcc cgc gtc tcg gtc cca gcg tcg cgc cgg gtt gcg gat				720
Asn Asp Leu Ala Arg Val Ser Val Pro Ala Ser Arg Arg Val Ala Asp	225	230	235	240
ctt ttg cag gtg gat cgc tat tcc cgc gtg atg cac ttg gtg tcc cgt				768
Leu Leu Gln Val Asp Arg Tyr Ser Arg Val Met His Leu Val Ser Arg	245	250	255	
gtg acg gcg acg ttg gac cca gag ctt gat gct ttg gac gcc tat cgg				816
Val Thr Ala Thr Leu Asp Pro Glu Leu Asp Ala Leu Asp Ala Tyr Arg	260	265	270	
gcg tgc atg aat atg ggc acg ttg acc ggc gct ccg aag ttg cgc gct				864
Ala Cys Met Asn Met Gly Thr Leu Thr Gly Ala Pro Lys Leu Arg Ala	275	280	285	
atg gag ctg ttg cgc ggc gtc gaa aag cgc agg cgt ggt tct tat ggt				912
Met Glu Leu Leu Arg Gly Val Glu Lys Arg Arg Arg Gly Ser Tyr Gly	290	295	300	
ggg gca gtg ggg tac ctg cgc ggc aat ggc gat atg gat aat tgc att				960
Gly Ala Val Gly Tyr Leu Arg Gly Asn Gly Asp Met Asp Asn Cys Ile	305	310	315	320
gtt att cgt tcg gcg ttt gtc cag gat ggt gtg gct gct gtg cag gct				1008
Val Ile Arg Ser Ala Phe Val Gln Asp Gly Val Ala Ala Val Gln Ala	325	330	335	
ggt gct ggt gtg gtc cgc gat tct aat cct caa tct gaa gcc gat gag				1056
Gly Ala Gly Val Val Arg Asp Ser Asn Pro Gln Ser Glu Ala Asp Glu	340	345	350	
acg ttg cac aag gcg tat gcc gtg ttg aat gcc att gcg ctt gct gct				1104
Thr Leu His Lys Ala Tyr Ala Val Leu Asn Ala Ile Ala Leu Ala Ala	355	360	365	
ggt tcc act ttg gag gtc atc cga tgacacacgt tgtttctcatt gat				1151
Gly Ser Thr Leu Glu Val Ile Arg	370	375		

&lt;210&gt; 422

&lt;211&gt; 376

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 422

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Asp Phe Leu Glu Thr Phe Glu Thr Leu Pro Ala Val Glu Glu Ser Val
  1              5              10              15

Asn Thr Tyr Pro Asp Tyr Gln Phe Val Leu Ala Glu Ile Val Leu Asp
      20              25              30

Ile Asn His Gln Asp Gln Thr Ala Lys Leu Ala Gly Val Ser Asn Ala
      35              40              45

Pro Gly Glu Leu Glu Ala Glu Leu Asn Lys Leu Ser Leu Leu Ile Asp
      50              55              60

Ala Ala Leu Pro Ala Thr Glu His Ala Tyr Gln Thr Thr Pro His Asp
      65              70              75              80

Gly Asp Thr Leu Arg Val Val Ala Asp Ile Pro Asp Ala Gln Phe Arg
      85              90              95

Thr Gln Ile Asn Glu Leu Lys Glu Asn Ile Tyr Asn Gly Asp Ile Tyr
      100              105              110

Gln Val Val Pro Ala Arg Thr Phe Thr Ala Pro Cys Pro Asp Ala Phe
      115              120              125

Ala Ala Tyr Leu Gln Leu Arg Ala Thr Asn Pro Ser Pro Tyr Met Phe
      130              135              140

Tyr Ile Arg Gly Leu Asn Glu Gly Arg Ser Tyr Glu Leu Phe Gly Ala
      145              150              155              160

Ser Pro Glu Ser Asn Leu Lys Phe Thr Ala Ala Asn Arg Glu Leu Gln
      165              170              175

Leu Tyr Pro Ile Ala Gly Thr Arg Pro Arg Gly Leu Asn Pro Asp Gly
      180              185              190

Ser Ile Asn Asp Glu Leu Asp Ile Arg Asn Glu Leu Asp Met Arg Thr
      195              200              205

Asp Ala Lys Glu Ile Ala Glu His Thr Met Leu Val Asp Leu Ala Arg
      210              215              220

Asn Asp Leu Ala Arg Val Ser Val Pro Ala Ser Arg Arg Val Ala Asp
      225              230              235              240

Leu Leu Gln Val Asp Arg Tyr Ser Arg Val Met His Leu Val Ser Arg
      245              250              255

Val Thr Ala Thr Leu Asp Pro Glu Leu Asp Ala Leu Asp Ala Tyr Arg
      260              265              270

Ala Cys Met Asn Met Gly Thr Leu Thr Gly Ala Pro Lys Leu Arg Ala
      275              280              285

Met Glu Leu Leu Arg Gly Val Glu Lys Arg Arg Arg Gly Ser Tyr Gly
      290              295              300

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Gly Ala Val Gly Tyr Leu Arg Gly Asn Gly Asp Met Asp Asn Cys Ile  
 305 310 315 320

Val Ile Arg Ser Ala Phe Val Gln Asp Gly Val Ala Ala Val Gln Ala  
 325 330 335

Gly Ala Gly Val Val Arg Asp Ser Asn Pro Gln Ser Glu Ala Asp Glu  
 340 345 350

Thr Leu His Lys Ala Tyr Ala Val Leu Asn Ala Ile Ala Leu Ala Ala  
 355 360 365

Gly Ser Thr Leu Glu Val Ile Arg  
 370 375

&lt;210&gt; 423

&lt;211&gt; 1068

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1045)

&lt;223&gt; RXA02687

&lt;400&gt; 423

caaaaccatg ctcggcgggg gagagttggg ccaagcgggt cgctaattga gcaacagaca 60

tggacaccca ccttagttcg gcgggttaag ctgtgtaacc atg agc gac gca cca 115  
 Met Ser Asp Ala Pro  
 1 5

act gtt gtg gcc tat ttg ggg cct gcc gga acc ttc acc gaa gaa gcc 163  
 Thr Val Val Ala Tyr Leu Gly Pro Ala Gly Thr Phe Thr Glu Glu Ala  
 10 15 20

ctc tac aaa ttt gcc gac gcc ggc gta ttc ggc gac ggt gag atc gag 211  
 Leu Tyr Lys Phe Ala Asp Ala Gly Val Phe Gly Asp Gly Glu Ile Glu  
 25 30 35

cag cta cca gcc aaa tcg cca caa gaa gct gtc gac gcc gtc cgc cac 259  
 Gln Leu Pro Ala Lys Ser Pro Gln Glu Ala Val Asp Ala Val Arg His  
 40 45 50

ggc acc gcc cag ttc gcg gtg gtc gcc atc gaa aac ttc gtc gac ggc 307  
 Gly Thr Ala Gln Phe Ala Val Val Ala Ile Glu Asn Phe Val Asp Gly  
 55 60 65

ccc gtc acc ccc acc ttc gac gcc ctt gac cag ggc tcc aac gtg caa 355  
 Pro Val Thr Pro Thr Phe Asp Ala Leu Asp Gln Gly Ser Asn Val Gln  
 70 75 80 85

atc atc gcc gaa gaa gaa ctc gac atc gcc ttt tcc atc atg gtc cgg 403  
 Ile Ile Ala Glu Glu Glu Leu Asp Ile Ala Phe Ser Ile Met Val Arg  
 90 95 100

cca ggg act tcg ctt gcc gac gtc aaa acc ctc gcc acc cac ccg gtt 451  
 Pro Gly Thr Ser Leu Ala Asp Val Lys Thr Leu Ala Thr His Pro Val  
 105 110 115

ggg tac caa caa gtg aaa aac tgg atg gca acc acc att ccg gac gcc 499  
 Gly Tyr Gln Gln Val Lys Asn Trp Met Ala Thr Thr Ile Pro Asp Ala  
 120 125 130

atg tat ctt tca gca agc tcc aac ggc gcc ggc gca caa atg gtt gcc 547  
 Met Tyr Leu Ser Ala Ser Ser Asn Gly Ala Gly Ala Gln Met Val Ala  
 135 140 145

gaa gga acc gcc gac gca gcc gca gcg ccc tcc cgc gca gcc gaa ctc 595  
 Glu Gly Thr Ala Asp Ala Ala Ala Pro Ser Arg Ala Ala Glu Leu  
 150 155 160 165

ttc gga ctg gaa cgc ctt gtt gat gat gtc gcc gac gtc cgt ggc gcc 643  
 Phe Gly Leu Glu Arg Leu Val Asp Asp Val Ala Asp Val Arg Gly Ala  
 170 175 180

cgc acc cgc ttc gtt gct gtc caa gcc caa gca gcc gtt tcc gaa ccg 691  
 Arg Thr Arg Phe Val Ala Val Gln Ala Gln Ala Ala Val Ser Glu Pro  
 185 190 195

acc ggc cac gac cgc acc tcc gtc att ttc tcc cta ccg aat gtg cca 739  
 Thr Gly His Asp Arg Thr Ser Val Ile Phe Ser Leu Pro Asn Val Pro  
 200 205 210

ggc agc ctc gtg cgc gcc ctc aac gaa ttc gcc atc cgc ggc gtt gac 787  
 Gly Ser Leu Val Arg Ala Leu Asn Glu Phe Ala Ile Arg Gly Val Asp  
 215 220 225

ctc acc cgc atc gaa tcc cgc ccc acc cgc aaa gtc ttc gga acc tac 835  
 Leu Thr Arg Ile Glu Ser Arg Pro Thr Arg Lys Val Phe Gly Thr Tyr  
 230 235 240 245

cgc ttc cac ctg gac ata tcc gga cat atc cgc gat atc ccc gtc gcc 883  
 Arg Phe His Leu Asp Ile Ser Gly His Ile Arg Asp Ile Pro Val Ala  
 250 255 260

gaa gcc ctc cgc gca ctc cac ctc caa gcc gaa gaa ctc gtc ttc gtc 931  
 Glu Ala Leu Arg Ala Leu His Leu Gln Ala Glu Glu Leu Val Phe Val  
 265 270 275

ggc tcc tgg ccc tcc aac cgt gcg gaa gac agc acg ccc caa acc gac 979  
 Gly Ser Trp Pro Ser Asn Arg Ala Glu Asp Ser Thr Pro Gln Thr Asp  
 280 285 290

caa cta gct aag cta cac aag gcg gac gaa tgg gtt cgc gca gca agc 1027  
 Gln Leu Ala Lys Leu His Lys Ala Asp Glu Trp Val Arg Ala Ala Ser  
 295 300 305

gaa gga agg aaa ctt aac tagccatggc cggccggatt att 1068  
 Glu Gly Arg Lys Leu Asn  
 310 315

&lt;210&gt; 424

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 424

Met Ser Asp Ala Pro Thr Val Val Ala Tyr Leu Gly Pro Ala Gly Thr  
 1 5 10 15

Phe Thr Glu Glu Ala Leu Tyr Lys Phe Ala Asp Ala Gly Val Phe Gly  
                     20                    25                    30  
 Asp Gly Glu Ile Glu Gln Leu Pro Ala Lys Ser Pro Gln Glu Ala Val  
                     35                    40                    45  
 Asp Ala Val Arg His Gly Thr Ala Gln Phe Ala Val Val Ala Ile Glu  
                     50                    55                    60  
 Asn Phe Val Asp Gly Pro Val Thr Pro Thr Phe Asp Ala Leu Asp Gln  
                     65                    70                    75                    80  
 Gly Ser Asn Val Gln Ile Ile Ala Glu Glu Glu Leu Asp Ile Ala Phe  
                     85                    90                    95  
 Ser Ile Met Val Arg Pro Gly Thr Ser Leu Ala Asp Val Lys Thr Leu  
                     100                    105                    110  
 Ala Thr His Pro Val Gly Tyr Gln Gln Val Lys Asn Trp Met Ala Thr  
                     115                    120                    125  
 Thr Ile Pro Asp Ala Met Tyr Leu Ser Ala Ser Ser Asn Gly Ala Gly  
                     130                    135                    140  
 Ala Gln Met Val Ala Glu Gly Thr Ala Asp Ala Ala Ala Pro Ser  
                     145                    150                    155                    160  
 Arg Ala Ala Glu Leu Phe Gly Leu Glu Arg Leu Val Asp Asp Val Ala  
                     165                    170                    175  
 Asp Val Arg Gly Ala Arg Thr Arg Phe Val Ala Val Gln Ala Gln Ala  
                     180                    185                    190  
 Ala Val Ser Glu Pro Thr Gly His Asp Arg Thr Ser Val Ile Phe Ser  
                     195                    200                    205  
 Leu Pro Asn Val Pro Gly Ser Leu Val Arg Ala Leu Asn Glu Phe Ala  
                     210                    215                    220  
 Ile Arg Gly Val Asp Leu Thr Arg Ile Glu Ser Arg Pro Thr Arg Lys  
                     225                    230                    235                    240  
 Val Phe Gly Thr Tyr Arg Phe His Leu Asp Ile Ser Gly His Ile Arg  
                     245                    250                    255  
 Asp Ile Pro Val Ala Glu Ala Leu Arg Ala Leu His Leu Gln Ala Glu  
                     260                    265                    270  
 Glu Leu Val Phe Val Gly Ser Trp Pro Ser Asn Arg Ala Glu Asp Ser  
                     275                    280                    285  
 Thr Pro Gln Thr Asp Gln Leu Ala Lys Leu His Lys Ala Asp Glu Trp  
                     290                    295                    300  
 Val Arg Ala Ala Ser Glu Gly Arg Lys Leu Asn  
                     305                    310                    315

&lt;210&gt; 425

&lt;211&gt; 1353

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1330)

&lt;223&gt; RXN01698

&lt;400&gt; 425

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cgctagtgcc tgcagttatg tcgcttttttg acgtcgaaaa gcaatttttaa aaagcccttg 60
gggtgggctg gatacgtctt ctgcggcctt tcgtgcgata atg cta ggc atg ctt 115
                                         Met Leu Gly Met Leu
                                         1 5

cga tgg act aca gca ggt gaa tcc cac ggc cag gcg ctt atc gcc acg 163
Arg Trp Thr Thr Ala Gly Glu Ser His Gly Gln Ala Leu Ile Ala Thr
                        10 15 20

gtt gaa cac atg cca gca ggc gtg ccc gtg act aaa gat gag gtc tcg 211
Val Glu His Met Pro Ala Gly Val Pro Val Thr Lys Asp Glu Val Ser
                        25 30 35

tat caa ttg gcg cgc cga cgc ctt gga tat ggt cgc ggc gct cgc atg 259
Tyr Gln Leu Ala Arg Arg Arg Leu Gly Tyr Gly Arg Gly Ala Arg Met
                        40 45 50

aag ttt gag caa gac gcg ttg acc ttc ctc acc ggc atc cgc cac ggc 307
Lys Phe Glu Gln Asp Ala Leu Thr Phe Leu Thr Gly Ile Arg His Gly
                        55 60 65

ctc act ttg ggt agc ccc atc tca atc atg atc ggc aac act gag tgg 355
Leu Thr Leu Gly Ser Pro Ile Ser Ile Met Ile Gly Asn Thr Glu Trp
                        70 75 80 85

gat aag tgg acc acc atc atg tcc tct gac gct ttg gac atg gaa gac 403
Asp Lys Trp Thr Thr Ile Met Ser Ser Asp Ala Leu Asp Met Glu Asp
                        90 95 100

cca gat aac gtt gcg gcg atg tct tcg ggt cgg ggc gca aaa ctg act 451
Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg Gly Ala Lys Leu Thr
                        105 110 115

cgt ccg cgt cca ggc cac gct gat tac gca ggc atg ctc aag tac gga 499
Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly Met Leu Lys Tyr Gly
                        120 125 130

ttc gat gat gcc cgc aac gtg ctg gag cgt tct tca gcc cgt gag acg 547
Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser Ser Ala Arg Glu Thr
                        135 140 145

gca gca cgc gtg gca gca gca acc gtt gcg cgt tcc ttc ctg cgt gaa 595
Ala Ala Arg Val Ala Ala Ala Thr Val Ala Arg Ser Phe Leu Arg Glu
                        150 155 160 165

acc ttg ggc gtg gaa gtg ctt tcc cac gta att tcc att ggt gcg tcc 643
Thr Leu Gly Val Glu Val Leu Ser His Val Ile Ser Ile Gly Ala Ser
                        170 175 180

gag cct tac act ggc gcg gag cca acc ttt gca gat att caa gca atc 691
Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala Asp Ile Gln Ala Ile

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185					190					195						
gat	gat	tcc	cca	gtt	cgt	gca	ttc	ggg	aaa	gac	gct	gaa	gaa	tcc	atg	739
Asp	Asp	Ser	Pro	Val	Arg	Ala	Phe	Gly	Lys	Asp	Ala	Glu	Glu	Ser	Met	
		200					205					210				
atc	gcg	gaa	atc	gag	gcc	gca	aag	aaa	gcc	ggc	gat	acc	ctc	ggg	ggc	787
Ile	Ala	Glu	Ile	Glu	Ala	Ala	Lys	Lys	Ala	Gly	Asp	Thr	Leu	Gly	Gly	
	215					220					225					
atc	gtg	gaa	gtg	att	gtt	gaa	ggc	ctg	ccc	atc	ggg	ttg	ggc	tca	cac	835
Ile	Val	Glu	Val	Ile	Val	Glu	Gly	Leu	Pro	Ile	Gly	Leu	Gly	Ser	His	
	230					235				240					245	
att	tct	ggc	gaa	gat	cgc	ctc	gat	gcg	cag	atc	gca	gct	gca	ctc	atg	883
Ile	Ser	Gly	Glu	Asp	Arg	Leu	Asp	Ala	Gln	Ile	Ala	Ala	Ala	Leu	Met	
				250					255					260		
ggc	att	cag	gcc	atc	aag	ggc	gtg	gaa	atc	ggg	gac	ggg	ttc	gaa	gaa	931
Gly	Ile	Gln	Ala	Ile	Lys	Gly	Val	Glu	Ile	Gly	Asp	Gly	Phe	Glu	Glu	
		265						270					275			
gct	cgt	cga	cgt	ggc	tcc	gaa	gcc	cac	gat	gaa	gtg	ttc	ctg	gat	gac	979
Ala	Arg	Arg	Arg	Gly	Ser	Glu	Ala	His	Asp	Glu	Val	Phe	Leu	Asp	Asp	
		280					285					290				
aac	ggc	gta	tac	cgc	aac	acc	aac	cgt	gca	ggg	ggc	ctc	gaa	ggc	ggc	1027
Asn	Gly	Val	Tyr	Arg	Asn	Thr	Asn	Arg	Ala	Gly	Gly	Leu	Glu	Gly	Gly	
	295					300					305					
atg	acc	aac	ggg	gaa	acc	ctg	cgc	gtt	cgt	gct	ggc	atg	aag	cca	att	1075
Met	Thr	Asn	Gly	Glu	Thr	Leu	Arg	Val	Arg	Ala	Gly	Met	Lys	Pro	Ile	
	310					315				320					325	
tct	act	gtg	cct	cgc	gcc	ctg	aaa	acc	att	gat	atg	gaa	aac	ggc	aag	1123
Ser	Thr	Val	Pro	Arg	Ala	Leu	Lys	Thr	Ile	Asp	Met	Glu	Asn	Gly	Lys	
				330					335					340		
gca	gca	acc	gga	atc	cac	cag	cgt	tcc	gac	gtg	tgc	gct	gtt	cca	gcc	1171
Ala	Ala	Thr	Gly	Ile	His	Gln	Arg	Ser	Asp	Val	Cys	Ala	Val	Pro	Ala	
		345					350						355			
gcc	ggg	gtc	gtt	gca	gaa	gca	atg	gtc	acc	ctg	gtt	ctc	gcc	cgc	gca	1219
Ala	Gly	Val	Val	Ala	Glu	Ala	Met	Val	Thr	Leu	Val	Leu	Ala	Arg	Ala	
		360					365					370				
gtc	ctg	cag	aaa	ttc	ggc	ggg	gac	tcc	ctg	agc	gaa	acc	aag	agc	aac	1267
Val	Leu	Gln	Lys	Phe	Gly	Gly	Asp	Ser	Leu	Ser	Glu	Thr	Lys	Ser	Asn	
	375					380					385					
att	gac	acc	tac	ctc	aaa	aac	att	gag	gaa	cga	atg	aaa	ttc	gaa	ggg	1315
Ile	Asp	Thr	Tyr	Leu	Lys	Asn	Ile	Glu	Glu	Arg	Met	Lys	Phe	Glu	Gly	
	390					395				400					405	
tta	gag	gat	gga	gcg	taatgaagtg	aatgatcaaa	ttc									1353
Leu	Glu	Asp	Gly	Ala												
				410												

&lt;210&gt; 426

&lt;211&gt; 410

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 426

Met	Leu	Gly	Met	Leu	Arg	Trp	Thr	Thr	Ala	Gly	Glu	Ser	His	Gly	Gln
1				5					10					15	
Ala	Leu	Ile	Ala	Thr	Val	Glu	His	Met	Pro	Ala	Gly	Val	Pro	Val	Thr
			20					25					30		
Lys	Asp	Glu	Val	Ser	Tyr	Gln	Leu	Ala	Arg	Arg	Arg	Leu	Gly	Tyr	Gly
		35					40					45			
Arg	Gly	Ala	Arg	Met	Lys	Phe	Glu	Gln	Asp	Ala	Leu	Thr	Phe	Leu	Thr
	50					55					60				
Gly	Ile	Arg	His	Gly	Leu	Thr	Leu	Gly	Ser	Pro	Ile	Ser	Ile	Met	Ile
65					70					75					80
Gly	Asn	Thr	Glu	Trp	Asp	Lys	Trp	Thr	Thr	Ile	Met	Ser	Ser	Asp	Ala
				85					90					95	
Leu	Asp	Met	Glu	Asp	Pro	Asp	Asn	Val	Ala	Ala	Met	Ser	Ser	Gly	Arg
			100					105						110	
Gly	Ala	Lys	Leu	Thr	Arg	Pro	Arg	Pro	Gly	His	Ala	Asp	Tyr	Ala	Gly
		115					120					125			
Met	Leu	Lys	Tyr	Gly	Phe	Asp	Asp	Ala	Arg	Asn	Val	Leu	Glu	Arg	Ser
	130					135					140				
Ser	Ala	Arg	Glu	Thr	Ala	Ala	Arg	Val	Ala	Ala	Ala	Thr	Val	Ala	Arg
145					150					155					160
Ser	Phe	Leu	Arg	Glu	Thr	Leu	Gly	Val	Glu	Val	Leu	Ser	His	Val	Ile
				165					170					175	
Ser	Ile	Gly	Ala	Ser	Glu	Pro	Tyr	Thr	Gly	Ala	Glu	Pro	Thr	Phe	Ala
			180					185						190	
Asp	Ile	Gln	Ala	Ile	Asp	Asp	Ser	Pro	Val	Arg	Ala	Phe	Gly	Lys	Asp
		195					200					205			
Ala	Glu	Glu	Ser	Met	Ile	Ala	Glu	Ile	Glu	Ala	Ala	Lys	Lys	Ala	Gly
	210					215						220			
Asp	Thr	Leu	Gly	Gly	Ile	Val	Glu	Val	Ile	Val	Glu	Gly	Leu	Pro	Ile
225					230					235					240
Gly	Leu	Gly	Ser	His	Ile	Ser	Gly	Glu	Asp	Arg	Leu	Asp	Ala	Gln	Ile
				245					250					255	
Ala	Ala	Ala	Leu	Met	Gly	Ile	Gln	Ala	Ile	Lys	Gly	Val	Glu	Ile	Gly
			260					265					270		
Asp	Gly	Phe	Glu	Glu	Ala	Arg	Arg	Arg	Gly	Ser	Glu	Ala	His	Asp	Glu
		275					280					285			
Val	Phe	Leu	Asp	Asp	Asn	Gly	Val	Tyr	Arg	Asn	Thr	Asn	Arg	Ala	Gly
		290				295					300				



Gly Leu Glu Gly Gly Met Thr Asn Gly Glu Thr Leu Arg Val Arg Ala  
 305 310 315 320  
 Gly Met Lys Pro Ile Ser Thr Val Pro Arg Ala Leu Lys Thr Ile Asp  
 325 330 335  
 Met Glu Asn Gly Lys Ala Ala Thr Gly Ile His Gln Arg Ser Asp Val  
 340 345 350  
 Cys Ala Val Pro Ala Ala Gly Val Val Ala Glu Ala Met Val Thr Leu  
 355 360 365  
 Val Leu Ala Arg Ala Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser  
 370 375 380  
 Glu Thr Lys Ser Asn Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg  
 385 390 395 400  
 Met Lys Phe Glu Gly Leu Glu Asp Gly Ala  
 405 410

<210> 427  
 <211> 1013  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(990)  
 <223> FRXA01698

<400> 427  
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 Gly Asn Thr Glu Trp Asp Lys Trp Thr Thr Ile Met Ser Ser Asp Ala  
 1 5 10 15  
 ttg gac atg gaa gac cca gat aac gtt gcg gcg atg tct tcg ggt cgg 96  
 Leu Asp Met Glu Asp Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg  
 20 25 30  
 ggc gca aaa ctg act cgt ccg cgt cca ggc cac gct gat tac gca ggc 144  
 Gly Ala Lys Leu Thr Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly  
 35 40 45  
 atg ctc aag tac gga ttc gat gat gcc cgc aac gtg ctg gag cgt tct 192  
 Met Leu Lys Tyr Gly Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser  
 50 55 60  
 tca gcc cgt gag acg gca gca cgc gtg gca gca gca acc gtt gcg cgt 240  
 Ser Ala Arg Glu Thr Ala Ala Arg Val Ala Ala Ala Thr Val Ala Arg  
 65 70 75 80  
 tcc ttc ctg cgt gaa acc ttg ggc gtg gaa gtg ctt tcc cac gta att 288  
 Ser Phe Leu Arg Glu Thr Leu Gly Val Glu Val Leu Ser His Val Ile  
 85 90 95  
 tcc att ggt gcg tcc gag cct tac act ggc gcg gag cca acc ttt gca 336  
 Ser Ile Gly Ala Ser Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala  
 100 105 110

gat att caa gca atc gat gat tcc cca gtt cgt gca ttc ggt aaa gac	384
Asp Ile Gln Ala Ile Asp Asp Ser Pro Val Arg Ala Phe Gly Lys Asp	
115 120 125	
gct gaa gaa tcc atg atc gcg gaa atc gag gcc gca aag aaa gcc ggc	432
Ala Glu Glu Ser Met Ile Ala Glu Ile Glu Ala Ala Lys Lys Ala Gly	
130 135 140	
gat acc ctc ggt ggc atc gtg gaa gtg att gtt gaa ggc ctg ccc atc	480
Asp Thr Leu Gly Gly Ile Val Glu Val Ile Val Glu Gly Leu Pro Ile	
145 150 155 160	
ggt ttg ggc tca cac att tct ggc gaa gat cgc ctc gat gcg cag atc	528
Gly Leu Gly Ser His Ile Ser Gly Glu Asp Arg Leu Asp Ala Gln Ile	
165 170 175	
gca gct gca ctc atg ggc att cag gcc atc aag ggc gtg gaa atc ggt	576
Ala Ala Ala Leu Met Gly Ile Gln Ala Ile Lys Gly Val Glu Ile Gly	
180 185 190	
gac ggt ttc gaa gaa gct cgt cga cgt ggc tcc gaa gcc cac gat gaa	624
Asp Gly Phe Glu Glu Ala Arg Arg Arg Gly Ser Glu Ala His Asp Glu	
195 200 205	
gtg ttc ctg gat gac aac ggc gta tac cgc aac acc aac cgt gca ggt	672
Val Phe Leu Asp Asp Asn Gly Val Tyr Arg Asn Thr Asn Arg Ala Gly	
210 215 220	
ggc ctc gaa ggc ggc atg acc aac ggt gaa acc ctg cgc gtt cgt gct	720
Gly Leu Glu Gly Gly Met Thr Asn Gly Glu Thr Leu Arg Val Arg Ala	
225 230 235 240	
ggc atg aag cca att tct act gtg cct cgc gcc ctg aaa acc att gat	768
Gly Met Lys Pro Ile Ser Thr Val Pro Arg Ala Leu Lys Thr Ile Asp	
245 250 255	
atg gaa aac ggc aag gca gca acc gga atc cac cag cgt tcc gac gtg	816
Met Glu Asn Gly Lys Ala Ala Thr Gly Ile His Gln Arg Ser Asp Val	
260 265 270	
tgc gct gtt cca gcc gcc ggt gtc gtt gca gaa gca atg gtc acc ctg	864
Cys Ala Val Pro Ala Ala Gly Val Val Ala Glu Ala Met Val Thr Leu	
275 280 285	
gtt ctc gcc cgc gca gtc ctg cag aaa ttc ggc ggt gac tcc ctg agc	912
Val Leu Ala Arg Ala Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser	
290 295 300	
gaa acc aag agc aac att gac acc tac ctc aaa aac att gag gaa cga	960
Glu Thr Lys Ser Asn Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg	
305 310 315 320	
atg aaa ttc gaa ggt tta gag gat gga gcg taatgaagtg aatgatcaaa	1010
Met Lys Phe Glu Gly Leu Glu Asp Gly Ala	
325 330	
ttc	1013

&lt;210&gt; 428

&lt;211&gt; 330

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 428

Gly Asn Thr Glu Trp Asp Lys Trp Thr Thr Ile Met Ser Ser Asp Ala  
 1 5 10 15  
 Leu Asp Met Glu Asp Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg  
 20 25 30  
 Gly Ala Lys Leu Thr Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly  
 35 40 45  
 Met Leu Lys Tyr Gly Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser  
 50 55 60  
 Ser Ala Arg Glu Thr Ala Ala Arg Val Ala Ala Ala Thr Val Ala Arg  
 65 70 75 80  
 Ser Phe Leu Arg Glu Thr Leu Gly Val Glu Val Leu Ser His Val Ile  
 85 90 95  
 Ser Ile Gly Ala Ser Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala  
 100 105 110  
 Asp Ile Gln Ala Ile Asp Asp Ser Pro Val Arg Ala Phe Gly Lys Asp  
 115 120 125  
 Ala Glu Glu Ser Met Ile Ala Glu Ile Glu Ala Ala Lys Lys Ala Gly  
 130 135 140  
 Asp Thr Leu Gly Gly Ile Val Glu Val Ile Val Glu Gly Leu Pro Ile  
 145 150 155 160  
 Gly Leu Gly Ser His Ile Ser Gly Glu Asp Arg Leu Asp Ala Gln Ile  
 165 170 175  
 Ala Ala Ala Leu Met Gly Ile Gln Ala Ile Lys Gly Val Glu Ile Gly  
 180 185 190  
 Asp Gly Phe Glu Glu Ala Arg Arg Arg Gly Ser Glu Ala His Asp Glu  
 195 200 205  
 Val Phe Leu Asp Asp Asn Gly Val Tyr Arg Asn Thr Asn Arg Ala Gly  
 210 215 220  
 Gly Leu Glu Gly Gly Met Thr Asn Gly Glu Thr Leu Arg Val Arg Ala  
 225 230 235 240  
 Gly Met Lys Pro Ile Ser Thr Val Pro Arg Ala Leu Lys Thr Ile Asp  
 245 250 255  
 Met Glu Asn Gly Lys Ala Ala Thr Gly Ile His Gln Arg Ser Asp Val  
 260 265 270  
 Cys Ala Val Pro Ala Ala Gly Val Val Ala Glu Ala Met Val Thr Leu  
 275 280 285  
 Val Leu Ala Arg Ala Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser  
 290 295 300

Glu Thr Lys Ser Asn Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg  
 305 310 315 320

Met Lys Phe Glu Gly Leu Glu Asp Gly Ala  
 325 330

<210> 429

<211> 906

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(883)

<223> RXA01095

<400> 429

gaaaccccag gtcaaagcta ggggtgtggca ccttgatttc tttcgccatg tgtgttcggg 60  
 ataaccttaa acacagcatt gggttgaagg aggttggggc atg gtt gca aca gag 115  
 Met Val Ala Thr Glu  
 1 5  
 aac cgc atg ttg atg gaa atc gct gcg gaa ata tcg gct cgg gaa gca 163  
 Asn Arg Met Leu Met Glu Ile Ala Ala Glu Ile Ser Ala Arg Glu Ala  
 10 15 20  
 acg ctt ggt ttt caa gaa gtc aaa act aaa tct cga tca gca ggt ctc 211  
 Thr Leu Gly Phe Gln Glu Val Lys Thr Lys Ser Arg Ser Ala Gly Leu  
 25 30 35  
 acg gcg gct ttc gat att gct tca gtc ttt ttt tcg tct gga tgt aat 259  
 Thr Ala Ala Phe Asp Ile Ala Ser Val Phe Phe Ser Ser Gly Cys Asn  
 40 45 50  
 gtc gta gtc gcc ttt gat cgt ttt gca tcc aat tgg tct gat cat tcg 307  
 Val Val Val Ala Phe Asp Arg Phe Ala Ser Asn Trp Ser Asp His Ser  
 55 60 65  
 gat cat gtg gac tac gct gca cag gtt gcg ggt ttt ggc gca tca atg 355  
 Asp His Val Asp Tyr Ala Ala Gln Val Ala Gly Phe Gly Ala Ser Met  
 70 75 80 85  
 ctt gca tat acg gtg cgc agg gga cag ttt gat acc gca gta cgc gat 403  
 Leu Ala Tyr Thr Val Arg Arg Gly Gln Phe Asp Thr Ala Val Arg Asp  
 90 95 100  
 atc agg gac atc aaa tct gaa gta gac att ccc att ctg ctt cat gat 451  
 Ile Arg Asp Ile Lys Ser Glu Val Asp Ile Pro Ile Leu Leu His Asp  
 105 110 115  
 ccc atc atc gat ccg tat caa atc cac gaa gcc cgc gtc atg ggc atc 499  
 Pro Ile Ile Asp Pro Tyr Gln Ile His Glu Ala Arg Val Met Gly Ile  
 120 125 130  
 gac gct ctt caa ttc ccc gta tgg gcg atg gaa caa gct cga ctg gaa 547  
 Asp Ala Leu Gln Phe Pro Val Trp Ala Met Glu Gln Ala Arg Leu Glu  
 135 140 145  
 tct ttg gtg gac cgc acc gaa tca ttg ggc atg aca gcc atc gtg tct 595

Ser Leu Val Asp Arg Thr Glu Ser Leu Gly Met Thr Ala Ile Val Ser  
 150 155 160 165

gtg cga aac cac gaa gaa gcg cat cgt gca gtg gac gca gga gcg aca 643  
 Val Arg Asn His Glu Glu Ala His Arg Ala Val Asp Ala Gly Ala Thr  
 170 175 180

gtg gta gca att gat att act ggt tat acc ggc tca ctc act ttg cct 691  
 Val Val Ala Ile Asp Ile Thr Gly Tyr Thr Gly Ser Leu Thr Leu Pro  
 185 190 195

gaa gcg ttt tgc ggt atc acc caa ttc atg ccc aaa gag gta gcc cgc 739  
 Glu Ala Phe Ser Gly Ile Thr Gln Phe Met Pro Lys Glu Val Ala Arg  
 200 205 210

att gtg ctc gga ggt tgc agc agc cct aaa gaa ctc atg cgg ttt gca 787  
 Ile Val Leu Gly Gly Cys Ser Ser Pro Lys Glu Leu Met Arg Phe Ala  
 215 220 225

cga cat tct gca gac gcc atc ttt gtt cca cat gca gac ctc gcc acc 835  
 Arg His Ser Ala Asp Ala Ile Phe Val Pro His Ala Asp Leu Ala Thr  
 230 235 240 245

aca aaa tct ctt gtg aca gca ggt atg cat cca gcg tgc cca tgc cgt 883  
 Thr Lys Ser Leu Val Thr Ala Gly Met His Pro Ala Cys Pro Ser Arg  
 250 255 260

tgaagagggtg ctctgtggtc agc 906

&lt;210&gt; 430

&lt;211&gt; 261

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 430

Met Val Ala Thr Glu Asn Arg Met Leu Met Glu Ile Ala Ala Glu Ile  
 1 5 10 15

Ser Ala Arg Glu Ala Thr Leu Gly Phe Gln Glu Val Lys Thr Lys Ser  
 20 25 30

Arg Ser Ala Gly Leu Thr Ala Ala Phe Asp Ile Ala Ser Val Phe Phe  
 35 40 45

Ser Ser Gly Cys Asn Val Val Val Ala Phe Asp Arg Phe Ala Ser Asn  
 50 55 60

Trp Ser Asp His Ser Asp His Val Asp Tyr Ala Ala Gln Val Ala Gly  
 65 70 75 80

Phe Gly Ala Ser Met Leu Ala Tyr Thr Val Arg Arg Gly Gln Phe Asp  
 85 90 95

Thr Ala Val Arg Asp Ile Arg Asp Ile Lys Ser Glu Val Asp Ile Pro  
 100 105 110

Ile Leu Leu His Asp Pro Ile Ile Asp Pro Tyr Gln Ile His Glu Ala  
 115 120 125

Arg Val Met Gly Ile Asp Ala Leu Gln Phe Pro Val Trp Ala Met Glu

130	135	140
Gln Ala Arg Leu Glu Ser Leu Val Asp Arg Thr Glu Ser Leu Gly Met		
145	150	155 160
Thr Ala Ile Val Ser Val Arg Asn His Glu Glu Ala His Arg Ala Val		
	165	170 175
Asp Ala Gly Ala Thr Val Val Ala Ile Asp Ile Thr Gly Tyr Thr Gly		
	180	185 190
Ser Leu Thr Leu Pro Glu Ala Phe Ser Gly Ile Thr Gln Phe Met Pro		
	195	200 205
Lys Glu Val Ala Arg Ile Val Leu Gly Gly Cys Ser Ser Pro Lys Glu		
	210	215 220
Leu Met Arg Phe Ala Arg His Ser Ala Asp Ala Ile Phe Val Pro His		
	225	230 235 240
Ala Asp Leu Ala Thr Thr Lys Ser Leu Val Thr Ala Gly Met His Pro		
	245	250 255
Ala Cys Pro Ser Arg		
	260	

<210> 431  
 <211> 1545  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1522)  
 <223> RXA00955

<400> 431  
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 aagcacgaag agatcgatta ctcagaaaag gagtcttcca atg act agt aat aat 115  
 Met Thr Ser Asn Asn  
 1 5  
 ctg ccc aca gtg ttg gaa agc atc gtc gag ggt cgt cgc gga cac ctg 163  
 Leu Pro Thr Val Leu Glu Ser Ile Val Glu Gly Arg Arg Gly His Leu  
 10 15 20  
 gag gaa att cgc gct cgc atc gct cac gtg gat gtg gat gcg ctt cca 211  
 Glu Glu Ile Arg Ala Arg Ile Ala His Val Asp Val Asp Ala Leu Pro  
 25 30 35  
 aaa tcc acc cgt tct ctg ttt gat tcc ctc aac cag ggt agg gga ggg 259  
 Lys Ser Thr Arg Ser Leu Phe Asp Ser Leu Asn Gln Gly Arg Gly Gly  
 40 45 50  
 gcg cgt ttc atc atg gag tgc aag tcc gca tcg cct tct ttg gga atg 307  
 Ala Arg Phe Ile Met Glu Cys Lys Ser Ala Ser Pro Ser Leu Gly Met  
 55 60 65  
 att cgt gag cac tac cag ccg ggt gaa atc gct cgc gtg tac tct cgc 355

Ile	Arg	Glu	His	Tyr	Gln	Pro	Gly	Glu	Ile	Ala	Arg	Val	Tyr	Ser	Arg		
70					75					80					85		
tac	gcc	agc	ggc	att	tcc	gtg	ctg	tgc	gag	ccg	gat	cgt	ttt	ggg	ggc		403
Tyr	Ala	Ser	Gly	Ile	Ser	Val	Leu	Cys	Glu	Pro	Asp	Arg	Phe	Gly	Gly		
				90				95						100			
gat	tac	gat	cac	ctc	gct	acc	gtt	gcc	gct	acc	tct	cat	ctt	ccg	gtg		451
Asp	Tyr	Asp	His	Leu	Ala	Thr	Val	Ala	Ala	Thr	Ser	His	Leu	Pro	Val		
			105					110					115				
ctg	tgc	aaa	gac	ttc	atc	att	gat	cct	gtc	cag	gta	cac	gcg	gcg	cgt		499
Leu	Cys	Lys	Asp	Phe	Ile	Ile	Asp	Pro	Val	Gln	Val	His	Ala	Ala	Arg		
		120					125					130					
tac	ttt	ggg	gct	gat	gcc	atc	ctg	ctc	atg	ctc	tct	gtg	ctt	gat	gat		547
Tyr	Phe	Gly	Ala	Asp	Ala	Ile	Leu	Leu	Met	Leu	Ser	Val	Leu	Asp	Asp		
	135					140					145						
gaa	gag	tac	gca	gca	ctc	gct	gcc	gag	gct	gcg	cgt	ttt	gat	ctg	gat		595
Glu	Glu	Tyr	Ala	Ala	Leu	Ala	Ala	Glu	Ala	Ala	Arg	Phe	Asp	Leu	Asp		
150					155					160					165		
atc	ctc	acc	gag	gtt	att	gat	gag	gag	gaa	gtc	gcc	cgc	gcc	atc	aag		643
Ile	Leu	Thr	Glu	Val	Ile	Asp	Glu	Glu	Glu	Val	Ala	Arg	Ala	Ile	Lys		
				170				175						180			
ctg	ggg	gcg	aag	atc	ttt	ggc	gtc	aac	cac	cgc	aac	ctg	cat	gat	ctg		691
Leu	Gly	Ala	Lys	Ile	Phe	Gly	Val	Asn	His	Arg	Asn	Leu	His	Asp	Leu		
			185					190					195				
tcc	att	gat	ttg	gat	cgt	tca	cgt	cgc	ctg	tcc	aag	ctc	att	cca	gca		739
Ser	Ile	Asp	Leu	Asp	Arg	Ser	Arg	Arg	Leu	Ser	Lys	Leu	Ile	Pro	Ala		
		200					205					210					
gat	gcc	gtg	ctc	gtg	tct	gag	tct	ggc	gtg	cgc	gat	acc	gaa	acc	gtc		787
Asp	Ala	Val	Leu	Val	Ser	Glu	Ser	Gly	Val	Arg	Asp	Thr	Glu	Thr	Val		
	215					220					225						
cgc	cag	cta	ggg	ggg	cac	tcc	aat	gca	ttc	ctc	gtt	ggc	tcc	cag	ctg		835
Arg	Gln	Leu	Gly	Gly	His	Ser	Asn	Ala	Phe	Leu	Val	Gly	Ser	Gln	Leu		
230					235					240					245		
acc	agc	cag	gaa	aac	gtc	gat	ctg	gca	gcc	cgc	gaa	tta	gtc	tac	ggc		883
Thr	Ser	Gln	Glu	Asn	Val	Asp	Leu	Ala	Ala	Arg	Glu	Leu	Val	Tyr	Gly		
				250				255						260			
ccc	aac	aaa	gtc	tgc	gga	ctc	acc	tca	cca	agt	gca	gca	caa	acc	gct		931
Pro	Asn	Lys	Val	Cys	Gly	Leu	Thr	Ser	Pro	Ser	Ala	Ala	Gln	Thr	Ala		
			265				270						275				
cgc	gca	gcg	ggg	gcg	gtc	tac	ggc	ggg	ctc	atc	ttc	gaa	gag	gca	tcg		979
Arg	Ala	Ala	Gly	Ala	Val	Tyr	Gly	Gly	Leu	Ile	Phe	Glu	Glu	Ala	Ser		
		280					285					290					
cca	cgc	aat	gtt	tca	cgt	gaa	aca	ttg	caa	aaa	atc	atc	gcc	gca	gag		1027
Pro	Arg	Asn	Val	Ser	Arg	Glu	Thr	Leu	Gln	Lys	Ile	Ile	Ala	Ala	Glu		
		295				300					305						
ccc	aac	ctg	cgc	tac	gtc	gcg	gtc	agc	cgt	cgc	acc	tcc	ggg	tac	aag		1075
Pro	Asn	Leu	Arg	Tyr	Val	Ala	Val	Ser	Arg	Arg	Thr	Ser	Gly	Tyr	Lys		

310	315	320	325	
gat ttg ctt gtc gac ggc atc ttc gcc gta caa atc cac gcc cca ctg				1123
Asp Leu Leu Val Asp Gly Ile Phe Ala Val Gln Ile His Ala Pro Leu				
	330	335	340	
cag gac agc gtc gaa gca gaa aag gca ttg atc gcc gcc gtt cgt gaa				1171
Gln Asp Ser Val Glu Ala Glu Lys Ala Leu Ile Ala Ala Val Arg Glu				
	345	350	355	
gag gtt gga ccg cag gtc cag gtc tgg cgc gcg atc tcg atg tcc agc				1219
Glu Val Gly Pro Gln Val Gln Val Trp Arg Ala Ile Ser Met Ser Ser				
	360	365	370	
ccc ttg ggg gct gaa gtg gca gct gcg gtg gag ggt gac gtc gat aag				1267
Pro Leu Gly Ala Glu Val Ala Ala Val Glu Gly Asp Val Asp Lys				
	375	380	385	
cta att ctt gat gcc cat gaa ggt ggc agc ggg gaa gta ttc gac tgg				1315
Leu Ile Leu Asp Ala His Glu Gly Gly Ser Gly Glu Val Phe Asp Trp				
	390	395	400	405
gct acg gtg ccg gcc gct gtg aag gca aag tct ttg ctc gcg gga ggc				1363
Ala Thr Val Pro Ala Ala Val Lys Ala Lys Ser Leu Leu Ala Gly Gly				
	410	415	420	
atc tct ccg gac aac gct gcg cag gca ctc gct gtg ggc tgc gca ggt				1411
Ile Ser Pro Asp Asn Ala Ala Gln Ala Leu Ala Val Gly Cys Ala Gly				
	425	430	435	
ttg gac atc aac tct ggc gtg gaa tac ccc gcc ggt gca ggc acg tgg				1459
Leu Asp Ile Asn Ser Gly Val Glu Tyr Pro Ala Gly Ala Gly Thr Trp				
	440	445	450	
gct ggg gcg aaa gac gcc ggc gcg ctg ctg aaa att tta gcg acc atc				1507
Ala Gly Ala Lys Asp Ala Gly Ala Leu Leu Lys Ile Leu Ala Thr Ile				
	455	460	465	
tcc aca ttc cat tac taaagggttta aataggatca tga				1545
Ser Thr Phe His Tyr				
470				

&lt;210&gt; 432

&lt;211&gt; 474

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 432

Met Thr Ser Asn Asn Leu Pro Thr Val Leu Glu Ser Ile Val Glu Gly
1 5 10 15

Arg Arg Gly His Leu Glu Glu Ile Arg Ala Arg Ile Ala His Val Asp
20 25 30

Val Asp Ala Leu Pro Lys Ser Thr Arg Ser Leu Phe Asp Ser Leu Asn
35 40 45

Gln Gly Arg Gly Gly Ala Arg Phe Ile Met Glu Cys Lys Ser Ala Ser
50 55 60



Pro Ser Leu Gly Met Ile Arg Glu His Tyr Gln Pro Gly Glu Ile Ala  
 65 70 75 80  
 Arg Val Tyr Ser Arg Tyr Ala Ser Gly Ile Ser Val Leu Cys Glu Pro  
 85 90 95  
 Asp Arg Phe Gly Gly Asp Tyr Asp His Leu Ala Thr Val Ala Ala Thr  
 100 105 110  
 Ser His Leu Pro Val Leu Cys Lys Asp Phe Ile Ile Asp Pro Val Gln  
 115 120 125  
 Val His Ala Ala Arg Tyr Phe Gly Ala Asp Ala Ile Leu Leu Met Leu  
 130 135 140  
 Ser Val Leu Asp Asp Glu Glu Tyr Ala Ala Leu Ala Ala Glu Ala Ala  
 145 150 155 160  
 Arg Phe Asp Leu Asp Ile Leu Thr Glu Val Ile Asp Glu Glu Glu Val  
 165 170 175  
 Ala Arg Ala Ile Lys Leu Gly Ala Lys Ile Phe Gly Val Asn His Arg  
 180 185 190  
 Asn Leu His Asp Leu Ser Ile Asp Leu Asp Arg Ser Arg Arg Leu Ser  
 195 200 205  
 Lys Leu Ile Pro Ala Asp Ala Val Leu Val Ser Glu Ser Gly Val Arg  
 210 215 220  
 Asp Thr Glu Thr Val Arg Gln Leu Gly Gly His Ser Asn Ala Phe Leu  
 225 230 235 240  
 Val Gly Ser Gln Leu Thr Ser Gln Glu Asn Val Asp Leu Ala Ala Arg  
 245 250 255  
 Glu Leu Val Tyr Gly Pro Asn Lys Val Cys Gly Leu Thr Ser Pro Ser  
 260 265 270  
 Ala Ala Gln Thr Ala Arg Ala Ala Gly Ala Val Tyr Gly Gly Leu Ile  
 275 280 285  
 Phe Glu Glu Ala Ser Pro Arg Asn Val Ser Arg Glu Thr Leu Gln Lys  
 290 295 300  
 Ile Ile Ala Ala Glu Pro Asn Leu Arg Tyr Val Ala Val Ser Arg Arg  
 305 310 315 320  
 Thr Ser Gly Tyr Lys Asp Leu Leu Val Asp Gly Ile Phe Ala Val Gln  
 325 330 335  
 Ile His Ala Pro Leu Gln Asp Ser Val Glu Ala Glu Lys Ala Leu Ile  
 340 345 350  
 Ala Ala Val Arg Glu Glu Val Gly Pro Gln Val Gln Val Trp Arg Ala  
 355 360 365  
 Ile Ser Met Ser Ser Pro Leu Gly Ala Glu Val Ala Ala Ala Val Glu  
 370 375 380  
 Gly Asp Val Asp Lys Leu Ile Leu Asp Ala His Glu Gly Gly Ser Gly

385		390		395		400
Glu Val Phe Asp Trp	Ala Thr Val Pro	Ala Ala Val Lys	Ala Lys Ser			
	405		410			415
Leu Leu Ala Gly	Gly Ile Ser Pro	Asn Ala Ala Gln	Ala Leu Ala			
	420		425			430
Val Gly Cys Ala Gly	Leu Asp Ile Asn	Ser Gly Val Glu	Tyr Pro Ala			
	435		440			445
Gly Ala Gly Thr Trp	Ala Gly Ala Lys	Asp Ala Gly	Ala Leu Leu Lys			
	450		455			460
Ile Leu Ala Thr Ile	Ser Thr Phe His	Tyr				
	465		470			

&lt;210&gt; 433

&lt;211&gt; 494

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(471)

&lt;223&gt; RXA02814

&lt;400&gt; 433

gcc aaa aac cta gaa gaa cac tcc tac gtg gtc aac cac ctg cgc acc	48
Ala Lys Asn Leu Glu Glu His Ser Tyr Val Val Asn His Leu Arg Thr	
1 5 10 15	
atc ctg gaa cca ctg tgc tca caa ttc gac gcc cca aca gtt cct gaa	96
Ile Leu Glu Pro Leu Cys Ser Gln Phe Asp Ala Pro Thr Val Pro Glu	
20 25 30	
ctg acc aaa acc aac gaa atg tgg cac ctc gca aca ccc atc gtt ggc	144
Leu Thr Lys Thr Asn Glu Met Trp His Leu Ala Thr Pro Ile Val Gly	
35 40 45	
acc ctc aag tac cca cac atc acc gca cta gaa cta gcc ata cga aca	192
Thr Leu Lys Tyr Pro His Ile Thr Ala Leu Glu Leu Ala Ile Arg Thr	
50 55 60	
cac ccc acc ccc gcg atc tgt ggc acc ccc acc gac gcc gcc gaa gcc	240
His Pro Thr Pro Ala Ile Cys Gly Thr Pro Thr Asp Ala Ala Glu Ala	
65 70 75 80	
ctc atc atc gaa gcg gaa tcc ccc cga aac ttc tac gcc gga gca gcc	288
Leu Ile Ile Glu Ala Glu Ser Pro Arg Asn Phe Tyr Ala Gly Ala Ala	
85 90 95	
ggc tgg tgt gac tcc acc gga gac ggc gaa tac atg gta gcc atc cgc	336
Gly Trp Cys Asp Ser Thr Gly Asp Gly Glu Tyr Met Val Ala Ile Arg	
100 105 110	
tgc gcc gaa gta tcc gaa gac gga acc tgg gcc aga gca tgg gca ggc	384
Cys Ala Glu Val Ser Glu Asp Gly Thr Trp Ala Arg Ala Trp Ala Gly	
115 120 125	

gga ggc atc gtc gcc gaa tca gac gcc caa gaa gag ttt gat gaa acc 432  
 Gly Gly Ile Val Ala Glu Ser Asp Ala Gln Glu Glu Phe Asp Glu Thr  
 130 135 140

acc gcg aag ctc caa acc atc atg cgc tcg ctt ggt ttg tgagatgtgg 481  
 Thr Ala Lys Leu Gln Thr Ile Met Arg Ser Leu Gly Leu  
 145 150 155

tcttaaaaca ccg 494

<210> 434

<211> 157

<212> PRT

<213> Corynebacterium glutamicum

<400> 434

Ala Lys Asn Leu Glu Glu His Ser Tyr Val Val Asn His Leu Arg Thr  
 1 5 10 15

Ile Leu Glu Pro Leu Cys Ser Gln Phe Asp Ala Pro Thr Val Pro Glu  
 20 25 30

Leu Thr Lys Thr Asn Glu Met Trp His Leu Ala Thr Pro Ile Val Gly  
 35 40 45

Thr Leu Lys Tyr Pro His Ile Thr Ala Leu Glu Leu Ala Ile Arg Thr  
 50 55 60

His Pro Thr Pro Ala Ile Cys Gly Thr Pro Thr Asp Ala Ala Glu Ala  
 65 70 75 80

Leu Ile Ile Glu Ala Glu Ser Pro Arg Asn Phe Tyr Ala Gly Ala Ala  
 85 90 95

Gly Trp Cys Asp Ser Thr Gly Asp Gly Glu Tyr Met Val Ala Ile Arg  
 100 105 110

Cys Ala Glu Val Ser Glu Asp Gly Thr Trp Ala Arg Ala Trp Ala Gly  
 115 120 125

Gly Gly Ile Val Ala Glu Ser Asp Ala Gln Glu Glu Phe Asp Glu Thr  
 130 135 140

Thr Ala Lys Leu Gln Thr Ile Met Arg Ser Leu Gly Leu  
 145 150 155

<210> 435

<211> 803

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(780)

<223> RXA00229

<400> 435

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 Glu Ala Lys Gly Leu Ala Gln Gly Arg Ala Thr Val Tyr Arg Arg Ile

1					5					10					15	
gac	acg	ctt	ggg	tcg	cgt	gct	tcc	ggg	caa	gat	tta	aat	acg	ctt	ctc	96
Asp	Thr	Leu	Gly	Ser	Arg	Ala	Ser	Gly	Gln	Asp	Leu	Asn	Thr	Leu	Leu	
			20					25					30			
gac	gcc	gcc	ctc	tac	ctt	ggc	ttc	agc	ggc	ctg	aac	atc	act	cac	ccg	144
Asp	Ala	Ala	Leu	Tyr	Leu	Gly	Phe	Ser	Gly	Leu	Asn	Ile	Thr	His	Pro	
		35					40					45				
tac	aag	caa	gca	gta	tta	ccc	ctg	ctt	ggc	gaa	gtc	tcc	gaa	caa	gcc	192
Tyr	Lys	Gln	Ala	Val	Leu	Pro	Leu	Leu	Gly	Glu	Val	Ser	Glu	Gln	Ala	
	50					55					60					
acc	caa	ctc	ggc	gca	gtg	aat	act	gtc	gtt	atg	gac	gcc	acc	ggc	cac	240
Thr	Gln	Leu	Gly	Ala	Val	Asn	Thr	Val	Val	Met	Asp	Ala	Thr	Gly	His	
	65				70				75						80	
acc	acc	ggc	cac	aac	acc	gac	gtc	tcc	gga	ttt	ggc	cgc	gga	atg	gaa	288
Thr	Thr	Gly	His	Asn	Thr	Asp	Val	Ser	Gly	Phe	Gly	Arg	Gly	Met	Glu	
				85					90					95		
gaa	ggc	ctc	ccc	aac	gcc	aag	ctc	gat	tcc	gtc	gtg	cag	gtc	ggc	gcc	336
Glu	Gly	Leu	Pro	Asn	Ala	Lys	Leu	Asp	Ser	Val	Val	Gln	Val	Gly	Ala	
			100					105					110			
ggc	ggc	gta	gaa	aac	gca	gtg	gca	tac	gcc	ctg	gtc	acc	cac	ggt	gtg	384
Gly	Gly	Val	Glu	Asn	Ala	Val	Ala	Tyr	Ala	Leu	Val	Thr	His	Gly	Val	
		115					120					125				
cag	aaa	ctt	cag	gtc	gct	gac	ctc	gac	act	tcc	cgc	gcg	cag	gca	ctg	432
Gln	Lys	Leu	Gln	Val	Ala	Asp	Leu	Asp	Thr	Ser	Arg	Ala	Gln	Ala	Leu	
	130					135					140					
gca	gat	gtc	atc	aac	aac	gca	gtc	ggc	cgt	gaa	gcc	gtc	gtg	gga	gta	480
Ala	Asp	Val	Ile	Asn	Asn	Ala	Val	Gly	Arg	Glu	Ala	Val	Val	Gly	Val	
	145				150					155					160	
gac	gcc	cgc	ggc	atc	gaa	gac	gtc	atc	gcc	gcc	gcc	gac	gga	gta	gtc	528
Asp	Ala	Arg	Gly	Ile	Glu	Asp	Val	Ile	Ala	Ala	Ala	Asp	Gly	Val	Val	
				165				170						175		
aac	gca	acc	ccc	atg	gga	atg	cca	gca	cac	ccc	ggc	acc	gcc	ttt	gat	576
Asn	Ala	Thr	Pro	Met	Gly	Met	Pro	Ala	His	Pro	Gly	Thr	Ala	Phe	Asp	
			180					185					190			
gtc	agc	tgc	ctc	acc	aag	gat	cac	tgg	gtt	ggc	gac	gtc	gtg	tac	atg	624
Val	Ser	Cys	Leu	Thr	Lys	Asp	His	Trp	Val	Gly	Asp	Val	Val	Tyr	Met	
		195					200					205				
ccc	atc	gaa	act	gaa	ctt	ctc	aaa	gcc	gcc	cgt	gcc	ctc	ggc	tgc	gaa	672
Pro	Ile	Glu	Thr	Glu	Leu	Leu	Lys	Ala	Ala	Arg	Ala	Leu	Gly	Cys	Glu	
	210					215					220					
acc	ctc	gac	gga	acc	cgc	atg	gca	atc	cac	caa	gcc	gtc	gat	gcc	ttc	720
Thr	Leu	Asp	Gly	Thr	Arg	Met	Ala	Ile	His	Gln	Ala	Val	Asp	Ala	Phe	
	225				230					235					240	
cga	ctg	ttc	acc	ggc	ctc	gaa	ccc	gac	gtc	tcc	cgc	atg	cgg	gaa	act	768
Arg	Leu	Phe	Thr	Gly	Leu	Glu	Pro	Asp	Val	Ser	Arg	Met	Arg	Glu	Thr	
				245				250						255		

ttc ctg tcc ctc taaaagagtc agtaaacct cga  
 Phe Leu Ser Leu  
 260

803

&lt;210&gt; 436

&lt;211&gt; 260

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 436

Glu Ala Lys Gly Leu Ala Gln Gly Arg Ala Thr Val Tyr Arg Arg Ile  
 1 5 10 15

Asp Thr Leu Gly Ser Arg Ala Ser Gly Gln Asp Leu Asn Thr Leu Leu  
 20 25 30

Asp Ala Ala Leu Tyr Leu Gly Phe Ser Gly Leu Asn Ile Thr His Pro  
 35 40 45

Tyr Lys Gln Ala Val Leu Pro Leu Leu Gly Glu Val Ser Glu Gln Ala  
 50 55 60

Thr Gln Leu Gly Ala Val Asn Thr Val Val Met Asp Ala Thr Gly His  
 65 70 75 80

Thr Thr Gly His Asn Thr Asp Val Ser Gly Phe Gly Arg Gly Met Glu  
 85 90 95

Glu Gly Leu Pro Asn Ala Lys Leu Asp Ser Val Val Gln Val Gly Ala  
 100 105 110

Gly Gly Val Glu Asn Ala Val Ala Tyr Ala Leu Val Thr His Gly Val  
 115 120 125

Gln Lys Leu Gln Val Ala Asp Leu Asp Thr Ser Arg Ala Gln Ala Leu  
 130 135 140

Ala Asp Val Ile Asn Asn Ala Val Gly Arg Glu Ala Val Val Gly Val  
 145 150 155 160

Asp Ala Arg Gly Ile Glu Asp Val Ile Ala Ala Ala Asp Gly Val Val  
 165 170 175

Asn Ala Thr Pro Met Gly Met Pro Ala His Pro Gly Thr Ala Phe Asp  
 180 185 190

Val Ser Cys Leu Thr Lys Asp His Trp Val Gly Asp Val Val Tyr Met  
 195 200 205

Pro Ile Glu Thr Glu Leu Leu Lys Ala Ala Arg Ala Leu Gly Cys Glu  
 210 215 220

Thr Leu Asp Gly Thr Arg Met Ala Ile His Gln Ala Val Asp Ala Phe  
 225 230 235 240

Arg Leu Phe Thr Gly Leu Glu Pro Asp Val Ser Arg Met Arg Glu Thr  
 245 250 255

Phe Leu Ser Leu

260

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<210> 437
<211> 927
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(904)  
<223> RXA02093
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<400> 437															
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ttgctcttcc tttgctccgc atgagtataa aatcactgtc atg gtc aac tac gtc 115															
Met Val Asn Tyr Val 5															
gac agg gaa aca acc ctg tgc atc tct ctc gct gct cgt cca tcc aac 163															
Asp Arg Glu Thr Thr Leu Cys Ile Ser Leu Ala Ala Arg Pro Ser Asn 20															
cat ggt gtt cgt ttc cac aac tgg ctt tac gct gaa ctt gga ttg aac 211															
His Gly Val Arg Phe His Asn Trp Leu Tyr Ala Glu Leu Gly Leu Asn 35															
tac ctg tac aag gct gtt gcc cca gca gat atc acc gct gca gtc gca 259															
Tyr Leu Tyr Lys Ala Val Ala Pro Ala Asp Ile Thr Ala Ala Val Ala 40 45 50															
ggc atc cgt ggt ctg aac att cgc ggc gca ggt gtc tcc atg cca tac 307															
Gly Ile Arg Gly Leu Asn Ile Arg Gly Ala Gly Val Ser Met Pro Tyr 55 60 65															
aag agc gat gtc atc cca ctc atc gat gag ttg cat cct tcc gca gag 355															
Lys Ser Asp Val Ile Pro Leu Ile Asp Glu Leu His Pro Ser Ala Glu 70 75 80 85															
cgc ata cgt tct gtt aac acc atc gtc aac aat gac gga cac ctt gtc 403															
Arg Ile Arg Ser Val Asn Thr Ile Val Asn Asn Asp Gly His Leu Val 90 95 100															
gga tac aac acc gac tac act gcg gtg tac cac ctc ctt gaa gaa cac 451															
Gly Tyr Asn Thr Asp Tyr Thr Ala Val Tyr His Leu Leu Glu Glu His 105 110 115															
cgc gtg aac ccc aat gca cga gta gct atc aag gga tcc ggc ggc atg 499															
Arg Val Asn Pro Asn Ala Arg Val Ala Ile Lys Gly Ser Gly Gly Met 120 125 130															
gcc aat gct gtt gtt gca gct ctt gct gag tat ggt ctg agt ggc acc 547															
Ala Asn Ala Val Val Ala Ala Leu Ala Glu Tyr Gly Leu Ser Gly Thr 135 140 145															
gtc gtt gcc cgc aac cac acc acc ggt tct gcg cta gct tcc cgt tac 595															
Val Val Ala Arg Asn His Thr Thr Gly Ser Ala Leu Ala Ser Arg Tyr 150 155 160 165															
ggc tgg gaa tac tcc gca act gtt ccg gaa gac gca aaa att ttg gtt 643															

Gly	Trp	Glu	Tyr	Ser	Ala	Thr	Val	Pro	Glu	Asp	Ala	Lys	Ile	Leu	Val		
				170					175					180			
aat	gta	acc	cca	atg	gga	atg	aat	gga	cct	gac	caa	gac	gtt	gta	tct	691	
Asn	Val	Thr	Pro	Met	Gly	Met	Asn	Gly	Pro	Asp	Gln	Asp	Val	Val	Ser		
			185					190					195				
ttt	ggt	gag	gat	gaa	gta	gac	cga	gcc	gac	gta	atc	ttt	gac	tgc	gta	739	
Phe	Gly	Glu	Asp	Glu	Val	Asp	Arg	Ala	Asp	Val	Ile	Phe	Asp	Cys	Val		
		200					205					210					
gca	ttc	ccc	gtc	gag	acc	cca	ctg	att	aag	ttg	gcc	aag	gaa	aag	ggt	787	
Ala	Phe	Pro	Val	Glu	Thr	Pro	Leu	Ile	Lys	Leu	Ala	Lys	Glu	Lys	Gly		
	215					220					225						
aag	caa	acc	atc	gac	ggc	gga	gaa	gtt	gcc	gct	ctt	cag	gca	gca	gag	835	
Lys	Gln	Thr	Ile	Asp	Gly	Gly	Glu	Val	Ala	Ala	Leu	Gln	Ala	Ala	Glu		
230					235				240						245		
cag	ttc	cac	ctc	tac	acc	gga	gtt	ctt	cca	acc	aac	gac	cag	atc	att	883	
Gln	Phe	His	Leu	Tyr	Thr	Gly	Val	Leu	Pro	Thr	Asn	Asp	Gln	Ile	Ile		
			250					255					260				
gct	gcg	gag	gag	ttc	tcc	aag	taaattttctc	tcccctatatt	tta							927	
Ala	Ala	Glu	Glu	Phe	Ser	Lys											
			265														

<210> 438  
 <211> 268  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 438  
 Met Val Asn Tyr Val Asp Arg Glu Thr Thr Leu Cys Ile Ser Leu Ala  
 1 5 10 15  
 Ala Arg Pro Ser Asn His Gly Val Arg Phe His Asn Trp Leu Tyr Ala  
 20 25 30  
 Glu Leu Gly Leu Asn Tyr Leu Tyr Lys Ala Val Ala Pro Ala Asp Ile  
 35 40 45  
 Thr Ala Ala Val Ala Gly Ile Arg Gly Leu Asn Ile Arg Gly Ala Gly  
 50 55 60  
 Val Ser Met Pro Tyr Lys Ser Asp Val Ile Pro Leu Ile Asp Glu Leu  
 65 70 75 80  
 His Pro Ser Ala Glu Arg Ile Arg Ser Val Asn Thr Ile Val Asn Asn  
 85 90 95  
 Asp Gly His Leu Val Gly Tyr Asn Thr Asp Tyr Thr Ala Val Tyr His  
 100 105 110  
 Leu Leu Glu Glu His Arg Val Asn Pro Asn Ala Arg Val Ala Ile Lys  
 115 120 125  
 Gly Ser Gly Gly Met Ala Asn Ala Val Val Ala Ala Leu Ala Glu Tyr  
 130 135 140

Gly Leu Ser Gly Thr Val Val Ala Arg Asn His Thr Thr Gly Ser Ala  
 145 150 155 160  
 Leu Ala Ser Arg Tyr Gly Trp Glu Tyr Ser Ala Thr Val Pro Glu Asp  
 165 170 175  
 Ala Lys Ile Leu Val Asn Val Thr Pro Met Gly Met Asn Gly Pro Asp  
 180 185 190  
 Gln Asp Val Val Ser Phe Gly Glu Asp Glu Val Asp Arg Ala Asp Val  
 195 200 205  
 Ile Phe Asp Cys Val Ala Phe Pro Val Glu Thr Pro Leu Ile Lys Leu  
 210 215 220  
 Ala Lys Glu Lys Gly Lys Gln Thr Ile Asp Gly Gly Glu Val Ala Ala  
 225 230 235 240  
 Leu Gln Ala Ala Glu Gln Phe His Leu Tyr Thr Gly Val Leu Pro Thr  
 245 250 255  
 Asn Asp Gln Ile Ile Ala Ala Glu Glu Phe Ser Lys  
 260 265

&lt;210&gt; 439

&lt;211&gt; 951

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(928)

&lt;223&gt; RXA02791

&lt;400&gt; 439

accgtgttca acgacacctt cgaagagcac gaagccgaca ttgagcaagc tttgaacagt 60

ggcgttcttag acagcaaccg ataaggatca gcgaataaaa ttg ggt tct cac atc 115  
 Leu Gly Ser His Ile  
 1 5

act cac cgg gcg gcc gta ctc ggc tca ccc atc gag cat tcc aaa tcc 163  
 Thr His Arg Ala Val Leu Gly Ser Pro Ile Glu His Ser Lys Ser  
 10 15 20

cca gtc ctc cac aac acc ggc tat aaa gcc ctc gga ctg gac caa tgg 211  
 Pro Val Leu His Asn Thr Gly Tyr Lys Ala Leu Gly Leu Asp Gln Trp  
 25 30 35

gaa tac gac cgc ttt gag tgc acc ggc gac atg ctc ccc ggc atc gtc 259  
 Glu Tyr Asp Arg Phe Glu Cys Thr Gly Asp Met Leu Pro Gly Ile Val  
 40 45 50

tcc ggc gct gat gaa acc tac tgc gga ttc tcc gtc acc atg ccg tct 307  
 Ser Gly Ala Asp Glu Thr Tyr Cys Gly Phe Ser Val Thr Met Pro Ser  
 55 60 65

aaa ttc gca gct ctt gaa ttc gcc gac gaa gta acc gaa cgc gcc tgc 355  
 Lys Phe Ala Ala Leu Glu Phe Ala Asp Glu Val Thr Glu Arg Ala Cys  
 70 75 80 85



gcc atc ggc tcc gca aac acc ttg ctg cgc acg gcc acc gga tgg cgc 403  
 Ala Ile Gly Ser Ala Asn Thr Leu Leu Arg Thr Ala Thr Gly Trp Arg  
 90 95 100  
  
 gcc gac aac acc gac gtc gac ggc atc agg gga gct ctc ggt gaa ctc 451  
 Ala Asp Asn Thr Asp Val Asp Gly Ile Arg Gly Ala Leu Gly Glu Leu  
 105 110 115  
  
 ctc ggc ggc gca tca ctg gcc ggc aaa cac gcc atc gtc atc ggc tcc 499  
 Leu Gly Gly Ala Ser Leu Ala Gly Lys His Ala Ile Val Ile Gly Ser  
 120 125 130  
  
 ggc ggc acc gca cgc ccc gcc atc tgg gca ctc atc gaa gcc ggg gtc 547  
 Gly Gly Thr Ala Arg Pro Ala Ile Trp Ala Leu Ile Glu Ala Gly Val  
 135 140 145  
  
 gcc cgg atc acg gtg ctc aac cgc tcc gat cgc acc gcc gaa ctg caa 595  
 Ala Arg Ile Thr Val Leu Asn Arg Ser Asp Arg Thr Ala Glu Leu Gln  
 150 155 160 165  
  
 acg ctt ttc gac gaa acc ccc acc acc ttg gcc tac gcc ccg ctc gag 643  
 Thr Leu Phe Asp Glu Thr Pro Thr Thr Leu Ala Tyr Ala Pro Leu Glu  
 170 175 180  
  
 cat ctc cac atc gaa gcc gac gtc gta gtc tct aca gtg ccc tcc gca 691  
 His Leu His Ile Glu Ala Asp Val Val Val Ser Thr Val Pro Ser Ala  
 185 190 195  
  
 gca atc gca ggc ctc gaa gac acc ctt gcg atc gcc cca gtc ctc gac 739  
 Ala Ile Ala Gly Leu Glu Asp Thr Leu Ala Ile Ala Pro Val Leu Asp  
 200 205 210  
  
 gtc atc tac gac ccc tgg cca aca cca ctc gta gaa gtc aca cga gcc 787  
 Val Ile Tyr Asp Pro Trp Pro Thr Pro Leu Val Glu Val Thr Arg Ala  
 215 220 225  
  
 aaa ggc ctc aaa gct gtc gga ggc cac gtc atg ctg gca cac cag tcc 835  
 Lys Gly Leu Lys Ala Val Gly Gly His Val Met Leu Ala His Gln Ser  
 230 235 240 245  
  
 tac gga cag ttt gaa caa ttc acc gga atg gat gca ccc cgc gat gcc 883  
 Tyr Gly Gln Phe Glu Gln Phe Thr Gly Met Asp Ala Pro Arg Asp Ala  
 250 255 260  
  
 atg cgt gag gct ttg gaa gag tct tta ggc atc tca gaa gaa cac 928  
 Met Arg Glu Ala Leu Glu Glu Ser Leu Gly Ile Ser Glu Glu His  
 265 270 275  
  
 taagtcctcg ccacctctc aac 951

&lt;210&gt; 440

&lt;211&gt; 276

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 440

Leu Gly Ser His Ile Thr His Arg Ala Ala Val Leu Gly Ser Pro Ile  
 1 5 10 15

Glu His Ser Lys Ser Pro Val Leu His Asn Thr Gly Tyr Lys Ala Leu  
                   20                                  25                                  30  
 Gly Leu Asp Gln Trp Glu Tyr Asp Arg Phe Glu Cys Thr Gly Asp Met  
                   35                                  40                                  45  
 Leu Pro Gly Ile Val Ser Gly Ala Asp Glu Thr Tyr Cys Gly Phe Ser  
                   50                                  55                                  60  
 Val Thr Met Pro Ser Lys Phe Ala Ala Leu Glu Phe Ala Asp Glu Val  
                   65                                  70                                  75                                  80  
 Thr Glu Arg Ala Cys Ala Ile Gly Ser Ala Asn Thr Leu Leu Arg Thr  
                                   85                                  90                                  95  
 Ala Thr Gly Trp Arg Ala Asp Asn Thr Asp Val Asp Gly Ile Arg Gly  
                   100                                  105                                  110  
 Ala Leu Gly Glu Leu Leu Gly Gly Ala Ser Leu Ala Gly Lys His Ala  
                   115                                  120                                  125  
 Ile Val Ile Gly Ser Gly Gly Thr Ala Arg Pro Ala Ile Trp Ala Leu  
                   130                                  135                                  140  
 Ile Glu Ala Gly Val Ala Arg Ile Thr Val Leu Asn Arg Ser Asp Arg  
                   145                                  150                                  155                                  160  
 Thr Ala Glu Leu Gln Thr Leu Phe Asp Glu Thr Pro Thr Thr Leu Ala  
                                   165                                  170                                  175  
 Tyr Ala Pro Leu Glu His Leu His Ile Glu Ala Asp Val Val Val Ser  
                   180                                  185                                  190  
 Thr Val Pro Ser Ala Ala Ile Ala Gly Leu Glu Asp Thr Leu Ala Ile  
                   195                                  200                                  205  
 Ala Pro Val Leu Asp Val Ile Tyr Asp Pro Trp Pro Thr Pro Leu Val  
                   210                                  215                                  220  
 Glu Val Thr Arg Ala Lys Gly Leu Lys Ala Val Gly Gly His Val Met  
                   225                                  230                                  235                                  240  
 Leu Ala His Gln Ser Tyr Gly Gln Phe Glu Gln Phe Thr Gly Met Asp  
                                   245                                  250                                  255  
 Ala Pro Arg Asp Ala Met Arg Glu Ala Leu Glu Glu Ser Leu Gly Ile  
                   260                                  265                                  270  
 Ser Glu Glu His  
                   275

<210> 441  
 <211> 693  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(670)  
 <223> RXA01699

&lt;400&gt; 441

ctgcagaaat tcggcgggtga ctccctgagc gaaaccaaga gcaacattga cacctacctc 60

aaaaacattg aggaacgaat gaaattcgaa ggttttagagg atg gag cgt aat gaa 115  
Met Glu Arg Asn Glu  
1 5

gtg aat gat caa att cac tta gat cat caa tca gat gac acc tct gaa 163  
Val Asn Asp Gln Ile His Leu Asp His Gln Ser Asp Asp Thr Ser Glu  
10 15 20

tgc tcc tgc ccg atc gtg gtt ctt gtg ggt ttg cca gga gct gga aaa 211  
Cys Ser Cys Pro Ile Val Val Leu Val Gly Leu Pro Gly Ala Gly Lys  
25 30 35

tcc acc att gga cgt cga tta gcg cgc gcc tta aac act gaa ctc gtc 259  
Ser Thr Ile Gly Arg Arg Leu Ala Arg Ala Leu Asn Thr Glu Leu Val  
40 45 50

gac tcc gac gaa ctg att gag cgc gcc acc gga aaa gcc tgt ggc gcc 307  
Asp Ser Asp Glu Leu Ile Glu Arg Ala Thr Gly Lys Ala Cys Gly Ala  
55 60 65

gtg ttc agc gag ctc ggc gag cca gcc ttc cgc gag ctc gag gcc atc 355  
Val Phe Ser Glu Leu Gly Glu Pro Ala Phe Arg Glu Leu Glu Ala Ile  
70 75 80 85

cac gtg gcc gaa gca ctg aaa tcc tcc gga gtg gtg agc ttg gga ggc 403  
His Val Ala Glu Ala Leu Lys Ser Ser Gly Val Val Ser Leu Gly Gly  
90 95 100

gga tct gtg ctg aca gaa tcc acc cgt gaa ctg ctc aaa ggc cag gac 451  
Gly Ser Val Leu Thr Glu Ser Thr Arg Glu Leu Leu Lys Gly Gln Asp  
105 110 115

gtg gtc tgg atc gac gtg cca gta gaa gaa ggc atc agg cgc acc gca 499  
Val Val Trp Ile Asp Val Pro Val Glu Glu Gly Ile Arg Arg Thr Ala  
120 125 130

aac gag cgt tcc cgc ccc gtg ctg caa gcc gcc gac ccc gcc gag cac 547  
Asn Glu Arg Ser Arg Pro Val Leu Gln Ala Ala Asp Pro Ala Glu His  
135 140 145

tac cgc aac ctg gtg aaa gtg cgc acc ccg ttg tac gaa gag gtg gca 595  
Tyr Arg Asn Leu Val Lys Val Arg Thr Pro Leu Tyr Glu Glu Val Ala  
150 155 160 165

acc tac cga ctt cgc acc aac aac cgc agc ccc cag caa gtg gtg gca 643  
Thr Tyr Arg Leu Arg Thr Asn Asn Arg Ser Pro Gln Gln Val Val Ala  
170 175 180

gca gtg ttg cat cat cta gaa atc gat taattaaacc gggcacctga 690  
Ala Val Leu His His Leu Glu Ile Asp  
185 190

tta 693

&lt;210&gt; 442

&lt;211&gt; 190

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 442

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Met Glu Arg Asn Glu Val Asn Asp Gln Ile His Leu Asp His Gln Ser
 1              5              10              15

Asp Asp Thr Ser Glu Cys Ser Cys Pro Ile Val Val Leu Val Gly Leu
          20              25              30

Pro Gly Ala Gly Lys Ser Thr Ile Gly Arg Arg Leu Ala Arg Ala Leu
          35              40              45

Asn Thr Glu Leu Val Asp Ser Asp Glu Leu Ile Glu Arg Ala Thr Gly
 50              55              60

Lys Ala Cys Gly Ala Val Phe Ser Glu Leu Gly Glu Pro Ala Phe Arg
 65              70              75              80

Glu Leu Glu Ala Ile His Val Ala Glu Ala Leu Lys Ser Ser Gly Val
          85              90              95

Val Ser Leu Gly Gly Gly Ser Val Leu Thr Glu Ser Thr Arg Glu Leu
          100              105              110

Leu Lys Gly Gln Asp Val Val Trp Ile Asp Val Pro Val Glu Glu Gly
          115              120              125

Ile Arg Arg Thr Ala Asn Glu Arg Ser Arg Pro Val Leu Gln Ala Ala
          130              135              140

Asp Pro Ala Glu His Tyr Arg Asn Leu Val Lys Val Arg Thr Pro Leu
          145              150              155              160

Tyr Glu Glu Val Ala Thr Tyr Arg Leu Arg Thr Asn Asn Arg Ser Pro
          165              170              175

Gln Gln Val Val Ala Ala Val Leu His His Leu Glu Ile Asp
          180              185              190

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&lt;210&gt; 443

&lt;211&gt; 959

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (97) .. (936)

&lt;223&gt; RXA00952

&lt;400&gt; 443

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catcctcgtc tccctatccg gccgtggcga caaggacgtt gaccacgtgc gccgcaccct 60

cgaagaaaat ccagaactga tcctgaagga caaccgatg agc cgt tac gac gat      114
                    Met Ser Arg Tyr Asp Asp
                    1              5

ctt ttt gca cgc ctc gac acg gca ggg gag ggc gcc ttt gtt ccc ttc      162
Leu Phe Ala Arg Leu Asp Thr Ala Gly Glu Gly Ala Phe Val Pro Phe
          10              15              20

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atc	atg	ctg	agc	gac	cct	tca	cca	gag	gag	gct	ttc	cag	atc	atc	tcc	210
Ile	Met	Leu	Ser	Asp	Pro	Ser	Pro	Glu	Glu	Ala	Phe	Gln	Ile	Ile	Ser	
		25					30					35				
aca	gca	atc	gaa	gct	ggc	gca	gat	gca	ctg	gaa	ctt	ggc	gta	cct	ttc	258
Thr	Ala	Ile	Glu	Ala	Gly	Ala	Asp	Ala	Leu	Glu	Leu	Gly	Val	Pro	Phe	
	40					45					50					
tcc	gac	cca	gtt	gcc	gat	ggc	ccc	acc	gtc	gcg	gaa	tcc	cac	ctc	cgc	306
Ser	Asp	Pro	Val	Ala	Asp	Gly	Pro	Thr	Val	Ala	Glu	Ser	His	Leu	Arg	
	55				60					65					70	
gca	ctc	gac	ggc	ggc	gcc	acc	gta	gac	agc	gca	ctc	gag	cag	atc	aag	354
Ala	Leu	Asp	Gly	Gly	Ala	Thr	Val	Asp	Ser	Ala	Leu	Glu	Gln	Ile	Lys	
			75					80						85		
cgc	gtg	cgc	gca	gcc	tac	cca	gag	gtt	ccc	atc	gga	atg	ctc	atc	tac	402
Arg	Val	Arg	Ala	Ala	Tyr	Pro	Glu	Val	Pro	Ile	Gly	Met	Leu	Ile	Tyr	
			90					95					100			
ggc	aac	gtt	cct	ttc	acc	cgt	ggc	ttg	gat	cgc	ttc	tac	caa	gag	ttc	450
Gly	Asn	Val	Pro	Phe	Thr	Arg	Gly	Leu	Asp	Arg	Phe	Tyr	Gln	Glu	Phe	
	105						110					115				
gct	gaa	gct	ggc	gca	gac	tcc	atc	ctc	ctg	cca	gac	gtc	cca	gtc	cga	498
Ala	Glu	Ala	Gly	Ala	Asp	Ser	Ile	Leu	Leu	Pro	Asp	Val	Pro	Val	Arg	
	120					125					130					
gaa	ggc	gca	ccg	ttt	tct	gca	gca	gct	gca	gca	gcc	gga	att	gat	ccc	546
Glu	Gly	Ala	Pro	Phe	Ser	Ala	Ala	Ala	Ala	Ala	Ala	Gly	Ile	Asp	Pro	
	135				140					145					150	
att	tac	atc	gct	ccg	gcc	aac	gcc	agc	gag	aaa	acc	ctc	gag	ggt	gtc	594
Ile	Tyr	Ile	Ala	Pro	Ala	Asn	Ala	Ser	Glu	Lys	Thr	Leu	Glu	Gly	Val	
			155						160					165		
tcc	gcc	gca	tca	aag	ggc	tac	atc	tac	gcc	atc	tcc	cgc	gac	ggc	gtc	642
Ser	Ala	Ala	Ser	Lys	Gly	Tyr	Ile	Tyr	Ala	Ile	Ser	Arg	Asp	Gly	Val	
			170					175					180			
acc	ggc	acc	gaa	cgt	gaa	tca	tcc	acc	gac	ggc	ctg	tcc	gca	gtg	gtg	690
Thr	Gly	Thr	Glu	Arg	Glu	Ser	Ser	Thr	Asp	Gly	Leu	Ser	Ala	Val	Val	
		185					190					195				
gac	aac	atc	aag	aaa	ttt	gat	ggc	gca	ccc	atc	ctc	ttg	ggc	ttc	ggc	738
Asp	Asn	Ile	Lys	Lys	Phe	Asp	Gly	Ala	Pro	Ile	Leu	Leu	Gly	Phe	Gly	
	200					205					210					
atc	tca	tcc	cct	cag	cac	gtg	gca	gac	gcg	att	gca	gcg	ggt	gct	tcc	786
Ile	Ser	Ser	Pro	Gln	His	Val	Ala	Asp	Ala	Ile	Ala	Ala	Gly	Ala	Ser	
	215				220				225						230	
ggt	gcg	atc	acg	ggt	tcc	gcg	atc	acc	aag	atc	att	gct	tcc	cac	tgc	834
Gly	Ala	Ile	Thr	Gly	Ser	Ala	Ile	Thr	Lys	Ile	Ile	Ala	Ser	His	Cys	
			235					240						245		
gaa	ggt	gag	cac	ccg	aac	ccg	tcc	acc	att	cga	gat	atg	gac	ggt	ttg	882
Glu	Gly	Glu	His	Pro	Asn	Pro	Ser	Thr	Ile	Arg	Asp	Met	Asp	Gly	Leu	
			250				255						260			

aag gtt taggccttta aatgtggcaa tgt 959  
Lys Val  
280

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<210> 444
<211> 280
<212> PRT
<213> Corynebacterium glutamicum
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<400>	444														
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1				5					10					15	
Gly	Ala	Phe	Val	Pro	Phe	Ile	Met	Leu	Ser	Asp	Pro	Ser	Pro	Glu	Glu
			20					25					30		
Ala	Phe	Gln	Ile	Ile	Ser	Thr	Ala	Ile	Glu	Ala	Gly	Ala	Asp	Ala	Leu
		35					40					45			
Glu	Leu	Gly	Val	Pro	Phe	Ser	Asp	Pro	Val	Ala	Asp	Gly	Pro	Thr	Val
	50					55					60				
Ala	Glu	Ser	His	Leu	Arg	Ala	Leu	Asp	Gly	Gly	Ala	Thr	Val	Asp	Ser
65					70					75					80
Ala	Leu	Glu	Gln	Ile	Lys	Arg	Val	Arg	Ala	Ala	Tyr	Pro	Glu	Val	Pro
				85					90					95	
Ile	Gly	Met	Leu	Ile	Tyr	Gly	Asn	Val	Pro	Phe	Thr	Arg	Gly	Leu	Asp
			100					105					110		
Arg	Phe	Tyr	Gln	Glu	Phe	Ala	Glu	Ala	Gly	Ala	Asp	Ser	Ile	Leu	Leu
		115					120					125			
Pro	Asp	Val	Pro	Val	Arg	Glu	Gly	Ala	Pro	Phe	Ser	Ala	Ala	Ala	Ala
	130					135					140				
Ala	Ala	Gly	Ile	Asp	Pro	Ile	Tyr	Ile	Ala	Pro	Ala	Asn	Ala	Ser	Glu
145					150					155					160
Lys	Thr	Leu	Glu	Gly	Val	Ser	Ala	Ala	Ser	Lys	Gly	Tyr	Ile	Tyr	Ala
				165					170					175	
Ile	Ser	Arg	Asp	Gly	Val	Thr	Gly	Thr	Glu	Arg	Glu	Ser	Ser	Thr	Asp
			180					185					190		
Gly	Leu	Ser	Ala	Val	Val	Asp	Asn	Ile	Lys	Lys	Phe	Asp	Gly	Ala	Pro
		195					200					205			
Ile	Leu	Leu	Gly	Phe	Gly	Ile	Ser	Ser	Pro	Gln	His	Val	Ala	Asp	Ala
	210					215					220				
Ile	Ala	Ala	Gly	Ala	Ser	Gly	Ala	Ile	Thr	Gly	Ser	Ala	Ile	Thr	Lys
225					230					235					240
Ile	Ile	Ala	Ser	His	Cys	Glu	Gly	Glu	His	Pro	Asn	Pro	Ser	Thr	Ile

	245		250		255
Arg Asp Met	Asp Gly Leu Lys Lys	Asp Leu Thr Glu Phe Ile Ser Ala			
	260	265	270		
Met Lys Ala Ala Thr Lys Lys Val					
275	280				

&lt;210&gt; 445

&lt;211&gt; 1237

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1237)

&lt;223&gt; RXN00956

&lt;400&gt; 445

gccggtgcag gcacgtgggc tggggcgaaa gacgccggcg cgctgctgaa aatttttagcg 60

accatctcca cattccatta ctaaagggttt aaataggatc	atg act gaa aaa gaa	115
	Met Thr Glu Lys Glu	
	1 5	

aac ttg ggc ggc tcc acg ctg ctg cct gca tac ttc ggt gaa ttc ggc	163
Asn Leu Gly Gly Ser Thr Leu Leu Pro Ala Tyr Phe Gly Glu Phe Gly	
10 15 20	

ggc cag ttc gtc ggc gaa tcc ctc ctg cct gct ctc gac cag ctg gag	211
Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala Leu Asp Gln Leu Glu	
25 30 35	

aag gcc ttc gtt gac ggc acc aac agc cca gag ttc cgc gaa gaa ctc	259
Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu Phe Arg Glu Glu Leu	
40 45 50	

ggc ggc tac ctc cgc gat tac ctc ggc cgc cca acc ccg ctg acc gaa	307
Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro Thr Pro Leu Thr Glu	
55 60 65	

tgc tcc aac ctg cca ctc gca ggc gaa ggc aaa ggc ttt gcg cgg atc	355
Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys Gly Phe Ala Arg Ile	
70 75 80 85	

ttc ctc aag cgc gaa gac ctc gtc cac ggc ggt gca cac aaa act aac	403
Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly Ala His Lys Thr Asn	
90 95 100	

cag gtg atc ggc cag gtg ctg ctt gcc aag cgc atg ggc aaa acc cgc	451
Gln Val Ile Gly Gln Val Leu Leu Ala Lys Arg Met Gly Lys Thr Arg	
105 110 115	

atc atc gca gag acc ggc gca ggc cag cac ggc acc gcc acc gct ctc	499
Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly Thr Ala Thr Ala Leu	
120 125 130	

gca tgt gcg ctc atg ggc ctc gag tgc gtt gtc tac atg ggc gcc aag	547
Ala Cys Ala Leu Met Gly Leu Glu Cys Val Val Tyr Met Gly Ala Lys	
135 140 145	

gac gtt gcc cgc cag cag ccc aac gtc tac cgc atg cag ctg cac ggc Asp Val Ala Arg Gln Gln Pro Asn Val Tyr Arg Met Gln Leu His Gly 150 155 160 165	595
gcg aag gtc atc ccc gtg gaa tct ggt tcc ggc acc ctg aag gac gcc Ala Lys Val Ile Pro Val Glu Ser Gly Ser Gly Thr Leu Lys Asp Ala 170 175 180	643
gtg aat gaa gcg ctg cgc gat tgg acc gca acc ttc cac gag tcc cac Val Asn Glu Ala Leu Arg Asp Trp Thr Ala Thr Phe His Glu Ser His 185 190 195	691
tac ctt ctg ggc acc ccc gcc ggc ccg cac cca ttc cca acc atc gtg Tyr Leu Leu Gly Thr Pro Ala Gly Pro His Pro Phe Pro Thr Ile Val 200 205 210	739
cgt gaa ttc cac aag gtg atc tct gag gaa gcc aag gca cag atg cta Arg Glu Phe His Lys Val Ile Ser Glu Glu Ala Lys Ala Gln Met Leu 215 220 225	787
gag cgc acc ggc aag ctt ccc gac gtt gtg gtc gcc tgt gtc ggt ggt Glu Arg Thr Gly Lys Leu Pro Asp Val Val Val Ala Cys Val Gly Gly 230 235 240 245	835
ggc tcc aac gcc atc ggc atg ttc gca gac ttc att gac gat gaa ggt Gly Ser Asn Ala Ile Gly Met Phe Ala Asp Phe Ile Asp Asp Glu Gly 250 255 260	883
gta gag ctg gtc ggc gct gag cca gcc ggt gaa ggc ctg gac tcc ggc Val Glu Leu Val Gly Ala Glu Pro Ala Gly Glu Gly Leu Asp Ser Gly 265 270 275	931
aag cac ggc gca acc atc acc aac ggt cag atc ggc atc ctg cac ggc Lys His Gly Ala Thr Ile Thr Asn Gly Gln Ile Gly Ile Leu His Gly 280 285 290	979
acc cgt tcc tac ctg atg cgc aac tcc gac ggc caa gtg gaa gag tcc Thr Arg Ser Tyr Leu Met Arg Asn Ser Asp Gly Gln Val Glu Glu Ser 295 300 305	1027
tac tcc atc tcc gcc gga ctt gat tac cca ggc gtc ggc cca cag cac Tyr Ser Ile Ser Ala Glu Leu Asp Tyr Pro Gly Val Gly Pro Gln His 310 315 320 325	1075
gca cac ctg cac gcc acc ggc cgc gcc acc tac gtt ggt atc acc gac Ala His Leu His Ala Thr Gly Arg Ala Thr Tyr Val Gly Ile Thr Asp 330 335 340	1123
gcc gaa gcc ctg caa gca ttc cag tac ctg gcc cgc tac gaa ggc atc Ala Glu Ala Leu Gln Ala Phe Gln Tyr Leu Ala Arg Tyr Glu Gly Ile 345 350 355	1171
atc ccc gca ctg gaa tcc tca cac gcg ttc gcc tac gca ctg aag cgc Ile Pro Ala Leu Glu Ser Ser His Ala Phe Ala Tyr Ala Leu Lys Arg 360 365 370	1219
gcc aag acc gcc gaa gta Ala Lys Thr Ala Glu Val 375	1237



&lt;210&gt; 446

&lt;211&gt; 379

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 446

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Met Thr Glu Lys Glu Asn Leu Gly Gly Ser Thr Leu Leu Pro Ala Tyr
 1          5          10          15

Phe Gly Glu Phe Gly Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala
    20          25          30

Leu Asp Gln Leu Glu Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu
    35          40          45

Phe Arg Glu Glu Leu Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro
    50          55          60

Thr Pro Leu Thr Glu Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys
    65          70          75          80

Gly Phe Ala Arg Ile Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly
          85          90          95

Ala His Lys Thr Asn Gln Val Ile Gly Gln Val Leu Leu Ala Lys Arg
    100          105          110

Met Gly Lys Thr Arg Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly
    115          120          125

Thr Ala Thr Ala Leu Ala Cys Ala Leu Met Gly Leu Glu Cys Val Val
    130          135          140

Tyr Met Gly Ala Lys Asp Val Ala Arg Gln Gln Pro Asn Val Tyr Arg
    145          150          155          160

Met Gln Leu His Gly Ala Lys Val Ile Pro Val Glu Ser Gly Ser Gly
          165          170          175

Thr Leu Lys Asp Ala Val Asn Glu Ala Leu Arg Asp Trp Thr Ala Thr
          180          185          190

Phe His Glu Ser His Tyr Leu Leu Gly Thr Pro Ala Gly Pro His Pro
    195          200          205

Phe Pro Thr Ile Val Arg Glu Phe His Lys Val Ile Ser Glu Glu Ala
    210          215          220

Lys Ala Gln Met Leu Glu Arg Thr Gly Lys Leu Pro Asp Val Val Val
    225          230          235          240

Ala Cys Val Gly Gly Gly Ser Asn Ala Ile Gly Met Phe Ala Asp Phe
          245          250          255

Ile Asp Asp Glu Gly Val Glu Leu Val Gly Ala Glu Pro Ala Gly Glu
    260          265          270

Gly Leu Asp Ser Gly Lys His Gly Ala Thr Ile Thr Asn Gly Gln Ile
    275          280          285

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Gly Ile Leu His Gly Thr Arg Ser Tyr Leu Met Arg Asn Ser Asp Gly  
 290 295 300

Gln Val Glu Glu Ser Tyr Ser Ile Ser Ala Gly Leu Asp Tyr Pro Gly  
 305 310 315 320

Val Gly Pro Gln His Ala His Leu His Ala Thr Gly Arg Ala Thr Tyr  
 325 330 335

Val Gly Ile Thr Asp Ala Glu Ala Leu Gln Ala Phe Gln Tyr Leu Ala  
 340 345 350

Arg Tyr Glu Gly Ile Ile Pro Ala Leu Glu Ser Ser His Ala Phe Ala  
 355 360 365

Tyr Ala Leu Lys Arg Ala Lys Thr Ala Glu Val  
 370 375

&lt;210&gt; 447

&lt;211&gt; 1231

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1231)

&lt;223&gt; FRXA00956

&lt;400&gt; 447

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accatctcca cattccatta ctaaaggttt aaataggatc atg act gaa aaa gaa 115  
 Met Thr Glu Lys Glu  
 1 5

aac ttg ggc ggc tcc acg ctg ctg cct gca tac ttc ggt gaa ttc ggc 163  
 Asn Leu Gly Gly Ser Thr Leu Leu Pro Ala Tyr Phe Gly Glu Phe Gly  
 10 15 20

ggc cag ttc gtc ggc gaa tcc ctc ctg cct gct ctc gac cag ctg gag 211  
 Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala Leu Asp Gln Leu Glu  
 25 30 35

aag gcc ttc gtt gac ggc acc aac agc cca gag ttc cgc gaa gaa ctc 259  
 Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu Phe Arg Glu Glu Leu  
 40 45 50

ggc ggc tac ctc cgc gat tac ctc ggc cgc cca acc ccg ctg acc gaa 307  
 Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro Thr Pro Leu Thr Glu  
 55 60 65

tgc tcc aac ctg cca ctc gca ggc gaa ggc aaa ggc ttt ggc cgg atc 355  
 Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys Gly Phe Ala Arg Ile  
 70 75 80 85

ttc ctc aag cgc gaa gac ctc gtc cac ggc ggt gca cac aaa act aac 403  
 Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly Ala His Lys Thr Asn  
 90 95 100

cag gtg atc ggc cag gtg ctg ctt gcc aag cgc atg ggc aaa acc cgc 451

Gln	Val	Ile	Gly	Gln	Val	Leu	Leu	Ala	Lys	Arg	Met	Gly	Lys	Thr	Arg	
			105					110					115			
atc	atc	gca	gag	acc	ggc	gca	ggc	cag	cac	ggc	acc	gcc	acc	gct	ctc	499
Ile	Ile	Ala	Glu	Thr	Gly	Ala	Gly	Gln	His	Gly	Thr	Ala	Thr	Ala	Leu	
		120					125					130				
gca	tgt	gcg	ctc	atg	ggc	ctc	gag	tgc	gtt	gtc	tac	atg	ggc	gcc	aag	547
Ala	Cys	Ala	Leu	Met	Gly	Leu	Glu	Cys	Val	Val	Tyr	Met	Gly	Ala	Lys	
	135					140					145					
gac	gtt	gcc	cgc	cag	cag	ccc	aac	gtc	tac	cgc	atg	cag	ctg	cac	ggc	595
Asp	Val	Ala	Arg	Gln	Gln	Pro	Asn	Val	Tyr	Arg	Met	Gln	Leu	His	Gly	
150					155					160					165	
gcg	aag	gtc	atc	ccc	gtg	gaa	tct	ggg	tcc	ggc	acc	ctg	aag	gac	gcc	643
Ala	Lys	Val	Ile	Pro	Val	Glu	Ser	Gly	Ser	Gly	Thr	Leu	Lys	Asp	Ala	
				170					175					180		
gtg	aat	gaa	gcg	ctg	cgc	gat	tgg	acc	gca	acc	ttc	cac	gag	tcc	cac	691
Val	Asn	Glu	Ala	Leu	Arg	Asp	Trp	Thr	Ala	Thr	Phe	His	Glu	Ser	His	
			185					190					195			
tac	ctt	ctc	ggc	acc	ccc	gcc	ggc	ccg	cac	cca	ttc	cca	acc	atc	gtg	739
Tyr	Leu	Leu	Gly	Thr	Pro	Ala	Gly	Pro	His	Pro	Phe	Pro	Thr	Ile	Val	
		200					205					210				
cgt	gaa	ttc	cac	aag	gtg	atc	tct	gag	gaa	gcc	aag	gca	cag	atg	cta	787
Arg	Glu	Phe	His	Lys	Val	Ile	Ser	Glu	Glu	Ala	Lys	Ala	Gln	Met	Leu	
	215					220					225					
gag	cgc	acc	ggc	aag	ctt	ccc	gac	gtt	gtg	gtc	gcc	tgt	gtc	ggt	ggt	835
Glu	Arg	Thr	Gly	Lys	Leu	Pro	Asp	Val	Val	Val	Ala	Cys	Val	Gly	Gly	
230					235					240				245		
ggc	tcc	aac	gcc	atc	ggc	atg	ttc	gca	gac	ttc	att	gac	gat	gaa	ggt	883
Gly	Ser	Asn	Ala	Ile	Gly	Met	Phe	Ala	Asp	Phe	Ile	Asp	Asp	Glu	Gly	
			250						255					260		
gta	gag	ctc	gtc	ggc	gct	gag	cca	gcc	ggg	gaa	ggc	ctc	gac	tcc	ggc	931
Val	Glu	Leu	Val	Gly	Ala	Glu	Pro	Ala	Gly	Glu	Gly	Leu	Asp	Ser	Gly	
			265					270					275			
aag	cac	ggc	gca	acc	atc	acc	aac	ggg	cag	atc	ggc	atc	ctg	cac	ggc	979
Lys	His	Gly	Ala	Thr	Ile	Thr	Asn	Gly	Gln	Ile	Gly	Ile	Leu	His	Gly	
		280					285					290				
acc	cgt	tcc	tac	ctg	atg	cgc	aac	tcc	gac	ggc	caa	gtg	gaa	gag	tcc	1027
Thr	Arg	Ser	Tyr	Leu	Met	Arg	Asn	Ser	Asp	Gly	Gln	Val	Glu	Glu	Ser	
		295				300					305					
tac	tcc	atc	tcc	gcc	gga	ctt	gat	tac	cca	ggc	gtc	ggc	cca	cag	cac	1075
Tyr	Ser	Ile	Ser	Ala	Gly	Leu	Asp	Tyr	Pro	Gly	Val	Gly	Pro	Gln	His	
310					315					320				325		
gca	cac	ctg	cac	gcc	acc	ggc	cgc	gcc	acc	tac	gtt	ggt	atc	acc	gac	1123
Ala	His	Leu	His	Ala	Thr	Gly	Arg	Ala	Thr	Tyr	Val	Gly	Ile	Thr	Asp	
			330					335					340			
gcc	gaa	gcc	ctc	caa	gca	ttc	cag	tac	ctc	gcc	cgc	tac	gaa	ggc	atc	1171
Ala	Glu	Ala	Leu	Gln	Ala	Phe	Gln	Tyr	Leu	Ala	Arg	Tyr	Glu	Gly	Ile	

345 350 355  
 atc ccc gca ctg gaa tcc tca cac gcg ttc gcc tac gca ctc aag cgc 1219  
 Ile Pro Ala Leu Glu Ser Ser His Ala Phe Ala Tyr Ala Leu Lys Arg  
 360 365 370

gcc aag acc gcc 1231  
 Ala Lys Thr Ala  
 375

<210> 448

<211> 377

<212> PRT

<213> Corynebacterium glutamicum

<400> 448

Met Thr Glu Lys Glu Asn Leu Gly Gly Ser Thr Leu Leu Pro Ala Tyr  
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Phe Gly Glu Phe Gly Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala  
 20 25 30

Leu Asp Gln Leu Glu Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu  
 35 40 45

Phe Arg Glu Glu Leu Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro  
 50 55 60

Thr Pro Leu Thr Glu Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys  
 65 70 75 80

Gly Phe Ala Arg Ile Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly  
 85 90 95

Ala His Lys Thr Asn Gln Val Ile Gly Gln Val Leu Leu Ala Lys Arg  
 100 105 110

Met Gly Lys Thr Arg Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly  
 115 120 125

Thr Ala Thr Ala Leu Ala Cys Ala Leu Met Gly Leu Glu Cys Val Val  
 130 135 140

Tyr Met Gly Ala Lys Asp Val Ala Arg Gln Gln Pro Asn Val Tyr Arg  
 145 150 155 160

Met Gln Leu His Gly Ala Lys Val Ile Pro Val Glu Ser Gly Ser Gly  
 165 170 175

Thr Leu Lys Asp Ala Val Asn Glu Ala Leu Arg Asp Trp Thr Ala Thr  
 180 185 190

Phe His Glu Ser His Tyr Leu Leu Gly Thr Pro Ala Gly Pro His Pro  
 195 200 205

Phe Pro Thr Ile Val Arg Glu Phe His Lys Val Ile Ser Glu Glu Ala  
 210 215 220

Lys Ala Gln Met Leu Glu Arg Thr Gly Lys Leu Pro Asp Val Val Val  
 225 230 235 240

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<210> 449
<211> 1401
<212> DNA
<213> Corynebacterium glutamicum
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ggtcgcgtcta ttttgccacc acatgcggag gtacgcagtt atg agt tca gtt tcg 115
Met Ser Ser Val Ser
1 5

ctg cag gat ttt gat gca gag cga att ggt ttg ttc cac gag gac att 163
Leu Gln Asp Phe Asp Ala Glu Arg Ile Gly Leu Phe His Glu Asp Ile
10 15 20

aag cgc aag ttt gat gag ctc aag tca aaa aat ctg aag ctg gat ctt 211
Lys Arg Lys Phe Asp Glu Leu Lys Ser Lys Asn Leu Lys Leu Asp Leu
25 30 35

act cgc ggt aag cct tcg tcg gag cag ttg gat ttc gct gat gag ttg 259
Thr Arg Gly Lys Pro Ser Ser Glu Gln Leu Asp Phe Ala Asp Glu Leu
40 45 50

ttg gcg ttg cct ggt aag ggt gat ttc aag gct gcg gat ggt act gat 307
Leu Ala Leu Pro Gly Lys Gly Asp Phe Lys Ala Ala Asp Gly Thr Asp
55 60 65

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gtc	cgt	aac	tat	ggc	ggg	ctg	gat	ggc	atc	gtt	gat	att	cgc	cag	att	355
Val	Arg	Asn	Tyr	Gly	Gly	Leu	Asp	Gly	Ile	Val	Asp	Ile	Arg	Gln	Ile	
70					75					80					85	
tgg	gcg	gat	ttg	ctg	ggt	gtt	cct	gtg	gag	cag	gtc	ttg	gcg	ggg	gat	403
Trp	Ala	Asp	Leu	Leu	Gly	Val	Pro	Val	Glu	Gln	Val	Leu	Ala	Gly	Asp	
				90					95					100		
gct	tcg	agc	ttg	aac	atc	atg	ttt	gat	gtg	atc	agc	tgg	tcg	tac	att	451
Ala	Ser	Ser	Leu	Asn	Ile	Met	Phe	Asp	Val	Ile	Ser	Trp	Ser	Tyr	Ile	
			105					110						115		
ttc	ggt	aac	aat	gat	tcg	gtt	cag	cct	tgg	tcg	aag	gaa	gaa	acc	gtt	499
Phe	Gly	Asn	Asn	Asp	Ser	Val	Gln	Pro	Trp	Ser	Lys	Glu	Glu	Thr	Val	
		120					125					130				
aag	tgg	att	tgc	cct	gtt	ccg	ggc	tat	gat	cgc	cat	ttc	tcc	atc	acg	547
Lys	Trp	Ile	Cys	Pro	Val	Pro	Gly	Tyr	Asp	Arg	His	Phe	Ser	Ile	Thr	
	135					140					145					
gag	cgt	ttc	ggc	ttt	gag	atg	att	tct	gtg	cca	atg	aat	gaa	gac	ggc	595
Glu	Arg	Phe	Gly	Phe	Glu	Met	Ile	Ser	Val	Pro	Met	Asn	Glu	Asp	Gly	
150					155					160					165	
cct	gat	atg	gat	gct	gtt	gag	gaa	ttg	gtg	aag	aat	ccg	cag	gtt	aag	643
Pro	Asp	Met	Asp	Ala	Val	Glu	Glu	Leu	Val	Lys	Asn	Pro	Gln	Val	Lys	
				170					175					180		
ggc	atg	tgg	gtt	gtt	ccg	gtg	ttt	tct	aac	ccg	act	ggg	ttc	acg	gtg	691
Gly	Met	Trp	Val	Val	Pro	Val	Phe	Ser	Asn	Pro	Thr	Gly	Phe	Thr	Val	
			185					190						195		
aca	gaa	gac	gtc	gca	aag	cgt	cta	agc	gca	atg	gaa	acc	gca	gct	ccg	739
Thr	Glu	Asp	Val	Ala	Lys	Arg	Leu	Ser	Ala	Met	Glu	Thr	Ala	Ala	Pro	
			200				205					210				
gac	ttc	cgc	gtt	gtg	tgg	gat	aat	gcc	tac	gcc	gtt	cat	acg	ctg	acc	787
Asp	Phe	Arg	Val	Val	Trp	Asp	Asn	Ala	Tyr	Ala	Val	His	Thr	Leu	Thr	
	215					220					225					
gat	gaa	ttc	cct	gag	gtt	atc	gat	atc	gtc	ggg	ctt	ggg	gag	gcc	gct	835
Asp	Glu	Phe	Pro	Glu	Val	Ile	Asp	Ile	Val	Gly	Leu	Gly	Glu	Ala	Ala	
230					235					240					245	
ggc	aac	ccg	aac	cgt	ttc	tgg	gcg	ttc	act	tct	act	tcg	aag	atc	act	883
Gly	Asn	Pro	Asn	Arg	Phe	Trp	Ala	Phe	Thr	Ser	Thr	Ser	Lys	Ile	Thr	
				250					255					260		
ctc	gcg	ggt	gcg	ggc	gtg	tcg	ttc	ttc	ctc	acc	tct	gcg	gag	aac	cgc	931
Leu	Ala	Gly	Ala	Gly	Val	Ser	Phe	Phe	Leu	Thr	Ser	Ala	Glu	Asn	Arg	
			265					270					275			
aag	tgg	tac	acc	ggc	cat	gcg	ggt	atc	cgt	ggc	att	ggc	cct	aac	aag	979
Lys	Trp	Tyr	Thr	Gly	His	Ala	Gly	Ile	Arg	Gly	Ile	Gly	Pro	Asn	Lys	
		280					285					290				
gtc	aat	cag	ttg	gct	cat	gcg	cgt	tac	ttt	ggc	gat	gct	gag	gga	gtg	1027
Val	Asn	Gln	Leu	Ala	His	Ala	Arg	Tyr	Phe	Gly	Asp	Ala	Glu	Gly	Val	
	295					300					305					

cgc gcg gtg atg cgt aag cat gct gcg tcg ttg gct ccg aag ttc aac 1075  
 Arg Ala Val Met Arg Lys His Ala Ala Ser Leu Ala Pro Lys Phe Asn  
 310 315 320 325

aag gtt ctg gag att ctg gat tct cgc ctt gct gag tac ggt gtc gcg 1123  
 Lys Val Leu Glu Ile Leu Asp Ser Arg Leu Ala Glu Tyr Gly Val Ala  
 330 335 340

cag tgg act gtc cct gcg ggc ggt tac ttc att tcc ctt gat gtg gtt 1171  
 Gln Trp Thr Val Pro Ala Gly Gly Tyr Phe Ile Ser Leu Asp Val Val  
 345 350 355

cct ggt acg gcg tct cgc gtg gct gag ttg gct aag gaa gcc ggc atc 1219  
 Pro Gly Thr Ala Ser Arg Val Ala Glu Leu Ala Lys Glu Ala Gly Ile  
 360 365 370

gcg ttg acg ggt gcg ggt tct tct tac ccg ctg cgt cag gat ccg gag 1267  
 Ala Leu Thr Gly Ala Gly Ser Ser Tyr Pro Leu Arg Gln Asp Pro Glu  
 375 380 385

aac aaa aat ctc cgt ttg gca ccg tcg ctg cct cca gtt gag gaa ctt 1315  
 Asn Lys Asn Leu Arg Leu Ala Pro Ser Leu Pro Pro Val Glu Glu Leu  
 390 395 400 405

gag gtt gcc atg gat ggc gtg gct acc tgt gtg ctg ttg gca gca gcg 1363  
 Glu Val Ala Met Asp Gly Val Ala Thr Cys Val Leu Leu Ala Ala Ala  
 410 415 420

gag cat tac gct aac taaaagttaa tacagcggag aca 1401  
 Glu His Tyr Ala Asn  
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<210> 450  
 <211> 426  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 450  
 Met Ser Ser Val Ser Leu Gln Asp Phe Asp Ala Glu Arg Ile Gly Leu  
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Phe His Glu Asp Ile Lys Arg Lys Phe Asp Glu Leu Lys Ser Lys Asn  
 20 25 30

Leu Lys Leu Asp Leu Thr Arg Gly Lys Pro Ser Ser Glu Gln Leu Asp  
 35 40 45

Phe Ala Asp Glu Leu Leu Ala Leu Pro Gly Lys Gly Asp Phe Lys Ala  
 50 55 60

Ala Asp Gly Thr Asp Val Arg Asn Tyr Gly Gly Leu Asp Gly Ile Val  
 65 70 75 80

Asp Ile Arg Gln Ile Trp Ala Asp Leu Leu Gly Val Pro Val Glu Gln  
 85 90 95

Val Leu Ala Gly Asp Ala Ser Ser Leu Asn Ile Met Phe Asp Val Ile  
 100 105 110

Ser Trp Ser Tyr Ile Phe Gly Asn Asn Asp Ser Val Gln Pro Trp Ser

115					120					125						
Lys	Glu	Glu	Thr	Val	Lys	Trp	Ile	Cys	Pro	Val	Pro	Gly	Tyr	Asp	Arg	
130					135					140						
His	Phe	Ser	Ile	Thr	Glu	Arg	Phe	Gly	Phe	Glu	Met	Ile	Ser	Val	Pro	
145					150					155					160	
Met	Asn	Glu	Asp	Gly	Pro	Asp	Met	Asp	Ala	Val	Glu	Glu	Leu	Val	Lys	
165					170					175						
Asn	Pro	Gln	Val	Lys	Gly	Met	Trp	Val	Val	Pro	Val	Phe	Ser	Asn	Pro	
180					185					190						
Thr	Gly	Phe	Thr	Val	Thr	Glu	Asp	Val	Ala	Lys	Arg	Leu	Ser	Ala	Met	
195					200					205						
Glu	Thr	Ala	Ala	Pro	Asp	Phe	Arg	Val	Val	Trp	Asp	Asn	Ala	Tyr	Ala	
210					215					220						
Val	His	Thr	Leu	Thr	Asp	Glu	Phe	Pro	Glu	Val	Ile	Asp	Ile	Val	Gly	
225					230					235					240	
Leu	Gly	Glu	Ala	Ala	Gly	Asn	Pro	Asn	Arg	Phe	Trp	Ala	Phe	Thr	Ser	
245					250					255						
Thr	Ser	Lys	Ile	Thr	Leu	Ala	Gly	Ala	Gly	Val	Ser	Phe	Phe	Leu	Thr	
260					265					270						
Ser	Ala	Glu	Asn	Arg	Lys	Trp	Tyr	Thr	Gly	His	Ala	Gly	Ile	Arg	Gly	
275					280					285						
Ile	Gly	Pro	Asn	Lys	Val	Asn	Gln	Leu	Ala	His	Ala	Arg	Tyr	Phe	Gly	
290					295					300						
Asp	Ala	Glu	Gly	Val	Arg	Ala	Val	Met	Arg	Lys	His	Ala	Ala	Ser	Leu	
305					310					315					320	
Ala	Pro	Lys	Phe	Asn	Lys	Val	Leu	Glu	Ile	Leu	Asp	Ser	Arg	Leu	Ala	
325					330					335						
Glu	Tyr	Gly	Val	Ala	Gln	Trp	Thr	Val	Pro	Ala	Gly	Gly	Tyr	Phe	Ile	
340					345					350						
Ser	Leu	Asp	Val	Val	Pro	Gly	Thr	Ala	Ser	Arg	Val	Ala	Glu	Leu	Ala	
355					360					365						
Lys	Glu	Ala	Gly	Ile	Ala	Leu	Thr	Gly	Ala	Gly	Ser	Ser	Tyr	Pro	Leu	
370					375					380						
Arg	Gln	Asp	Pro	Glu	Asn	Lys	Asn	Leu	Arg	Leu	Ala	Pro	Ser	Leu	Pro	
385					390					395					400	
Pro	Val	Glu	Glu	Leu	Glu	Val	Ala	Met	Asp	Gly	Val	Ala	Thr	Cys	Val	
405					410					415						
Leu	Leu	Ala	Ala	Ala	Glu	His	Tyr	Ala	Asn							
420					425											

&lt;210&gt; 451



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<220>  
<221> CDS  
<222> (101)..(1120)  
<223> RXN00448
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ccatttacct tcaactaagg tagccgtaac tgcaaagctc aggccatcct cttcagtgtt 60

gtc cca tcc cga gtt ggc cca cac gat gca gca gca gca cga gtg tct 691

Val	Pro	Ser	Arg	Val	Gly	Pro	His	Asp	Ala	Ala	Ala	Ala	Arg	Val	Ser		
			185					190						195			
cat	tta	aca	cac	atc	ctg	gct	gaa	acc	ctc	gcc	atc	gtc	ggg	gac	aac	739	
His	Leu	Thr	His	Ile	Leu	Ala	Glu	Thr	Leu	Ala	Ile	Val	Gly	Asp	Asn		
		200					205					210					
ggg	ggc	gca	ctg	tct	ctc	tct	tta	gcc	gct	ggc	agc	tac	cgc	gac	tcc	787	
Gly	Gly	Ala	Leu	Ser	Leu	Ser	Leu	Ala	Ala	Gly	Ser	Tyr	Arg	Asp	Ser		
	215					220					225						
acc	cgc	gtt	gca	ggc	acc	gac	cca	gga	ctc	gtc	cgc	gcc	atg	tgt	gaa	835	
Thr	Arg	Val	Ala	Gly	Thr	Asp	Pro	Gly	Leu	Val	Arg	Ala	Met	Cys	Glu		
230					235					240					245		
agc	aac	gcc	ggc	cca	ctg	gtc	aaa	gcc	ctc	gac	gaa	gca	ctg	gcg	atc	883	
Ser	Asn	Ala	Gly	Pro	Leu	Val	Lys	Ala	Leu	Asp	Glu	Ala	Leu	Ala	Ile		
				250					255						260		
ctc	cac	gaa	gcc	cgc	gaa	ggc	ctc	acc	gca	gaa	cag	cca	aac	atc	gag	931	
Leu	His	Glu	Ala	Arg	Glu	Gly	Leu	Thr	Ala	Glu	Gln	Pro	Asn	Ile	Glu		
			265					270						275			
caa	ctt	gcc	gac	aac	ggc	tac	cga	tcc	cgc	atc	cgc	tac	gaa	gcc	cgc	979	
Gln	Leu	Ala	Asp	Asn	Gly	Tyr	Arg	Ser	Arg	Ile	Arg	Tyr	Glu	Ala	Arg		
		280					285					290					
tcc	ggc	cag	cga	cgc	gcc	aaa	gaa	tcc	gtt	agc	cct	acc	atc	acc	tca	1027	
Ser	Gly	Gln	Arg	Arg	Ala	Lys	Glu	Ser	Val	Ser	Pro	Thr	Ile	Thr	Ser		
	295					300					305						
tcc	agg	cca	gtg	ctc	cgt	ctc	cac	ccg	ggc	aca	cca	aac	tggt	gag	aag	1075	
Ser	Arg	Pro	Val	Leu	Arg	Leu	His	Pro	Gly	Thr	Pro	Asn	Trp	Glu	Lys		
310					315					320					325		
cag	ctc	atc	cac	gct	gaa	acc	ctc	ggc	gca	cgg	atc	gaa	gtg	ttc		1120	
Gln	Leu	Ile	His	Ala	Glu	Thr	Leu	Gly	Ala	Arg	Ile	Glu	Val	Phe			
				330					335					340			
tagttttatc	ggctgatgat	tct														1143	

&lt;210&gt; 452

&lt;211&gt; 340

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 452

Val	Thr	Thr	Lys	Asp	Ile	Ser	Arg	Pro	Val	Cys	Ile	Leu	Gly	Leu	Gly		
1				5					10					15			
Leu	Ile	Gly	Gly	Ser	Leu	Leu	Arg	Asp	Leu	His	Ala	Ala	Asn	His	Ser		
			20					25					30				
Val	Phe	Gly	Tyr	Asn	Arg	Ser	Arg	Ser	Gly	Ala	Lys	Ser	Ala	Val	Asp		
		35					40					45					
Glu	Gly	Phe	Asp	Val	Ser	Ala	Asp	Leu	Glu	Ala	Thr	Leu	Gln	Arg	Ala		
	50					55					60						
Ala	Ala	Glu	Asp	Ala	Leu	Ile	Val	Leu	Ala	Val	Pro	Met	Thr	Ala	Ile		

65					70					75					80
Asp	Ser	Leu	Leu	Asp	Ala	Val	His	Thr	His	Ala	Pro	Asn	Asn	Gly	Phe
				85					90					95	
Thr	Asp	Val	Val	Ser	Val	Lys	Thr	Ala	Val	Tyr	Asp	Ala	Val	Lys	Ala
		100						105					110		
Arg	Asn	Met	Gln	His	Arg	Tyr	Val	Gly	Ser	His	Pro	Met	Ala	Gly	Thr
		115					120					125			
Ala	Asn	Ser	Gly	Trp	Ser	Ala	Ser	Met	Asp	Gly	Leu	Phe	Lys	Arg	Ala
	130					135					140				
Val	Trp	Val	Val	Thr	Phe	Asp	Gln	Leu	Phe	Asp	Gly	Thr	Asp	Ile	Asn
145					150					155					160
Ser	Thr	Trp	Ile	Ser	Ile	Trp	Lys	Asp	Val	Val	Gln	Met	Ala	Leu	Ala
				165					170					175	
Val	Gly	Ala	Glu	Val	Val	Pro	Ser	Arg	Val	Gly	Pro	His	Asp	Ala	Ala
			180					185					190		
Ala	Ala	Arg	Val	Ser	His	Leu	Thr	His	Ile	Leu	Ala	Glu	Thr	Leu	Ala
			195				200					205			
Ile	Val	Gly	Asp	Asn	Gly	Gly	Ala	Leu	Ser	Leu	Ser	Leu	Ala	Ala	Gly
	210					215					220				
Ser	Tyr	Arg	Asp	Ser	Thr	Arg	Val	Ala	Gly	Thr	Asp	Pro	Gly	Leu	Val
225					230					235					240
Arg	Ala	Met	Cys	Glu	Ser	Asn	Ala	Gly	Pro	Leu	Val	Lys	Ala	Leu	Asp
				245					250					255	
Glu	Ala	Leu	Ala	Ile	Leu	His	Glu	Ala	Arg	Glu	Gly	Leu	Thr	Ala	Glu
			260					265					270		
Gln	Pro	Asn	Ile	Glu	Gln	Leu	Ala	Asp	Asn	Gly	Tyr	Arg	Ser	Arg	Ile
		275					280					285			
Arg	Tyr	Glu	Ala	Arg	Ser	Gly	Gln	Arg	Arg	Ala	Lys	Glu	Ser	Val	Ser
	290					295					300				
Pro	Thr	Ile	Thr	Ser	Ser	Arg	Pro	Val	Leu	Arg	Leu	His	Pro	Gly	Thr
305					310					315					320
Pro	Asn	Trp	Glu	Lys	Gln	Leu	Ile	His	Ala	Glu	Thr	Leu	Gly	Ala	Arg
				325					330					335	
Ile	Glu	Val	Phe												
			340												

&lt;210&gt; 453

&lt;211&gt; 689

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

<223> FRXA00448

tat	gtg	gga	tcc	cac	ccc	atg	gca	ggc	acc	gcc	aac	tcc	ggc	tgg	agc	48
Tyr	Val	Gly	Ser	His	Pro	Met	Ala	Gly	Thr	Ala	Asn	Ser	Gly	Trp	Ser	
1				5				10						15		
gca	tcc	atg	gac	gga	ctg	ttc	aaa	cga	gca	gta	tgg	gtg	gtc	acc	ttc	96
Ala	Ser	Met	Asp	Gly	Leu	Phe	Lys	Arg	Ala	Val	Trp	Val	Val	Thr	Phe	
			20				25						30			
gac	cag	ctt	ttc	gac	ggc	acc	gac	atc	aac	tcc	acc	tgg	atc	agc	atc	144
Asp	Gln	Leu	Phe	Asp	Gly	Thr	Asp	Ile	Asn	Ser	Thr	Trp	Ile	Ser	Ile	
		35					40					45				
tgg	aaa	gac	gtc	gtc	caa	atg	gca	ctc	gcc	gtg	ggc	gct	gaa	gtt	gtc	192
Trp	Lys	Asp	Val	Val	Gln	Met	Ala	Leu	Ala	Val	Gly	Ala	Glu	Val	Val	
	50					55					60					
cca	tcc	cga	gtt	ggc	cca	cac	gat	gca	gca	gca	gca	cga	gtg	tct	cat	240
Pro	Ser	Arg	Val	Gly	Pro	His	Asp	Ala	Ala	Ala	Ala	Arg	Val	Ser	His	
65				70				75							80	
tta	aca	cac	atc	ctg	gct	gaa	acc	ctc	gcc	atc	gtc	ggc	gac	aac	ggc	288
Leu	Thr	His	Ile	Leu	Ala	Glu	Thr	Leu	Ala	Ile	Val	Gly	Asp	Asn	Gly	
				85				90						95		
ggc	gca	ctg	tct	ctc	tct	tta	gcc	gct	ggc	agc	tac	cgc	gac	tcc	acc	336
Gly	Ala	Leu	Ser	Leu	Ser	Leu	Ala	Ala	Gly	Ser	Tyr	Arg	Asp	Ser	Thr	
			100				105						110			
cgc	gtt	gca	ggc	acc	gac	cca	gga	ctc	gtc	cgc	gcc	atg	tgt	gaa	agc	384
Arg	Val	Ala	Gly	Thr	Asp	Pro	Gly	Leu	Val	Arg	Ala	Met	Cys	Glu	Ser	
		115					120					125				
aac	gcc	ggc	cca	ctg	gtc	aaa	gcc	ctc	gac	gaa	gca	ctg	gcg	atc	ctc	432
Asn	Ala	Gly	Pro	Leu	Val	Lys	Ala	Leu	Asp	Glu	Ala	Leu	Ala	Ile	Leu	
	130					135					140					
cac	gaa	gcc	cgc	gaa	ggc	ctc	acc	gca	gaa	cag	cca	aac	atc	gag	caa	480
His	Glu	Ala	Arg	Glu	Gly	Leu	Thr	Ala	Glu	Gln	Pro	Asn	Ile	Glu	Gln	
145				150				155							160	
ctt	gcc	gac	aac	ggc	tac	cga	tcc	cgc	atc	cgc	tac	gaa	gcc	cgc	tcc	528
Leu	Ala	Asp	Asn	Gly	Tyr	Arg	Ser	Arg	Ile	Arg	Tyr	Glu	Ala	Arg	Ser	
			165					170						175		
ggc	cag	cga	cgc	gcc	aaa	gaa	tcc	gtt	agc	cct	acc	atc	acc	tca	tcc	576
Gly	Gln	Arg	Arg	Ala	Lys	Glu	Ser	Val	Ser	Pro	Thr	Ile	Thr	Ser	Ser	
			180				185						190			
agg	cca	gtg	ctc	cgt	ctc	cac	ccg	ggc	aca	cca	aac	tgg	gag	aag	cag	624
Arg	Pro	Val	Leu	Arg	Leu	His	Pro	Gly	Thr	Pro	Asn	Trp	Glu	Lys	Gln	
		195					200					205				
ctc	atc	cac	gct	gaa	acc	ctc	ggc	gca	cgg	atc	gaa	gtg	tt			

&lt;210&gt; 454

&lt;211&gt; 222

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 454

Tyr Val Gly Ser His Pro Met Ala Gly Thr Ala Asn Ser Gly Trp Ser  
 1 5 10 15

Ala Ser Met Asp Gly Leu Phe Lys Arg Ala Val Trp Val Val Thr Phe  
 20 25 30

Asp Gln Leu Phe Asp Gly Thr Asp Ile Asn Ser Thr Trp Ile Ser Ile  
 35 40 45

Trp Lys Asp Val Val Gln Met Ala Leu Ala Val Gly Ala Glu Val Val  
 50 55 60

Pro Ser Arg Val Gly Pro His Asp Ala Ala Ala Ala Arg Val Ser His  
 65 70 75 80

Leu Thr His Ile Leu Ala Glu Thr Leu Ala Ile Val Gly Asp Asn Gly  
 85 90 95

Gly Ala Leu Ser Leu Ser Leu Ala Ala Gly Ser Tyr Arg Asp Ser Thr  
 100 105 110

Arg Val Ala Gly Thr Asp Pro Gly Leu Val Arg Ala Met Cys Glu Ser  
 115 120 125

Asn Ala Gly Pro Leu Val Lys Ala Leu Asp Glu Ala Leu Ala Ile Leu  
 130 135 140

His Glu Ala Arg Glu Gly Leu Thr Ala Glu Gln Pro Asn Ile Glu Gln  
 145 150 155 160

Leu Ala Asp Asn Gly Tyr Arg Ser Arg Ile Arg Tyr Glu Ala Arg Ser  
 165 170 175

Gly Gln Arg Arg Ala Lys Glu Ser Val Ser Pro Thr Ile Thr Ser Ser  
 180 185 190

Arg Pro Val Leu Arg Leu His Pro Gly Thr Pro Asn Trp Glu Lys Gln  
 195 200 205

Leu Ile His Ala Glu Thr Leu Gly Ala Arg Ile Glu Val Phe  
 210 215 220

&lt;210&gt; 455

&lt;211&gt; 346

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(346)

&lt;223&gt; FRXA00452

&lt;400&gt; 455

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ccatttacct tcaactaagg tagccgtaac tgcaaagctc aggccatcct cttcagtgtt 60
catagagata accgtagtag gtatgtgcca cacttgtcag gtg act acc aaa gac 115
                               Val Thr Thr Lys Asp
                               1                               5

att tcc cgc cca gta tgc atc ctg ggc ctc ggc ctc atc ggc gga tcc 163
Ile Ser Arg Pro Val Cys Ile Leu Gly Leu Gly Leu Ile Gly Gly Ser
                               10                               15                               20

ctc ctc cgc gac ctc cat gca gcc aac cac tcc gtc ttc ggc tac aac 211
Leu Leu Arg Asp Leu His Ala Ala Asn His Ser Val Phe Gly Tyr Asn
                               25                               30                               35

cgc tca cgc tcc ggc gct aaa tca gcc gtc gac gaa ggc ttc gac gtt 259
Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp Glu Gly Phe Asp Val
                               40                               45                               50

tcc gcc gat ctt gaa gca acc ctc cag cgt gca gcc gcc gaa gat gcg 307
Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala Ala Ala Glu Asp Ala
                               55                               60                               65

ctc atc gtc ctc gcg gtc ccc atg acc gca atc gat tcg 346
Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile Asp Ser
70                               75                               80

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&lt;210&gt; 456

&lt;211&gt; 82

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 456

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Val Thr Thr Lys Asp Ile Ser Arg Pro Val Cys Ile Leu Gly Leu Gly
  1                               5                               10                               15

Leu Ile Gly Gly Ser Leu Leu Arg Asp Leu His Ala Ala Asn His Ser
                20                25                30

Val Phe Gly Tyr Asn Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp
                35                40                45

Glu Gly Phe Asp Val Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala
  50                55                60

Ala Ala Glu Asp Ala Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile
  65                70                75                80

Asp Ser

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&lt;210&gt; 457

&lt;211&gt; 1248

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1225)

&lt;223&gt; RXA00584

&lt;400&gt; 457

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tagttgtgcc acctaaaacg cgaacagaac cggagtcgag cagcacctcc ccgcaagggt 60

agaggggctg cttttttgtt tcctaaattc accccatccc atg cat agc cct gaa 115
                                         Met His Ser Pro Glu
                                         1           5

agg caa gaa aaa atg agt tct cca gtc tca ctc gaa aac gcg gcg tca 163
Arg Gln Glu Lys Met Ser Ser Pro Val Ser Leu Glu Asn Ala Ala Ser
              10                      15                      20

acc agc aac aag cgc gtc gtg gct ttc cac gag ctg cct agc cct aca 211
Thr Ser Asn Lys Arg Val Val Ala Phe His Glu Leu Pro Ser Pro Thr
              25                      30                      35

gat ctc atc gcc gca aac cca ctg aca cca aag cag gct tcc aag gtg 259
Asp Leu Ile Ala Ala Asn Pro Leu Thr Pro Lys Gln Ala Ser Lys Val
              40                      45                      50

gag cag gat cgc cag gac atc gct gat atc ttc gct ggc gac gat gac 307
Glu Gln Asp Arg Gln Asp Ile Ala Asp Ile Phe Ala Gly Asp Asp Asp
              55                      60                      65

cgc ctc gtt gtc gtt gtg gga cct tgc tca gtt cac gat cct gaa gca 355
Arg Leu Val Val Val Val Gly Pro Cys Ser Val His Asp Pro Glu Ala
              70                      75                      80                      85

gcc atc gat tac gca aac cgc ctg gct ccg ctg gca aag cgc ctt gat 403
Ala Ile Asp Tyr Ala Asn Arg Leu Ala Pro Leu Ala Lys Arg Leu Asp
              90                      95                      100

cag gac ctc aag att gtc atg cgc gtg tac ttc gag aag cct cgc acc 451
Gln Asp Leu Lys Ile Val Met Arg Val Tyr Phe Glu Lys Pro Arg Thr
              105                      110                      115

atc gtc gga tgg aag gga ttg atc aat gat cct cac ctc aac gaa acc 499
Ile Val Gly Trp Lys Gly Leu Ile Asn Asp Pro His Leu Asn Glu Thr
              120                      125                      130

tac gac atc cca gag ggc ttg cgc att gcg cgc aaa gtg ctt atc gac 547
Tyr Asp Ile Pro Glu Gly Leu Arg Ile Ala Arg Lys Val Leu Ile Asp
              135                      140                      145

gtt gtg aac ctt gat ctc cca gtc ggc tgc gaa ttc ctc gaa cca aac 595
Val Val Asn Leu Asp Leu Pro Val Gly Cys Glu Phe Leu Glu Pro Asn
              150                      155                      160                      165

agc cct cag tac tac gcc gac act gtc gca tgg gga gca atc ggc gct 643
Ser Pro Gln Tyr Tyr Ala Asp Thr Val Ala Trp Gly Ala Ile Gly Ala
              170                      175                      180

cgt acc acc gaa tct cag gtg cac cgc cag ctg gct tct ggg atg tct 691
Arg Thr Thr Glu Ser Gln Val His Arg Gln Leu Ala Ser Gly Met Ser
              185                      190                      195

atg cca att ggt ttc aag aac gga act gac gga aac atc cag gtt gca 739
Met Pro Ile Gly Phe Lys Asn Gly Thr Asp Gly Asn Ile Gln Val Ala
              200                      205                      210

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gtc gac gcg gta cag gct gcc cag aac cca cac ttc ttc ttc gga acc 787  
 Val Asp Ala Val Gln Ala Ala Gln Asn Pro His Phe Phe Phe Gly Thr  
 215 220 225

tcc gac gac ggc gcg ctg agc gtc gtg gag acc gca ggc aac agc aac 835  
 Ser Asp Asp Gly Ala Leu Ser Val Val Glu Thr Ala Gly Asn Ser Asn  
 230 235 240 245

tcc cac atc att ttg cgc ggc ggt acc tcc ggc ccg aat cat gat gca 883  
 Ser His Ile Ile Leu Arg Gly Gly Thr Ser Gly Pro Asn His Asp Ala  
 250 255 260

gct tcg gtg gag gcc gtc gtc gag aag ctt ggt gaa aac gct cgt ctc 931  
 Ala Ser Val Glu Ala Val Val Glu Lys Leu Gly Glu Asn Ala Arg Leu  
 265 270 275

atg atc gat gct tcc cat gct aac tcc ggc aag gat cat atc cga cag 979  
 Met Ile Asp Ala Ser His Ala Asn Ser Gly Lys Asp His Ile Arg Gln  
 280 285 290

gtt gag gtt gtt cgt gaa atc gca gag cag att tct ggc ggt tct gaa 1027  
 Val Glu Val Val Arg Glu Ile Ala Glu Gln Ile Ser Gly Gly Ser Glu  
 295 300 305

gct gtg gct gga atc atg att gag tcc ttc ctc gtt ggt ggc gca cag 1075  
 Ala Val Ala Gly Ile Met Ile Glu Ser Phe Leu Val Gly Gly Ala Gln  
 310 315 320 325

aac ctt gat cct gcg aaa ttg cgc atc aat ggc ggt gaa ggc ctg gtg 1123  
 Asn Leu Asp Pro Ala Lys Leu Arg Ile Asn Gly Gly Glu Gly Leu Val  
 330 335 340

tac gga cag tct gtg acc gat aag tgc atc gat att gac acc acc atc 1171  
 Tyr Gly Gln Ser Val Thr Asp Lys Cys Ile Asp Ile Asp Thr Thr Ile  
 345 350 355

gat ttg ctc gct gag ctg gcc gca gca gta agg gaa cgc cga gca gca 1219  
 Asp Leu Leu Ala Glu Leu Ala Ala Ala Val Arg Glu Arg Arg Ala Ala  
 360 365 370

gcc aag taattaaggg cgctagactg tta 1248  
 Ala Lys  
 375

&lt;210&gt; 458

&lt;211&gt; 375

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 458

Met His Ser Pro Glu Arg Gln Glu Lys Met Ser Ser Pro Val Ser Leu  
 1 5 10 15

Glu Asn Ala Ala Ser Thr Ser Asn Lys Arg Val Val Ala Phe His Glu  
 20 25 30

Leu Pro Ser Pro Thr Asp Leu Ile Ala Ala Asn Pro Leu Thr Pro Lys  
 35 40 45

Gln Ala Ser Lys Val Glu Gln Asp Arg Gln Asp Ile Ala Asp Ile Phe



50	55	60
Ala Gly Asp Asp Asp Arg Leu Val Val Val Val Gly Pro Cys Ser Val 65 70 75 80		
His Asp Pro Glu Ala Ala Ile Asp Tyr Ala Asn Arg Leu Ala Pro Leu 85 90 95		
Ala Lys Arg Leu Asp Gln Asp Leu Lys Ile Val Met Arg Val Tyr Phe 100 105 110		
Glu Lys Pro Arg Thr Ile Val Gly Trp Lys Gly Leu Ile Asn Asp Pro 115 120 125		
His Leu Asn Glu Thr Tyr Asp Ile Pro Glu Gly Leu Arg Ile Ala Arg 130 135 140		
Lys Val Leu Ile Asp Val Val Asn Leu Asp Leu Pro Val Gly Cys Glu 145 150 155 160		
Phe Leu Glu Pro Asn Ser Pro Gln Tyr Tyr Ala Asp Thr Val Ala Trp 165 170 175		
Gly Ala Ile Gly Ala Arg Thr Thr Glu Ser Gln Val His Arg Gln Leu 180 185 190		
Ala Ser Gly Met Ser Met Pro Ile Gly Phe Lys Asn Gly Thr Asp Gly 195 200 205		
Asn Ile Gln Val Ala Val Asp Ala Val Gln Ala Ala Gln Asn Pro His 210 215 220		
Phe Phe Phe Gly Thr Ser Asp Asp Gly Ala Leu Ser Val Val Glu Thr 225 230 235 240		
Ala Gly Asn Ser Asn Ser His Ile Ile Leu Arg Gly Gly Thr Ser Gly 245 250 255		
Pro Asn His Asp Ala Ala Ser Val Glu Ala Val Val Glu Lys Leu Gly 260 265 270		
Glu Asn Ala Arg Leu Met Ile Asp Ala Ser His Ala Asn Ser Gly Lys 275 280 285		
Asp His Ile Arg Gln Val Glu Val Val Arg Glu Ile Ala Glu Gln Ile 290 295 300		
Ser Gly Gly Ser Glu Ala Val Ala Gly Ile Met Ile Glu Ser Phe Leu 305 310 315 320		
Val Gly Gly Ala Gln Asn Leu Asp Pro Ala Lys Leu Arg Ile Asn Gly 325 330 335		
Gly Glu Gly Leu Val Tyr Gly Gln Ser Val Thr Asp Lys Cys Ile Asp 340 345 350		
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				Met	Arg	Val	Leu	Ile								5
				1												
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Ile	Asp	Asn	Tyr	Asp	Ser	Phe	Thr	Phe	Asn	Leu	Ala	Thr	Tyr	Val	Glu	20
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Glu	Val	Thr	Gly	Gln	Ala	Pro	Val	Val	Val	Pro	Asn	Asp	Gln	Glu	Ile	35
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Asp	Glu	Met	Leu	Phe	Asp	Ala	Val	Ile	Leu	Ser	Pro	Gly	Pro	Gly	His	50
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Ala	Gly	Val	Ala	Ala	Asp	Phe	Gly	Ile	Cys	Ala	Gly	Val	Ile	Glu	Arg	65
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Ala	Arg	Val	Pro	Ile	Leu	Gly	Val	Cys	Leu	Gly	His	Gln	Gly	Ile	Ala	85
	70											75				
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Leu	Ala	Tyr	Gly	Gly	Asp	Val	Asp	Leu	Ala	Pro	Arg	Pro	Val	His	Gly	90
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Glu	Val	Ser	Gln	Ile	Thr	His	Asp	Gly	Ser	Gly	Leu	Phe	Ala	Gly	Ile	110
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Pro	Glu	Thr	Phe	Glu	Ala	Val	Arg	Tyr	His	Ser	Met	Val	Ala	Thr	Arg	120
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Leu	Pro	Glu	Ser	Leu	Lys	Ala	Thr	Ala	Thr	Ser	Asp	Asp	Gly	Leu	Ile	135
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Met	Ala	Leu	Ala	His	Glu	Val	Leu	Pro	Gln	Trp	Gly	Val	Gln	Phe	His	150
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ccg	gaa	tct	att	ggt	gga	caa	ttc	ggc	cat	cag	atc	att	aag	aac	ttc	643
Pro	Glu	Ser	Ile	Gly	Gly	Gln	Phe	Gly	His	Gln	Ile	Ile	Lys	Asn	Phe	

				170				175				180							
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Leu	Asn	Leu	Ala	Arg	Thr	Tyr	Arg	Trp	Gln	Leu	Thr	Glu	Lys	Thr	Ile				
185								190				195							
ccg	ctc	agc	gtt	gat	tca	gca	gcg	gtt	ttt	gaa	aca	ttc	ttt	gcc	cat	739			
Pro	Leu	Ser	Val	Asp	Ser	Ala	Ala	Val	Phe	Glu	Thr	Phe	Phe	Ala	His				
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Ser	Ser	His	Ala	Phe	Trp	Leu	Asp	Asp	Ala	Gln	Gly	Thr	Ser	Tyr	Leu				
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Gly	Asp	Ala	Ser	Gly	Pro	Leu	Ala	Arg	Thr	Lys	Thr	His	Asn	Val	Gly				
230								235				240				245			
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Glu	Gly	Asp	Phe	Phe	Thr	Trp	Leu	Lys	Glu	Asp	Leu	Ala	Ala	Asn	Ser				
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Val	Ala	Pro	Gly	Gln	Gly	Phe	Arg	Leu	Gly	Trp	Val	Gly	Tyr	Val	Gly				
265								270				275							
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Tyr	Glu	Leu	Lys	Ala	Glu	Ala	Gly	Ala	Arg	Ala	Ala	His	Thr	Ser	Ser				
280								285				290							
ctt	ccg	gat	gcg	cac	ctc	att	ttt	gcc	gat	cgc	gcc	atc	gca	gtg	gaa	1027			
Leu	Pro	Asp	Ala	His	Leu	Ile	Phe	Ala	Asp	Arg	Ala	Ile	Ala	Val	Glu				
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Ser	Asp	Gln	Val	Arg	Leu	Leu	Ala	Leu	Gly	Glu	Gln	Asp	Glu	Trp	Phe				
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gaa	gaa	acc	atc	aag	aag	ctg	cat	aat	ctt	gtc	gcc	ccg	cgg	ata	cct	1123			
Glu	Glu	Thr	Ile	Lys	Lys	Leu	His	Asn	Leu	Val	Ala	Pro	Arg	Ile	Pro				
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Ala	Ser	Gly	His	Leu	Ala	Leu	Gln	Val	Arg	Asp	Ser	Lys	Asp	Glu	Tyr				
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ctc	gac	aaa	att	cgc	aga	gcc	cag	gag	ctg	att	act	cgc	ggc	gaa	tcg	1219			
Leu	Asp	Lys	Ile	Arg	Arg	Ala	Gln	Glu	Leu	Ile	Thr	Arg	Gly	Glu	Ser				
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tat	gaa	atc	tgc	ctg	acc	aca	aaa	ctt	cag	ggc	acc	act	gat	gtg	gcc	1267			
Tyr	Glu	Ile	Cys	Leu	Thr	Thr	Lys	Leu	Gln	Gly	Thr	Thr	Asp	Val	Ala				
375				380				385											
cct	ctg	gct	gcc	tat	cta	gca	ctg	cgt	ggg	gcc	aat	ccc	acc	gca	tat	1315			
Pro	Leu	Ala	Ala	Tyr	Leu	Ala	Leu	Arg	Gly	Ala	Asn	Pro	Thr	Ala	Tyr				
390				395				400				405							
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Gly	Ala	Tyr	Leu	Gln	Leu	Gly	Asp	Thr	Ser	Ile	Leu	Ser	Ser	Ser	Pro				
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 Glu Arg Phe Ile Thr Ile Asp Ser Ala Gly Tyr Val Glu Ser Lys Pro  
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 att aaa ggc acc agg ccg cgt ggg cga aca gcg caa gaa gac caa gaa 1459  
 Ile Lys Gly Thr Arg Pro Arg Gly Arg Thr Ala Gln Glu Asp Gln Glu  
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 Ile Ile Ala Glu Leu Arg Ser Asn Pro Lys Asp Arg Ala Glu Asn Leu  
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 Met Ile Val Asp Leu Val Arg Asn Asp Leu Ala Arg Gly Ala Leu Pro  
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 Thr Thr Val Lys Thr Ser Lys Leu Phe Asp Val Glu Thr Tyr Ala Thr  
 490 495 500  
  
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 Val His Gln Leu Val Ser Thr Val Ser Ala Glu Leu Gly Pro Arg Ser  
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 ccg att gag tgc gtg cgc gca gca ttc ccc ggt ggt tcg atg act ggt 1699  
 Pro Ile Glu Cys Val Arg Ala Ala Phe Pro Gly Gly Ser Met Thr Gly  
 520 525 530  
  
 gcc cca aag ctg cgc acc atg gag atc atc gat gag ctg gag gca gct 1747  
 Ala Pro Lys Leu Arg Thr Met Glu Ile Ile Asp Glu Leu Glu Ala Ala  
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 cct cgc ggt att tac tca ggt ggc ttg gga tat ttt tcc ctc gac ggc 1795  
 Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr Phe Ser Leu Asp Gly  
 550 555 560 565  
  
 gca gtt gat ctc tcc atg gtg atc aga act ctc gtc atc cag aac aat 1843  
 Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu Val Ile Gln Asn Asn  
 570 575 580  
  
 cac gtg gag tac gga gtg ggc ggt gca ctt ctt gct ctg tct gat ccg 1891  
 His Val Glu Tyr Gly Val Gly Gly Ala Leu Leu Ala Leu Ser Asp Pro  
 585 590 595  
  
 gag gct gag tgg gag gaa atc cgc gtt aaa tca cgg cct ctg ctg aat 1939  
 Glu Ala Glu Trp Glu Glu Ile Arg Val Lys Ser Arg Pro Leu Leu Asn  
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 Leu Phe Gly Val Glu Phe Pro  
 615 620

&lt;210&gt; 460

&lt;211&gt; 620

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 460

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Ala Thr Tyr Val Glu Glu Val Thr Gly Gln Ala Pro Val Val Val Pro	20	25	30
Asn Asp Gln Glu Ile Asp Glu Met Leu Phe Asp Ala Val Ile Leu Ser	35	40	45
Pro Gly Pro Gly His Ala Gly Val Ala Ala Asp Phe Gly Ile Cys Ala	50	55	60
Gly Val Ile Glu Arg Ala Arg Val Pro Ile Leu Gly Val Cys Leu Gly	65	70	75
His Gln Gly Ile Ala Leu Ala Tyr Gly Gly Asp Val Asp Leu Ala Pro	85	90	95
Arg Pro Val His Gly Glu Val Ser Gln Ile Thr His Asp Gly Ser Gly	100	105	110
Leu Phe Ala Gly Ile Pro Glu Thr Phe Glu Ala Val Arg Tyr His Ser	115	120	125
Met Val Ala Thr Arg Leu Pro Glu Ser Leu Lys Ala Thr Ala Thr Ser	130	135	140
Asp Asp Gly Leu Ile Met Ala Leu Ala His Glu Val Leu Pro Gln Trp	145	150	155
Gly Val Gln Phe His Pro Glu Ser Ile Gly Gly Gln Phe Gly His Gln	165	170	175
Ile Ile Lys Asn Phe Leu Asn Leu Ala Arg Thr Tyr Arg Trp Gln Leu	180	185	190
Thr Glu Lys Thr Ile Pro Leu Ser Val Asp Ser Ala Ala Val Phe Glu	195	200	205
Thr Phe Phe Ala His Ser Ser His Ala Phe Trp Leu Asp Asp Ala Gln	210	215	220
Gly Thr Ser Tyr Leu Gly Asp Ala Ser Gly Pro Leu Ala Arg Thr Lys	225	230	235
Thr His Asn Val Gly Glu Gly Asp Phe Phe Thr Trp Leu Lys Glu Asp	245	250	255
Leu Ala Ala Asn Ser Val Ala Pro Gly Gln Gly Phe Arg Leu Gly Trp	260	265	270
Val Gly Tyr Val Gly Tyr Glu Leu Lys Ala Glu Ala Gly Ala Arg Ala	275	280	285
Ala His Thr Ser Ser Leu Pro Asp Ala His Leu Ile Phe Ala Asp Arg	290	295	300
Ala Ile Ala Val Glu Ser Asp Gln Val Arg Leu Leu Ala Leu Gly Glu	305	310	315
Gln Asp Glu Trp Phe Glu Glu Thr Ile Lys Lys Leu His Asn Leu Val	325	330	335

Ala Pro Arg Ile Pro Ala Ser Gly His Leu Ala Leu Gln Val Arg Asp  
 340 345 350  
 Ser Lys Asp Glu Tyr Leu Asp Lys Ile Arg Arg Ala Gln Glu Leu Ile  
 355 360 365  
 Thr Arg Gly Glu Ser Tyr Glu Ile Cys Leu Thr Thr Lys Leu Gln Gly  
 370 375 380  
 Thr Thr Asp Val Ala Pro Leu Ala Ala Tyr Leu Ala Leu Arg Gly Ala  
 385 390 395 400  
 Asn Pro Thr Ala Tyr Gly Ala Tyr Leu Gln Leu Gly Asp Thr Ser Ile  
 405 410 415  
 Leu Ser Ser Ser Pro Glu Arg Phe Ile Thr Ile Asp Ser Ala Gly Tyr  
 420 425 430  
 Val Glu Ser Lys Pro Ile Lys Gly Thr Arg Pro Arg Gly Arg Thr Ala  
 435 440 445  
 Gln Glu Asp Gln Glu Ile Ile Ala Glu Leu Arg Ser Asn Pro Lys Asp  
 450 455 460  
 Arg Ala Glu Asn Leu Met Ile Val Asp Leu Val Arg Asn Asp Leu Ala  
 465 470 475 480  
 Arg Gly Ala Leu Pro Thr Thr Val Lys Thr Ser Lys Leu Phe Asp Val  
 485 490 495  
 Glu Thr Tyr Ala Thr Val His Gln Leu Val Ser Thr Val Ser Ala Glu  
 500 505 510  
 Leu Gly Pro Arg Ser Pro Ile Glu Cys Val Arg Ala Ala Phe Pro Gly  
 515 520 525  
 Gly Ser Met Thr Gly Ala Pro Lys Leu Arg Thr Met Glu Ile Ile Asp  
 530 535 540  
 Glu Leu Glu Ala Ala Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr  
 545 550 555 560  
 Phe Ser Leu Asp Gly Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu  
 565 570 575  
 Val Ile Gln Asn Asn His Val Glu Tyr Gly Val Gly Gly Ala Leu Leu  
 580 585 590  
 Ala Leu Ser Asp Pro Glu Ala Glu Trp Glu Glu Ile Arg Val Lys Ser  
 595 600 605  
 Arg Pro Leu Leu Asn Leu Phe Gly Val Glu Phe Pro  
 610 615 620

&lt;210&gt; 461

&lt;211&gt; 747

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(724)

&lt;223&gt; RXA00958

&lt;400&gt; 461

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                                     Met Thr His Val Val
                                     1 5

ctc att gat aat cac gat tct ttt gtc tac aac ctg gtg gat gcg ttc 163
Leu Ile Asp Asn His Asp Ser Phe Val Tyr Asn Leu Val Asp Ala Phe
                                     10 15 20

gcc gtg gcc ggt tat aag tgc acg gtg ttc cgc aat acg gtg cca gtg 211
Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg Asn Thr Val Pro Val
                                     25 30 35

gaa acc att ttg gca gcc aac ccg gac ctg atc tgc ctt tca cct gga 259
Glu Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile Cys Leu Ser Pro Gly
                                     40 45 50

cct ggt tac cct gcc gat gcg ggc aac atg atg gcg ctg atc gag cgc 307
Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met Ala Leu Ile Glu Arg
                                     55 60 65

aca ctc ggc cag att cct tta ctg ggt att tgc ctc ggc tac cag gca 355
Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys Leu Gly Tyr Gln Ala
                                     70 75 80 85

ctc atc gaa tac cac ggc ggc aag gtt gag cct tgt ggc cct gtg cac 403
Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro Cys Gly Pro Val His
                                     90 95 100

ggc acc acc gac aac atg atc ctt act gat gca ggt gtg cag agc cct 451
Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala Gly Val Gln Ser Pro
                                     105 110 115

gtt ttt gca ggt ctt gcc act gat gtt gag cct gat cat cca gaa atc 499
Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro Asp His Pro Glu Ile
                                     120 125 130

cca ggc cgc aag gtt cca att ggc cgt tat cac tca ctg ggc tgc gtg 547
Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His Ser Leu Gly Cys Val
                                     135 140 145

gtt gcc cca gac ggt att gaa tca cta ggt acc tgt tcc tcg gag att 595
Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr Cys Ser Ser Glu Ile
                                     150 155 160 165

ggg gat gtc atc atg gcg gca cgc acc acc gat gga aag gcc att ggc 643
Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp Gly Lys Ala Ile Gly
                                     170 175 180

ctg cag ttt cac cct gag tca gtg cta agc cca acg ggt cct gtc att 691
Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro Thr Gly Pro Val Ile
                                     185 190 195

ttg tcc cgc tgt gtc gaa cag ctt ctc gcg aac taataaaaaa aggatttgat 744

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tca

747

<210> 462

<211> 208

<212> PRT

<213> Corynebacterium glutamicum

<400> 462

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20 25 30

Asn Thr Val Pro Val Glu Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile  
35 40 45

Cys Leu Ser Pro Gly Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met  
50 55 60

Ala Leu Ile Glu Arg Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys  
65 70 75 80

Leu Gly Tyr Gln Ala Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro  
85 90 95

Cys Gly Pro Val His Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala  
100 105 110

Gly Val Gln Ser Pro Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro  
115 120 125

Asp His Pro Glu Ile Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His  
130 135 140

Ser Leu Gly Cys Val Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr  
145 150 155 160

Cys Ser Ser Glu Ile Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp  
165 170 175

Gly Lys Ala Ile Gly Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro  
180 185 190

Thr Gly Pro Val Ile Leu Ser Arg Cys Val Glu Gln Leu Leu Ala Asn  
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<210> 463

<211> 469

<212> DNA

<213> Corynebacterium glutamicum

<220>



&lt;221&gt; CDS

&lt;222&gt; (101)..(469)

&lt;223&gt; RXN03007

&lt;400&gt; 463

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                                   Met Thr Ser Pro Ala
                                   1 5

aca ctg aaa gtt ctc aac gcc tac ttg gat aac ccc act cca acc ctg 163
Thr Leu Lys Val Leu Asn Ala Tyr Leu Asp Asn Pro Thr Pro Thr Leu
                                   10 15 20

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Glu Glu Ala Ile Glu Val Phe Thr Pro Leu Thr Val Gly Glu Tyr Asp
                                   25 30 35

gac gtg cac atc gca gcg ctg ctt gcc acc atc cgt act cgc ggt gag 259
Asp Val His Ile Ala Ala Leu Leu Ala Thr Ile Arg Thr Arg Gly Glu
                                   40 45 50

cag ttc gct gat att gcc ggc gct gcc aag gcg ttc ctc gcg gcg gct 307
Gln Phe Ala Asp Ile Ala Gly Ala Ala Lys Ala Phe Leu Ala Ala Ala
                                   55 60 65

cgt ccg ttc ccg att act ggc gca ggt ttg cta gat tcc gct ggt act 355
Arg Pro Phe Pro Ile Thr Gly Ala Gly Leu Leu Asp Ser Ala Gly Thr
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ggt ggc gac ggt gcc aac acc atc aac atc acc acc ggc gca tcc ctg 403
Gly Gly Asp Gly Ala Asn Thr Ile Asn Ile Thr Thr Gly Ala Ser Leu
                                   90 95 100

atc gca gca tcc ggt gga gtg aag ctg gtt aag cac ggc aac cgt tcg 451
Ile Ala Ala Ser Gly Gly Val Lys Leu Val Lys His Gly Asn Arg Ser
                                   105 110 115

gtg agc tcc aag tcc ggc 469
Val Ser Ser Lys Ser Gly
                                   120

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&lt;210&gt; 464

&lt;211&gt; 123

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 464

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Met Thr Ser Pro Ala Thr Leu Lys Val Leu Asn Ala Tyr Leu Asp Asn
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Pro Thr Pro Thr Leu Glu Glu Ala Ile Glu Val Phe Thr Pro Leu Thr
 20 25 30

Val Gly Glu Tyr Asp Asp Val His Ile Ala Ala Leu Leu Ala Thr Ile
 35 40 45

Arg Thr Arg Gly Glu Gln Phe Ala Asp Ile Ala Gly Ala Ala Lys Ala
 50 55 60

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Phe Leu Ala Ala Ala Arg Pro Phe Pro Ile Thr Gly Ala Gly Leu Leu  
 65 70 75 80  
 Asp Ser Ala Gly Thr Gly Gly Asp Gly Ala Asn Thr Ile Asn Ile Thr  
 85 90 95  
 Thr Gly Ala Ser Leu Ile Ala Ala Ser Gly Gly Val Lys Leu Val Lys  
 100 105 110  
 His Gly Asn Arg Ser Val Ser Ser Lys Ser Gly  
 115 120

&lt;210&gt; 465

&lt;211&gt; 564

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(541)

&lt;223&gt; RXN02918

&lt;400&gt; 465

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 Met Ser Glu Ile Leu  
 1 5  
 gaa acc tat tgg gca ccc cac ttt gga aaa acc gaa gaa gcc aca gca 163  
 Glu Thr Tyr Trp Ala Pro His Phe Gly Lys Thr Glu Glu Ala Thr Ala  
 10 15 20  
 ctc gtt tca tac ctg gca caa gct tcc ggc gat ccc att gag gtt cac 211  
 Leu Val Ser Tyr Leu Ala Gln Ala Ser Gly Asp Pro Ile Glu Val His  
 25 30 35  
 acc ctg ttc ggg gat tta ggt tta gac gga ctc tct gga aac tac acc 259  
 Thr Leu Phe Gly Asp Leu Gly Leu Asp Gly Leu Ser Gly Asn Tyr Thr  
 40 45 50  
 gac act gag att gac ggc tac ggc gac gca ttc ctg ctg gtt gca gcg 307  
 Asp Thr Glu Ile Asp Gly Tyr Gly Asp Ala Phe Leu Leu Val Ala Ala  
 55 60 65  
 cta tcc gtg ttg atg gct gaa aac aaa gca aca ggt ggc gtg aat ctg 355  
 Leu Ser Val Leu Met Ala Glu Asn Lys Ala Thr Gly Gly Val Asn Leu  
 70 75 80 85  
 ggt gag ctt ggg gga gct gat aaa tcg atc cgg ctg cat gtt gaa tcc 403  
 Gly Glu Leu Gly Gly Ala Asp Lys Ser Ile Arg Leu His Val Glu Ser  
 90 95 100  
 aag gag aac acc caa atc aac acc gca ttg aag tat ttt gcg ctc tcc 451  
 Lys Glu Asn Thr Gln Ile Asn Thr Ala Leu Lys Tyr Phe Ala Leu Ser  
 105 110 115  
 cca gaa gac cac gca gca gca gat cgc ttc gat gag gat gac ctg tct 499  
 Pro Glu Asp His Ala Ala Ala Asp Arg Phe Asp Glu Asp Asp Leu Ser

120 125 130  
gag ctt gcc aac ttg agt gaa gag ctg cgc gga cag ctg gac 541  
Glu Leu Ala Asn Leu Ser Glu Glu Leu Arg Gly Gln Leu Asp  
135 140 145

taattgtctc ccattttaagg agt 564

<210> 466  
<211> 147  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 466  
Met Ser Glu Ile Leu Glu Thr Tyr Trp Ala Pro His Phe Gly Lys Thr  
1 5 10 15  
Glu Glu Ala Thr Ala Leu Val Ser Tyr Leu Ala Gln Ala Ser Gly Asp  
20 25 30  
Pro Ile Glu Val His Thr Leu Phe Gly Asp Leu Gly Leu Asp Gly Leu  
35 40 45  
Ser Gly Asn Tyr Thr Asp Thr Glu Ile Asp Gly Tyr Gly Asp Ala Phe  
50 55 60  
Leu Leu Val Ala Ala Leu Ser Val Leu Met Ala Glu Asn Lys Ala Thr  
65 70 75 80  
Gly Gly Val Asn Leu Gly Glu Leu Gly Gly Ala Asp Lys Ser Ile Arg  
85 90 95  
Leu His Val Glu Ser Lys Glu Asn Thr Gln Ile Asn Thr Ala Leu Lys  
100 105 110  
Tyr Phe Ala Leu Ser Pro Glu Asp His Ala Ala Ala Asp Arg Phe Asp  
115 120 125  
Glu Asp Asp Leu Ser Glu Leu Ala Asn Leu Ser Glu Glu Leu Arg Gly  
130 135 140  
Gln Leu Asp  
145

<210> 467  
<211> 735  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(712)  
<223> RXN01116

<400> 467  
tgccaggaat ttacgtcaac cgcgtcgtcc acgttggacc gcaggaaacc ggaatcgaaa 60  
acaggacggt gtctaactaa tgacttggga tcataaccaa atg gca gcc cgc gtt 115  
Met Ala Ala Arg Val

	1	5	
gcc cag gaa ctt gaa gac ggc cag tac gtc aac ctc ggc atc ggc atg			163
Ala Gln Glu Leu Glu Asp Gly Gln Tyr Val Asn Leu Gly Ile Gly Met			
	10	20	
cct aca ctt atc ccc ggc tac ctg cct gag gga cta gag gtt atc ctt			211
Pro Thr Leu Ile Pro Gly Tyr Leu Pro Glu Gly Leu Glu Val Ile Leu			
	25	35	
cac tcc gaa aac ggt gtg ctg ggc gtt gga cct tac cca act gaa gag			259
His Ser Glu Asn Gly Val Leu Gly Val Gly Pro Tyr Pro Thr Glu Glu			
	40	50	
gaa ctt gat cct gag ctg atc aac gcc ggc aag gaa acc atc acg gtt			307
Glu Leu Asp Pro Glu Leu Ile Asn Ala Gly Lys Glu Thr Ile Thr Val			
	55	65	
gca cct ggc gca tcc tac ttc tcc tct tct gat tct ttc gcc atg atc			355
Ala Pro Gly Ala Ser Tyr Phe Ser Ser Ser Asp Ser Phe Ala Met Ile			
	70	80	85
cgc tcc aag tct gtc gac gtt gca gtc ttg ggc gtt atg gaa gtc tcc			403
Arg Ser Lys Ser Val Asp Val Ala Val Leu Gly Val Met Glu Val Ser			
	90	95	100
cag tac ggc gac ctg gcc aac tgg atg att ccc ggc aag ctg gtc aag			451
Gln Tyr Gly Asp Leu Ala Asn Trp Met Ile Pro Gly Lys Leu Val Lys			
	105	110	115
ggt atg ggt ggc gca atg gat ctg gtg cac ggc gca tcc aag atc atc			499
Gly Met Gly Gly Ala Met Asp Leu Val His Gly Ala Ser Lys Ile Ile			
	120	125	130
gcc atg acc gat cac atc acc aag aag ggc gct ccg aag atc ctt aag			547
Ala Met Thr Asp His Ile Thr Lys Lys Gly Ala Pro Lys Ile Leu Lys			
	135	140	145
gag tgt cgc ctc cca ctg act ggc gcg aag tgc gtg gac atg att gtc			595
Glu Cys Arg Leu Pro Leu Thr Gly Ala Lys Cys Val Asp Met Ile Val			
	150	155	160
acc acc cac gct gtg ttc tct gtg gac cct gaa gaa ggc ctc acg ctc			643
Thr Thr His Ala Val Phe Ser Val Asp Pro Glu Glu Gly Leu Thr Leu			
	170	175	180
atc gag tgc gcc gac ggt gtc acc gtt gag gaa ctc cgc gaa atc acc			691
Ile Glu Cys Ala Asp Gly Val Thr Val Glu Glu Leu Arg Glu Ile Thr			
	185	190	195
gaa gcc gat ttc aaa gtt gct taagcaaacg ctgcgcaatt aag			735
Glu Ala Asp Phe Lys Val Ala			
	200		

&lt;210&gt; 468

&lt;211&gt; 204

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 468

Met Ala Ala Arg Val Ala Gln Glu Leu Glu Asp Gly Gln Tyr Val Asn  
 1 5 10 15

Leu Gly Ile Gly Met Pro Thr Leu Ile Pro Gly Tyr Leu Pro Glu Gly  
 20 25 30

Leu Glu Val Ile Leu His Ser Glu Asn Gly Val Leu Gly Val Gly Pro  
 35 40 45

Tyr Pro Thr Glu Glu Glu Leu Asp Pro Glu Leu Ile Asn Ala Gly Lys  
 50 55 60

Glu Thr Ile Thr Val Ala Pro Gly Ala Ser Tyr Phe Ser Ser Ser Asp  
 65 70 75 80

Ser Phe Ala Met Ile Arg Ser Lys Ser Val Asp Val Ala Val Leu Gly  
 85 90 95

Val Met Glu Val Ser Gln Tyr Gly Asp Leu Ala Asn Trp Met Ile Pro  
 100 105 110

Gly Lys Leu Val Lys Gly Met Gly Gly Ala Met Asp Leu Val His Gly  
 115 120 125

Ala Ser Lys Ile Ile Ala Met Thr Asp His Ile Thr Lys Lys Gly Ala  
 130 135 140

Pro Lys Ile Leu Lys Glu Cys Arg Leu Pro Leu Thr Gly Ala Lys Cys  
 145 150 155 160

Val Asp Met Ile Val Thr Thr His Ala Val Phe Ser Val Asp Pro Glu  
 165 170 175

Glu Gly Leu Thr Leu Ile Glu Cys Ala Asp Gly Val Thr Val Glu Glu  
 180 185 190

Leu Arg Glu Ile Thr Glu Ala Asp Phe Lys Val Ala  
 195 200

&lt;210&gt; 469

&lt;211&gt; 876

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(853)

&lt;223&gt; RXN01115

&lt;400&gt; 469

ctcaccgcat gcagcgtgaa aacactcagt acggactggc caccatgtgc atcggtggcg 60

gccagggtct tgcagctgtc tttgaaaagg agaactaaaa atg gct att ttg cac 115  
 Met Ala Ile Leu His  
 1 5

agc gtt tcc tac gga act tcc gac aac acc ttg gtg ttc att ggc tcg 163  
 Ser Val Ser Tyr Gly Thr Ser Asp Asn Thr Leu Val Phe Ile Gly Ser  
 10 15 20

ttg ggt tcc acc acc gac atg tgg ctg cca cag ctg gat gcc ttg cat	211
Leu Gly Ser Thr Thr Asp Met Trp Leu Pro Gln Leu Asp Ala Leu His	
25 30 35	
aag gat ttc cgc gtc atc gct gtt gat cac cgc gga cat ggt ctg tct	259
Lys Asp Phe Arg Val Ile Ala Val Asp His Arg Gly His Gly Leu Ser	
40 45 50	
gaa ctc atc gaa ggc acc ccc act gtg gcg gat ctg gcg cag gat gtg	307
Glu Leu Ile Glu Gly Thr Pro Thr Val Ala Asp Leu Ala Gln Asp Val	
55 60 65	
ctg gat acc ctc gat gac ctg ggt gtc gga aac ttc ggc gtc atc gga	355
Leu Asp Thr Leu Asp Asp Leu Gly Val Gly Asn Phe Gly Val Ile Gly	
70 75 80 85	
cta tct ctc ggc gga gcg gtt gca caa tac ttg gcg gcc acc tct gat	403
Leu Ser Leu Gly Gly Ala Val Ala Gln Tyr Leu Ala Ala Thr Ser Asp	
90 95 100	
cgt gtc acc aag gca gca ttc atg tgt acc gct gca aaa ttc ggc gag	451
Arg Val Thr Lys Ala Ala Phe Met Cys Thr Ala Ala Lys Phe Gly Glu	
105 110 115	
ccc cag ggc tgg cta gat cgc gcc gca gcg tgc cgc gaa aac ggc act	499
Pro Gln Gly Trp Leu Asp Arg Ala Ala Ala Cys Arg Glu Asn Gly Thr	
120 125 130	
ggt tct ctg tcc gaa gct gtg atc cag cgc tgg ttc tcc ccc act tgg	547
Gly Ser Leu Ser Glu Ala Val Ile Gln Arg Trp Phe Ser Pro Thr Trp	
135 140 145	
ttg gag aac aac cca gcg tcc cgc gag cac ttc gaa gcc atg gtt gcc	595
Leu Glu Asn Asn Pro Ala Ser Arg Glu His Phe Glu Ala Met Val Ala	
150 155 160 165	
ggc acc cca tct gag ggt tac gcg ctg tgc tgc gag gcg ttg gca acc	643
Gly Thr Pro Ser Glu Gly Tyr Ala Leu Cys Cys Glu Ala Leu Ala Thr	
170 175 180	
tgg gat ttc acc gat cgc ctg gga gaa atc acc gtg cca gtg ctc acc	691
Trp Asp Phe Thr Asp Arg Leu Gly Glu Ile Thr Val Pro Val Leu Thr	
185 190 195	
atc gca ggt gcc gat gac ccc tcc act cct cca gca acc gtg cag atc	739
Ile Ala Gly Ala Asp Asp Pro Ser Thr Pro Pro Ala Thr Val Gln Ile	
200 205 210	
att gcc gat ggc gtt ggc ggc gag tcc cgc gca gag gtc cta agc cca	787
Ile Ala Asp Gly Val Gly Gly Glu Ser Arg Ala Glu Val Leu Ser Pro	
215 220 225	
gcc gcg cac gta cca acc gtg gaa cgt cca aac gag gta aat gaa ctg	835
Ala Ala His Val Pro Thr Val Glu Arg Pro Asn Glu Val Asn Glu Leu	
230 235 240 245	
cta gca cag cat ttc gct taatgttgta ggcatgttca caa	876
Leu Ala Gln His Phe Ala	
250	

&lt;210&gt; 470

&lt;211&gt; 251

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 470

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Met Ala Ile Leu His Ser Val Ser Tyr Gly Thr Ser Asp Asn Thr Leu
  1              5              10              15

Val Phe Ile Gly Ser Leu Gly Ser Thr Thr Asp Met Trp Leu Pro Gln
          20              25              30

Leu Asp Ala Leu His Lys Asp Phe Arg Val Ile Ala Val Asp His Arg
          35              40              45

Gly His Gly Leu Ser Glu Leu Ile Glu Gly Thr Pro Thr Val Ala Asp
  50              55              60

Leu Ala Gln Asp Val Leu Asp Thr Leu Asp Asp Leu Gly Val Gly Asn
  65              70              75              80

Phe Gly Val Ile Gly Leu Ser Leu Gly Gly Ala Val Ala Gln Tyr Leu
          85              90              95

Ala Ala Thr Ser Asp Arg Val Thr Lys Ala Ala Phe Met Cys Thr Ala
          100              105              110

Ala Lys Phe Gly Glu Pro Gln Gly Trp Leu Asp Arg Ala Ala Ala Cys
          115              120              125

Arg Glu Asn Gly Thr Gly Ser Leu Ser Glu Ala Val Ile Gln Arg Trp
          130              135              140

Phe Ser Pro Thr Trp Leu Glu Asn Asn Pro Ala Ser Arg Glu His Phe
          145              150              155              160

Glu Ala Met Val Ala Gly Thr Pro Ser Glu Gly Tyr Ala Leu Cys Cys
          165              170              175

Glu Ala Leu Ala Thr Trp Asp Phe Thr Asp Arg Leu Gly Glu Ile Thr
          180              185              190

Val Pro Val Leu Thr Ile Ala Gly Ala Asp Asp Pro Ser Thr Pro Pro
          195              200              205

Ala Thr Val Gln Ile Ile Ala Asp Gly Val Gly Gly Glu Ser Arg Ala
          210              215              220

Glu Val Leu Ser Pro Ala Ala His Val Pro Thr Val Glu Arg Pro Asn
          225              230              235              240

Glu Val Asn Glu Leu Leu Ala Gln His Phe Ala
          245              250

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&lt;210&gt; 471

&lt;211&gt; 1284

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1261)

&lt;223&gt; RXS00116

&lt;400&gt; 471

cgcggcacgc acgctggggg caagcgctcga caagcacaaa ctttttgctt aattgaatcc 60

tttgcgccacc aatcaatggg ggatcaaata tagtagctgc atg agt aat gac ttc 115  
Met Ser Asn Asp Phe  
1 5

gtc gtt tct agg ctt aga ccc ttt ggt gaa acg att ttt gca acc atg 163  
Val Val Ser Arg Leu Arg Pro Phe Gly Glu Thr Ile Phe Ala Thr Met  
10 15 20

acc cag cga gct gtt gag gcg ggt gca atc aat ctt ggt cag ggc ttt 211  
Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly Phe  
25 30 35

cct gat gag gat ggt cct cgt cgg atg tta gag atc gcg tcg gag cag 259  
Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu Gln  
40 45 50

att ctc ggg gga aat aat cag tat tcg gcg ggg cgt ggg gat gct tcg 307  
Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala Ser  
55 60 65

ttg agg gca gct gtg gct cgt gat cat ttg gag agg ttt gat ctg gag 355  
Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu Glu  
70 75 80 85

tac aac cct gat tcg gag gtg ttg atc acg gtg ggg gcc act gag gcg 403  
Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu Ala  
90 95 100

att acg gcg act gtg ttg ggt ttg gtg gag cct ggg gat gaa gtg atc 451  
Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val Ile  
105 110 115

gtt ttg gaa ccg tat tac gat gcg tat gcg gcg gct att gcg ttg gcg 499  
Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala Ala Ile Ala Leu Ala  
120 125 130

ggg gcg acg ccg gtg gcg gtt cct ttg cag gag gtg gag aac tcg tgg 547  
Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu Val Glu Asn Ser Trp  
135 140 145

gat gtg gat gtc gat aag ttg cat gcg gcg gtg act aag aag acg ccg 595  
Asp Val Asp Val Asp Lys Leu His Ala Ala Val Thr Lys Lys Thr Arg  
150 155 160 165

atg att atc gtt aat tcg ccg cat aat ccg acg ggt tcg gtg ttt tct 643  
Met Ile Ile Val Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe Ser  
170 175 180

aag aag gcg ttg aag cag ttg gcg ggt gtt gct cgt gcg tat gac ttg 691  
Lys Lys Ala Leu Lys Gln Leu Ala Gly Val Ala Arg Ala Tyr Asp Leu  
185 190 195

ttg gtg ttg tca gat gag gtg tat gag cat ctt gtt ttt gat gat cag 739  
Leu Val Leu Ser Asp Glu Val Tyr Glu His Leu Val Phe Asp Asp Gln



200	205	210	
aag cat gtg agt gtc gcg aag ctg ccc ggt atg tgg gat cgc acg gtg Lys His Val Ser Val Ala Lys Leu Pro Gly Met Trp Asp Arg Thr Val 215 220 225			787
acg gtg tcg tcg gcg gcg aaa acg ttc aat gtg act ggt tgg aag acg Thr Val Ser Ser Ala Ala Lys Thr Phe Asn Val Thr Gly Trp Lys Thr 230 235 240 245			835
ggg tgg gcg ttg gca ccg gag ccg ttg ttg gag gcg gtg ttg aag gcg Gly Trp Ala Leu Ala Pro Glu Pro Leu Leu Glu Ala Val Leu Lys Ala 250 255 260			883
aag cag ttt atg tct tat gtg ggg gct aca cct ttt cag ccg gct gtg Lys Gln Phe Met Ser Tyr Val Gly Ala Thr Pro Phe Gln Pro Ala Val 265 270 275			931
gcg cat gcg att gaa cat gag cag aag tgg gtg tca aag atg tct aag Ala His Ala Ile Glu His Glu Gln Lys Trp Val Ser Lys Met Ser Lys 280 285 290			979
ggg ctt gag ctc aag cgg gat att ttg cgt act gcg tta gat aag gcg Gly Leu Glu Leu Lys Arg Asp Ile Leu Arg Thr Ala Leu Asp Lys Ala 295 300 305			1027
ggg ctg aag act cat gac agt atg ggc acg tat ttc atc gtt gcg gat Gly Leu Lys Thr His Asp Ser Met Gly Thr Tyr Phe Ile Val Ala Asp 310 315 320 325			1075
att ggg gat cgt gat ggt gcg gag ttc tgt ttt gag ttg att gag aag Ile Gly Asp Arg Asp Gly Ala Glu Phe Cys Phe Glu Leu Ile Glu Lys 330 335 340			1123
gtt ggg gtg gcg gcg att ccg gtg cag gcg ttt gtg gat cat ccg aag Val Gly Val Ala Ala Ile Pro Val Gln Ala Phe Val Asp His Pro Lys 345 350 355			1171
aag tgg tcg tcg aag gtt cgt ttt gcg ttt tgc aaa aaa gaa gag acg Lys Trp Ser Ser Lys Val Arg Phe Ala Phe Cys Lys Lys Glu Glu Thr 360 365 370			1219
ctc cgc gaa gct gcg gag cgt ctc aag ggg att aag aaa cta Leu Arg Glu Ala Ala Glu Arg Leu Lys Gly Ile Lys Lys Leu 375 380 385			1261
tagtttgaac aggttgttgg ggg			1284

&lt;210&gt; 472

&lt;211&gt; 387

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 472

Met	Ser	Asn	Asp	Phe	Val	Val	Ser	Arg	Leu	Arg	Pro	Phe	Gly	Glu	Thr
1				5					10					15	

Ile	Phe	Ala	Thr	Met	Thr	Gln	Arg	Ala	Val	Glu	Ala	Gly	Ala	Ile	Asn
		20					25					30			

Leu Gly Gln Gly Phe Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu  
                   35                                  40                                  45  
 Ile Ala Ser Glu Gln Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly  
           50                                  55                                  60  
 Arg Gly Asp Ala Ser Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu  
       65                                  70                                  75                                  80  
 Arg Phe Asp Leu Glu Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val  
                   85                                  90                                  95  
 Gly Ala Thr Glu Ala Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro  
                  100                                 105                                 110  
 Gly Asp Glu Val Ile Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala  
          115                                 120                                 125  
 Ala Ile Ala Leu Ala Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu  
       130                                 135                                 140  
 Val Glu Asn Ser Trp Asp Val Asp Val Asp Lys Leu His Ala Ala Val  
   145                                 150                                 155                                 160  
 Thr Lys Lys Thr Arg Met Ile Ile Val Asn Ser Pro His Asn Pro Thr  
                  165                                 170                                 175  
 Gly Ser Val Phe Ser Lys Lys Ala Leu Lys Gln Leu Ala Gly Val Ala  
                  180                                 185                                 190  
 Arg Ala Tyr Asp Leu Leu Val Leu Ser Asp Glu Val Tyr Glu His Leu  
       195                                 200                                 205  
 Val Phe Asp Asp Gln Lys His Val Ser Val Ala Lys Leu Pro Gly Met  
       210                                 215                                 220  
 Trp Asp Arg Thr Val Thr Val Ser Ser Ala Ala Lys Thr Phe Asn Val  
   225                                 230                                 235                                 240  
 Thr Gly Trp Lys Thr Gly Trp Ala Leu Ala Pro Glu Pro Leu Leu Glu  
                  245                                 250                                 255  
 Ala Val Leu Lys Ala Lys Gln Phe Met Ser Tyr Val Gly Ala Thr Pro  
                  260                                 265                                 270  
 Phe Gln Pro Ala Val Ala His Ala Ile Glu His Glu Gln Lys Trp Val  
       275                                 280                                 285  
 Ser Lys Met Ser Lys Gly Leu Glu Leu Lys Arg Asp Ile Leu Arg Thr  
       290                                 295                                 300  
 Ala Leu Asp Lys Ala Gly Leu Lys Thr His Asp Ser Met Gly Thr Tyr  
   305                                 310                                 315                                 320  
 Phe Ile Val Ala Asp Ile Gly Asp Arg Asp Gly Ala Glu Phe Cys Phe  
                  325                                 330                                 335  
 Glu Leu Ile Glu Lys Val Gly Val Ala Ala Ile Pro Val Gln Ala Phe  
       340                                 345                                 350  
 Val Asp His Pro Lys Lys Trp Ser Ser Lys Val Arg Phe Ala Phe Cys

[illegible]

aat tcg ccg cat aat ccg acg ggt tcg gtg ttt tct aag aag gcg ttg 595  
 Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe Ser Lys Lys Ala Leu  
 150 155 160 165

aag cag ttg gcg 607  
 Lys Gln Leu Ala

<210> 474

<211> 169

<212> PRT

<213> Corynebacterium glutamicum

<400> 474

Met Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly  
 1 5 10 15

Phe Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu  
 20 25 30

Gln Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala  
 35 40 45

Ser Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu  
 50 55 60

Glu Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu  
 65 70 75 80

Ala Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val  
 85 90 95

Ile Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala Ala Ile Ala Leu  
 100 105 110

Ala Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu Val Glu Asn Ser  
 115 120 125

Trp Asp Val Asp Val Asp Lys Leu His Ala Ala Val Thr Lys Lys Thr  
 130 135 140

Arg Met Ile Ile Val Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe  
 145 150 155 160

Ser Lys Lys Ala Leu Lys Gln Leu Ala  
 165

<210> 475

<211> 843

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(820)

<223> RXS00391

<400> 475

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tttctccccc atccctgtac aagataaaac ccgtgcacag ttg ctg cgc gat tct																115
Leu Leu Arg Asp Ser																
caa cga gtt ggc ctc gcc atc gat cct tcg atc gct ttg gtg atg gcc																163
Gln Arg Val Gly Leu Ala Ile Asp Pro Ser Ile Ala Leu Val Met Ala																
act tct ggt tct aca ggt acc ccg aag ggc gct cag ctc act ccg ttg																211
Thr Ser Gly Ser Thr Gly Thr Pro Lys Gly Ala Gln Leu Thr Pro Leu																
aat ttg gtg agt tcc gcc gat gct acg cat cag ttt tta ggt ggc gaa																259
Asn Leu Val Ser Ser Ala Asp Ala Thr His Gln Phe Leu Gly Gly Glu																
ggc cag tgg ttg ctt gcc atg cca gca cac cac att gca ggc atg cag																307
Gly Gln Trp Leu Leu Ala Met Pro Ala His His Ile Ala Gly Met Gln																
gtg ctt ctt cga agc ctc att gct gga gtt gag cca cta gct att gat																355
Val Leu Leu Arg Ser Leu Ile Ala Gly Val Glu Pro Leu Ala Ile Asp																
ctc agc aca ggt ttt cac att gac gct ttc gca ggc gcc gcg gca gaa																403
Leu Ser Thr Gly Phe His Ile Asp Ala Phe Ala Gly Ala Ala Ala Glu																
ctg aaa aat acc ggc gac cgc gtc tat aca tcc ttg act cca atg cag																451
Leu Lys Asn Thr Gly Asp Arg Val Tyr Thr Ser Leu Thr Pro Met Gln																
tta ctt aaa gca atg gac tcc ttg caa ggc att gaa gcc ctg aaa ctt																499
Leu Leu Lys Ala Met Asp Ser Leu Gln Gly Ile Glu Ala Leu Lys Leu																
ttt gat gtc att ctt gtt ggc ggt gct gca ttg tct aag cag gcc cga																547
Phe Asp Val Ile Leu Val Gly Gly Ala Ala Leu Ser Lys Gln Ala Arg																
att tct gcg gag cag cta gac atc aac att gtc acc acc tac ggc tcc																595
Ile Ser Ala Glu Gln Leu Asp Ile Asn Ile Val Thr Thr Tyr Gly Ser																
tca gag act tca ggt ggc tgc gtt tat gat ggc aag ccc att ccc ggc																643
Ser Glu Thr Ser Gly Gly Cys Val Tyr Asp Gly Lys Pro Ile Pro Gly																
gcg aaa gtc cgt att tcg gat gag cgc att gag ttg ggt ggc ccg atg																691
Ala Lys Val Arg Ile Ser Asp Glu Arg Ile Glu Leu Gly Gly Pro Met																
att gcg cag ggc tac aga aat gca cct gaa cat ccg gat ttc gcc aac																739
Ile Ala Gln Gly Tyr Arg Asn Ala Pro Glu His Pro Asp Phe Ala Asn																
gag ggt tgg ttt acc acc tct gat tca ggt gaa ctc cac gac ggg att																787
Glu Gly Trp Phe Thr Thr Ser Asp Ser Gly Glu Leu His Asp Gly Ile																

ctc acc gtg act ggt cgc gtg gat acc cgt cat tgattccggt ggattgaagt 840  
 Leu Thr Val Thr Gly Arg Val Asp Thr Arg His  
 230 235 240

tgc

843

<210> 476

<211> 240

<212> PRT

<213> Corynebacterium glutamicum

<400> 476

Leu Leu Arg Asp Ser Gln Arg Val Gly Leu Ala Ile Asp Pro Ser Ile  
 1 5 10 15

Ala Leu Val Met Ala Thr Ser Gly Ser Thr Gly Thr Pro Lys Gly Ala  
 20 25 30

Gln Leu Thr Pro Leu Asn Leu Val Ser Ser Ala Asp Ala Thr His Gln  
 35 40 45

Phe Leu Gly Gly Glu Gly Gln Trp Leu Leu Ala Met Pro Ala His His  
 50 55 60

Ile Ala Gly Met Gln Val Leu Leu Arg Ser Leu Ile Ala Gly Val Glu  
 65 70 75 80

Pro Leu Ala Ile Asp Leu Ser Thr Gly Phe His Ile Asp Ala Phe Ala  
 85 90 95

Gly Ala Ala Ala Glu Leu Lys Asn Thr Gly Asp Arg Val Tyr Thr Ser  
 100 105 110

Leu Thr Pro Met Gln Leu Leu Lys Ala Met Asp Ser Leu Gln Gly Ile  
 115 120 125

Glu Ala Leu Lys Leu Phe Asp Val Ile Leu Val Gly Gly Ala Ala Leu  
 130 135 140

Ser Lys Gln Ala Arg Ile Ser Ala Glu Gln Leu Asp Ile Asn Ile Val  
 145 150 155 160

Thr Thr Tyr Gly Ser Ser Glu Thr Ser Gly Gly Cys Val Tyr Asp Gly  
 165 170 175

Lys Pro Ile Pro Gly Ala Lys Val Arg Ile Ser Asp Glu Arg Ile Glu  
 180 185 190

Leu Gly Gly Pro Met Ile Ala Gln Gly Tyr Arg Asn Ala Pro Glu His  
 195 200 205

Pro Asp Phe Ala Asn Glu Gly Trp Phe Thr Thr Ser Asp Ser Gly Glu  
 210 215 220

Leu His Asp Gly Ile Leu Thr Val Thr Gly Arg Val Asp Thr Arg His  
 225 230 235 240

<210> 477  
 <211> 1017  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(994)  
 <223> RXS00393

<400> 477

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aattgcgcga tcgagtatgt gatggggaaa gatagagggt atg tct cac acg gaa 115
                               Met Ser His Thr Glu
                               1           5

ccc cag ccg aat tct gta act ttg tcc gat tgg att caa ggc gca cgc 163
Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp Ile Gln Gly Ala Arg
                10                15                20

ccg cgt acc tgg gca aat gcg ttc gcg cct gtc att gcc ggt tca ggt 211
Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val Ile Ala Gly Ser Gly
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gtc gcc gct ttt cat gat ggt ttt gtg tgg tgg aag gcc ttg ctg gcg 259
Val Ala Ala Phe His Asp Gly Phe Val Trp Trp Lys Ala Leu Leu Ala
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ctt gtc gtg gcg tgg gct ttg atc atc ggt gtg aat tac gcc aat gat 307
Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val Asn Tyr Ala Asn Asp
                55                60                65

tac tct gat ggc att cgt ggc acc gat gaa gac cgc acc ggt cct ctg 355
Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp Arg Thr Gly Pro Leu
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cga ctc act ggt tct ggg ttg gct gag ccg aag aaa gtg aaa gct gcg 403
Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys Lys Val Lys Ala Ala
                90                95                100

gcg ttt att tct ttc ggt atc gca ggt gtc gcc ggc acc gcg ctg agc 451
Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala Gly Thr Ala Leu Ser
                105                110                115

ctg ttg agc gcg tgg tgg ctg atc ctc atc ggc atc ctg tgt gtg ctg 499
Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly Ile Leu Cys Val Leu
                120                125                130

ggc gcg tgg ttc tac acc ggc ggt aaa aat cct tat ggt tac cgc ggg 547
Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro Tyr Gly Tyr Arg Gly
                135                140                145

ctc ggc gag att gct gtg ttc atc ttc ttc ggc ctc gtc gcg gtc atg 595
Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly Leu Val Ala Val Met
                150                155                160                165

gga acg cag ttc acc caa acc ggt tcc gtc agc tgg gcc ggt ttg gcc 643
Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser Trp Ala Gly Leu Ala
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170										175					180					
gcc	gca	gtt	ggc	gtg	ggg	tcg	atg	tct	gct	ggc	gtg	aac	ttg	gcc	aac	691				
Ala	Ala	Val	Gly	Val	Gly	Ser	Met	Ser	Ala	Gly	Val	Asn	Leu	Ala	Asn					
			185				190						195							
aat	att	cgc	gat	att	cca	acc	gat	agc	aag	acc	gga	aaa	att	acc	ctc	739				
Asn	Ile	Arg	Asp	Ile	Pro	Thr	Asp	Ser	Lys	Thr	Gly	Lys	Ile	Thr	Leu					
			200				205						210							
gcg	gtc	cgc	ctg	ggc	gat	gcg	ggg	gct	cgt	aag	ctg	ttc	ctc	gcg	ctg	787				
Ala	Val	Arg	Leu	Gly	Asp	Ala	Gly	Ala	Arg	Lys	Leu	Phe	Leu	Ala	Leu					
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Ile	Ser	Thr	Pro	Phe	Ile	Met	Ser	Ile	Cys	Leu	Ala	Phe	Val	Ala	Trp					
230						235						240			245					
cca	gcg	ctg	atc	gcg	atc	atc	gtt	ttc	ccg	ctg	gca	ctg	aaa	gcc	gca	883				
Pro	Ala	Leu	Ile	Ala	Ile	Ile	Val	Phe	Pro	Leu	Ala	Leu	Lys	Ala	Ala					
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ggg	ccg	atc	cgc	aac	aac	gcc	acc	ggc	aag	gat	ctc	atc	ccc	gtc	atc	931				
Gly	Pro	Ile	Arg	Asn	Asn	Ala	Thr	Gly	Lys	Asp	Leu	Ile	Pro	Val	Ile					
			265						270						275					
ggc	tca	aca	ggg	cgc	gcc	atg	gcg	ttg	tgg	gcc	gtg	ctc	acg	ggc	ctg	979				
Gly	Ser	Thr	Gly	Arg	Ala	Met	Ala	Leu	Trp	Ala	Val	Leu	Thr	Gly	Leu					
			280						285						290					
gca	tta	gcg	ttt	agc	taaaacgctt	ttcgacgctc	ccc									1017				
Ala	Leu	Ala	Phe	Ser																
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			20						25						30					
Ile	Ala	Gly	Ser	Gly	Val	Ala	Ala	Phe	His	Asp	Gly	Phe	Val	Trp	Trp					
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Lys	Ala	Leu	Leu	Ala	Leu	Val	Val	Ala	Trp	Ala	Leu	Ile	Ile	Gly	Val					
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Asn	Tyr	Ala	Asn	Asp	Tyr	Ser	Asp	Gly	Ile	Arg	Gly	Thr	Asp	Glu	Asp					
65						70						75			80					
Arg	Thr	Gly	Pro	Leu	Arg	Leu	Thr	Gly	Ser	Gly	Leu	Ala	Glu	Pro	Lys					
			85						90						95					
Lys	Val	Lys	Ala	Ala	Ala	Phe	Ile	Ser	Phe	Gly	Ile	Ala	Gly	Val	Ala					
			100						105						110					



Gly Thr Ala Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly  
 115 120 125  
 Ile Leu Cys Val Leu Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro  
 130 135 140  
 Tyr Gly Tyr Arg Gly Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly  
 145 150 155 160  
 Leu Val Ala Val Met Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser  
 165 170 175  
 Trp Ala Gly Leu Ala Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly  
 180 185 190  
 Val Asn Leu Ala Asn Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr  
 195 200 205  
 Gly Lys Ile Thr Leu Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys  
 210 215 220  
 Leu Phe Leu Ala Leu Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu  
 225 230 235 240  
 Ala Phe Val Ala Trp Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu  
 245 250 255  
 Ala Leu Lys Ala Ala Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp  
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<220>  
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 <223> FRXA00393

<400> 479  
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 Met Ser His Thr Glu  
 1 5  
 ccc cag ccg aat tct gta act ttg tcc gat tgg att caa ggc gca cgc 163  
 Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp Ile Gln Gly Ala Arg  
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 ccg cgt acc tgg gca aat gcg ttc gcg cct gtc att gcc ggt tca ggt 211  
 Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val Ile Ala Gly Ser Gly

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Val	Ala	Ala	Phe	His	Asp	Gly	Phe	Val	Trp	Trp	Lys	Ala	Leu	Leu	Ala					
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ctt	gtc	gtg	gcg	tgg	gct	ttg	atc	atc	ggt	gtg	aat	tac	gcc	aat	gat	307				
Leu	Val	Val	Ala	Trp	Ala	Leu	Ile	Ile	Gly	Val	Asn	Tyr	Ala	Asn	Asp					
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tac	tct	gat	ggc	att	cgt	ggc	acc	gat	gaa	gac	cgc	acc	ggt	cct	ctg	355				
Tyr	Ser	Asp	Gly	Ile	Arg	Gly	Thr	Asp	Glu	Asp	Arg	Thr	Gly	Pro	Leu					
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Arg	Leu	Thr	Gly	Ser	Gly	Leu	Ala	Glu	Pro	Lys	Lys	Val	Lys	Ala	Ala					
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Ala	Phe	Ile	Ser	Phe	Gly	Ile	Ala	Gly	Val	Ala	Gly	Thr	Ala	Leu	Ser					
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ctg	ttg	agc	gcg	tgg	tgg	ctg	atc	ctc	atc	ggc	atc	ctg	tgt	gtg	ctg	499				
Leu	Leu	Ser	Ala	Trp	Trp	Leu	Ile	Leu	Ile	Gly	Ile	Leu	Cys	Val	Leu					
120						125						130								
ggc	gcg	tgg	ttc	tac	acc	ggc	ggt	aaa	aat	cct	tat	ggt	tac	cgc	ggg	547				
Gly	Ala	Trp	Phe	Tyr	Thr	Gly	Gly	Lys	Asn	Pro	Tyr	Gly	Tyr	Arg	Gly					
135						140						145								
ctc	ggc	gag	att	gct	gtg	ttc	atc	ttc	ttc	ggc	ctc	gtc	gcg	gtc	atg	595				
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Gly	Thr	Gln	Phe	Thr	Gln	Thr	Gly	Ser	Val	Ser	Trp	Ala	Gly	Leu	Ala					
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gcc	gca	gtt	ggc	gtg	ggg	tcg	atg	tct	gct	ggc	gtg	aac	ttg	gcc	aac	691				
Ala	Ala	Val	Gly	Val	Gly	Ser	Met	Ser	Ala	Gly	Val	Asn	Leu	Ala	Asn					
			185			190						195								
aat	att	cgc	gat	att	cca	acc	gat	agc	aag	acc	gga	aaa	att	acc	ctc	739				
Asn	Ile	Arg	Asp	Ile	Pro	Thr	Asp	Ser	Lys	Thr	Gly	Lys	Ile	Thr	Leu					
200						205						210								
gcg	gtc	cgc	ctg	ggc	gat	gcg	ggt	gct	cgt	aag	ctg	ttc	ctc	gcg	ctg	787				
Ala	Val	Arg	Leu	Gly	Asp	Ala	Gly	Ala	Arg	Lys	Leu	Phe	Leu	Ala	Leu					
215						220			225											
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Ile	Ser	Thr	Pro	Phe	Ile	Met	Ser	Ile	Cys	Leu	Ala	Phe	Val	Ala	Trp					
230						235			240			245								
cca	gcg	ctg	atc	gcg	atc	atc	gtt	ttc	ccg	ctg	gca	ctg	aaa	gcc	gca	883				
Pro	Ala	Leu	Ile	Ala	Ile	Ile	Val	Phe	Pro	Leu	Ala	Leu	Lys	Ala	Ala					
			250						255			260								
ggg	ccg	atc	cgc	aac	aac	gcc	acc	ggc	aag	gat	ctc	atc	ccg	tca	tcg	931				
Gly	Pro	Ile	Arg	Asn	Asn	Ala	Thr	Gly	Lys	Asp	Leu	Ile	Pro	Ser	Ser					
			265			270						275								

cat tagcgtttag ctaaaacgct ttt 1005  
His

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Ile	Gln	Gly	Ala 20	Arg	Pro	Arg	Thr	Trp 25	Ala	Asn	Ala	Phe	Ala 30	Pro	Val
Ile	Ala	Gly 35	Ser	Gly	Val	Ala	Ala 40	Phe	His	Asp	Gly	Phe 45	Val	Trp	Trp
Lys 50	Ala	Leu	Leu	Ala	Leu	Val 55	Val	Ala	Trp	Ala	Leu 60	Ile	Ile	Gly	Val
Asn 65	Tyr	Ala	Asn	Asp	Tyr 70	Ser	Asp	Gly	Ile	Arg 75	Gly	Thr	Asp	Glu	Asp 80
Arg	Thr	Gly	Pro	Leu 85	Arg	Leu	Thr	Gly	Ser 90	Gly	Leu	Ala	Glu	Pro	Lys
Lys	Val	Lys	Ala 100	Ala	Ala	Phe	Ile	Ser 105	Phe	Gly	Ile	Ala	Gly 110	Val	Ala
Gly	Thr	Ala 115	Leu	Ser	Leu	Leu	Ser 120	Ala	Trp	Trp	Leu	Ile 125	Leu	Ile	Gly
Ile 130	Leu	Cys	Val	Leu	Gly	Ala 135	Trp	Phe	Tyr	Thr	Gly 140	Gly	Lys	Asn	Pro
Tyr 145	Gly	Tyr	Arg	Gly	Leu 150	Gly	Glu	Ile	Ala	Val 155	Phe	Ile	Phe	Phe	Gly 160
Leu	Val	Ala	Val	Met 165	Gly	Thr	Gln	Phe	Thr 170	Gln	Thr	Gly	Ser	Val 175	Ser
Trp	Ala	Gly	Leu 180	Ala	Ala	Ala	Val	Gly 185	Val	Gly	Ser	Met	Ser 190	Ala	Gly
Val	Asn 195	Leu	Ala	Asn	Asn	Ile	Arg 200	Asp	Ile	Pro	Thr	Asp 205	Ser	Lys	Thr
Gly 210	Lys	Ile	Thr	Leu	Ala	Val 215	Arg	Leu	Gly	Asp	Ala 220	Gly	Ala	Arg	Lys
Leu 225	Phe	Leu	Ala	Leu	Ile 230	Ser	Thr	Pro	Phe	Ile 235	Met	Ser	Ile	Cys	Leu 240

Ala Phe Val Ala Trp Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu  
 245 250 255

Ala Leu Lys Ala Ala Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp  
 260 265 270

Leu Ile Pro Ser Ser Ala Gln Gln Gly Ala Pro Trp Arg Cys Gly Pro  
 275 280 285

Cys Ser Arg Ala Trp His  
 290

&lt;210&gt; 481

&lt;211&gt; 987

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(964)

&lt;223&gt; RXS00446

&lt;400&gt; 481

tgctacgaag ttatctagta atgaagtttag tttttccct ctcccggcag cagttgatgc 60

ggtgacggag gctacttggg gggctaactcg gtaccgggat atg ggt gcg gtt gag 115  
 Met Gly Ala Val Glu  
 1 5

ctc cgt gag gct ctt gca gag cat tta gag gtt gag ttt gac cag gtc 163  
 Leu Arg Glu Ala Leu Ala Glu His Leu Glu Val Glu Phe Asp Gln Val  
 10 15 20

acg gta ggt tgc ggc tcg tct gcg ctg tgt caa cag ctg gtt cag gca 211  
 Thr Val Gly Cys Gly Ser Ser Ala Leu Cys Gln Gln Leu Val Gln Ala  
 25 30 35

acg tgc gct cag ggc gat gag gtc att ttt cca tgg cgc agc ttt gag 259  
 Thr Cys Ala Gln Gly Asp Glu Val Ile Phe Pro Trp Arg Ser Phe Glu  
 40 45 50

gct tat cca att ttc gcg cag gtc gcg ggc gcc act cct gtt gcc att 307  
 Ala Tyr Pro Ile Phe Ala Gln Val Ala Gly Ala Thr Pro Val Ala Ile  
 55 60 65

ccg ctg act gct gat cag aat cat gat ctt gat gcg atg gca gcc gcg 355  
 Pro Leu Thr Ala Asp Gln Asn His Asp Leu Asp Ala Met Ala Ala Ala  
 70 75 80 85

atc act gat aag acc cgc ctc att ttc atc tgc aac ccc aac aat cct 403  
 Ile Thr Asp Lys Thr Arg Leu Ile Phe Ile Cys Asn Pro Asn Asn Pro  
 90 95 100

tcg ggc acc acc atc acc cag gcg cag ttt gat aat ttc atg gaa aag 451  
 Ser Gly Thr Thr Ile Thr Gln Ala Gln Phe Asp Asn Phe Met Glu Lys  
 105 110 115

gtt cca aac gat gtc gtt gtt ggg ctg gat gag gct tat ttt gag ttc 499  
 Val Pro Asn Asp Val Val Val Gly Leu Asp Glu Ala Tyr Phe Glu Phe  
 120 125 130

aac cgc gcg gac gac acc cca gtt gcc act gag gaa atc cac cgc cac 547  
 Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile His Arg His  
 135 140 145  
  
 gac aac gtg att ggt ttg cgc acg ttc tcc aag gcg tat ggc ctg gcg 595  
 Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr Gly Leu Ala  
 150 155 160 165  
  
 ggc ttg cgt gtt ggt tac gcc ttc gga aac gca gag atc atc gca gcg 643  
 Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile Ile Ala Ala  
 170 175 180  
  
 atg aat aag gtg gct att cct ttc gcg gtg aat tca gca gct cag gcg 691  
 Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala Ala Gln Ala  
 185 190 195  
  
 gca gcg ctt gcg agt ttg aat tct gcc gat gag ttg atg gaa cgg gtg 739  
 Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met Glu Arg Val  
 200 205 210  
  
 gag gaa acc gtc gaa aag cgt gat gct gtg gtg tca gcg ctt ggt gct 787  
 Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala Leu Gly Ala  
 215 220 225  
  
 gcg ccg acg cag gcc aat ttc gtc tgg ctg ccg ggc gag ggc gcc gct 835  
 Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu Gly Ala Ala  
 230 235 240 245  
  
 gag ttg gcg gct aaa ttg gcc gag cac ggc atc gtg att cgc gcg ttc 883  
 Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile Arg Ala Phe  
 250 255 260  
  
 ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa act gac aag 931  
 Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu Thr Asp Lys  
 265 270 275  
  
 ctg ctg cgc gcg tgg gag gcc atc aat gct ggg tagtcttttg cgttttgcgg 984  
 Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly  
 280 285  
  
 tgc 987

&lt;210&gt; 482

&lt;211&gt; 288

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 482

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 Glu Phe Asp Gln Val Thr Val Gly Cys Gly Ser Ser Ala Leu Cys Gln  
 20 25 30  
  
 Gln Leu Val Gln Ala Thr Cys Ala Gln Gly Asp Glu Val Ile Phe Pro  
 35 40 45  
  
 Trp Arg Ser Phe Glu Ala Tyr Pro Ile Phe Ala Gln Val Ala Gly Ala  
 50 55 60

Thr Pro Val Ala Ile Pro Leu Thr Ala Asp Gln Asn His Asp Leu Asp  
 65 70 75 80  
 Ala Met Ala Ala Ala Ile Thr Asp Lys Thr Arg Leu Ile Phe Ile Cys  
 85 90 95  
 Asn Pro Asn Asn Pro Ser Gly Thr Thr Ile Thr Gln Ala Gln Phe Asp  
 100 105 110  
 Asn Phe Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu  
 115 120 125  
 Ala Tyr Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu  
 130 135 140  
 Glu Ile His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys  
 145 150 155 160  
 Ala Tyr Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala  
 165 170 175  
 Glu Ile Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn  
 180 185 190  
 Ser Ala Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu  
 195 200 205  
 Leu Met Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val  
 210 215 220  
 Ser Ala Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro  
 225 230 235 240  
 Gly Glu Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile  
 245 250 255  
 Val Ile Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala  
 260 265 270  
 Glu Glu Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly  
 275 280 285

&lt;210&gt; 483

&lt;211&gt; 545

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(522)

&lt;223&gt; FRXA00446

&lt;400&gt; 483

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 Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu Ala Tyr  
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ttt gag ttc aac cgc gcg gac gac acc cca gtt gcc act gag gaa atc 96  
 Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile  
                   20                                  25                                  30

cac cgc cac gac aac gtg att ggt ttg cgc acg ttc tcc aag gcg tat 144  
 His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr  
                   35                                  40                                  45

ggc ctg gcg ggc ttg cgt gtt ggt tac gcc ttc gga aac gca gag atc 192  
 Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile  
                   50                                  55                                  60

atc gca gcg atg aat aag gtg gct att cct ttc gcg gtg aat tca gca 240  
 Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala  
                   65                                  70                                  75                                  80

gct cag gcg gca gcg ctt gcg agt ttg aat tct gcc gat gag ttg atg 288  
 Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met  
                                   85                                  90                                  95

gaa cgg gtg gag gaa acc gtc gaa aag cgt gat gct gtg gtg tca gcg 336  
 Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala  
                   100                                  105                                  110

ctt ggt gct gcg ccg acg cag gcc aat ttc gtc tgg ctg ccg ggc gag 384  
 Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu  
                   115                                  120                                  125

ggc gcc gct gag ttg gcg gct aaa ttg gcc gag cac ggc atc gtg att 432  
 Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile  
                   130                                  135                                  140

cgc gcg ttc ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa 480  
 Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu  
                   145                                  150                                  155                                  160

act gac aag ctg ctg cgc gcg tgg gag gcc atc aat gct ggg 522  
 Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly  
                   165                                  170

tagtctttgg cgttttgcgg tgc 545

&lt;210&gt; 484

&lt;211&gt; 174

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 484

Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu Ala Tyr  
   1                  5                                  10                                  15

Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile  
                   20                                  25                                  30

His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr  
                   35                                  40                                  45

Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile  
                   50                                  55                                  60

Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala  
 65 70 75 80  
 Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met  
 85 90 95  
 Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala  
 100 105 110  
 Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu  
 115 120 125  
 Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile  
 130 135 140  
 Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu  
 145 150 155 160  
 Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly  
 165 170

<210> 485  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1207)  
 <223> RXS00618

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 Met Gln Met Leu Asp  
 1 5  
 cga gtc cac cgt cgc agg cgc gaa ggc aaa gac acc tta atg ttc tgc 163  
 Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp Thr Leu Met Phe Cys  
 10 15 20  
 gct ggc cag ccg tca act ggt gcg cca gaa gca gtc atc gaa gaa gca 211  
 Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala Val Ile Glu Glu Ala  
 25 30 35  
 gag atc gct ctt cgc tcg ggt cct ttg gga tac acc gag gtg att ggt 259  
 Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr Thr Glu Val Ile Gly  
 40 45 50  
 gat cgt gag ttc cgt gaa cgc atc gcc gat tgg cac tct gct act tat 307  
 Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp His Ser Ala Thr Tyr  
 55 60 65  
 gac gta gac acc aac cct gac aat gtt att gtc acc acc ggt tct tca 355  
 Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val Thr Thr Gly Ser Ser  
 70 75 80 85  
 ggt gga ttc gtg gca tcg ttt atc gcc acc ttg gat cac ggg gat tat 403



Gly	Gly	Phe	Val	Ala	Ser	Phe	Ile	Ala	Thr	Leu	Asp	His	Gly	Asp	Tyr	
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gtg	gca	atg	cct	acc	ccg	ggg	tac	ccg	gca	tat	cgc	aat	att	ctg	gaa	451
Val	Ala	Met	Pro	Thr	Pro	Gly	Tyr	Pro	Ala	Tyr	Arg	Asn	Ile	Leu	Glu	
			105					110					115			
tct	ttg	ggg	gcg	aag	gtt	ctg	aac	ctg	cgc	tgt	act	gca	gag	act	cgt	499
Ser	Leu	Gly	Ala	Lys	Val	Leu	Asn	Leu	Arg	Cys	Thr	Ala	Glu	Thr	Arg	
		120					125					130				
ttc	cag	cca	acc	gct	caa	atg	ttg	gag	gaa	ctg	cca	cac	aag	ccg	aag	547
Phe	Gln	Pro	Thr	Ala	Gln	Met	Leu	Glu	Glu	Leu	Pro	His	Lys	Pro	Lys	
	135					140					145					
gct	gtt	att	gtc	acc	agc	cca	gga	aac	cca	acg	ggc	acc	atc	att	gat	595
Ala	Val	Ile	Val	Thr	Ser	Pro	Gly	Asn	Pro	Thr	Gly	Thr	Ile	Ile	Asp	
150					155					160					165	
ccg	gaa	gag	cta	gag	cgc	atc	gcc	aag	tgg	tgc	gat	gac	aat	gat	gct	643
Pro	Glu	Glu	Leu	Glu	Arg	Ile	Ala	Lys	Trp	Cys	Asp	Asp	Asn	Asp	Ala	
			170						175					180		
gtt	ctt	atc	tct	gat	gag	gac	tac	cac	ggc	atg	agc	ttt	ggt	cgt	ccg	691
Val	Leu	Ile	Ser	Asp	Glu	Asp	Tyr	His	Gly	Met	Ser	Phe	Gly	Arg	Pro	
			185					190					195			
ctg	gca	act	gcg	cat	cag	ttt	tcc	aag	aac	gcc	atc	gtg	gtg	ggt	acc	739
Leu	Ala	Thr	Ala	His	Gln	Phe	Ser	Lys	Asn	Ala	Ile	Val	Val	Gly	Thr	
		200					205					210				
ttg	tcc	aag	tac	ttc	tcc	atg	acg	ggg	tgg	cgc	gtg	ggt	tgg	atc	atc	787
Leu	Ser	Lys	Tyr	Phe	Ser	Met	Thr	Gly	Trp	Arg	Val	Gly	Trp	Ile	Ile	
	215					220					225					
gtt	cca	gat	gag	ctg	gtc	aca	ccg	att	gaa	aac	ctg	cag	gct	tct	ctt	835
Val	Pro	Asp	Glu	Leu	Val	Thr	Pro	Ile	Glu	Asn	Leu	Gln	Ala	Ser	Leu	
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Ser	Leu	Cys	Ala	Pro	Ala	Ile	Gly	Gln	Ala	Ala	Gly	Arg	Ala	Ala	Phe	
			250					255					260			
act	ttg	gag	gct	ggg	gcc	gaa	ctt	gat	gcc	cac	gtt	gaa	gcg	tat	cgc	931
Thr	Leu	Glu	Ala	Gly	Ala	Glu	Leu	Asp	Ala	His	Val	Glu	Ala	Tyr	Arg	
		265					270					275				
gag	gcc	cgg	gag	gtg	ttc	gtc	gat	aag	ctc	cct	gaa	atc	ggg	ctt	ggc	979
Glu	Ala	Arg	Glu	Val	Phe	Val	Asp	Lys	Leu	Pro	Glu	Ile	Gly	Leu	Gly	
		280					285					290				
act	ttc	gcc	gac	ccg	gat	ggc	ggc	ctg	tat	ttg	tgg	gtc	gat	gtt	tct	1027
Thr	Phe	Ala	Asp	Pro	Asp	Gly	Gly	Leu	Tyr	Leu	Trp	Val	Asp	Val	Ser	
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gca	tac	acc	gat	gat	tca	gag	gaa	tgg	gca	ttg	cgt	ttg	ctc	gat	gaa	1075
Ala	Tyr	Thr	Asp	Asp	Ser	Glu	Glu	Trp	Ala	Leu	Arg	Leu	Leu	Asp	Glu	
310					315				320						325	
gcg	ggc	gtg	gcc	gtc	gcg	ccg	ggg	gtt	gat	ttt	gat	cct	gag	gaa	ggc	1123
Ala	Gly	Val	Ala	Val	Ala	Pro	Gly	Val	Asp	Phe	Asp	Pro	Glu	Glu	Gly	

	330	335	340	
cac aag tgg att cgt ttg agc ctg tgc gcg tca aag gaa gac acc att				1171
His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser Lys Glu Asp Thr Ile				
	345	350	355	
gaa ggt gtg cgc aaa atc gga gaa ttc atc aaa aaa tagcagcgac				1217
Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys Lys				
	360	365		
taggttagtt tcg				1230

&lt;210&gt; 486

&lt;211&gt; 369

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 486

Met Gln Met Leu Asp Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp				
1	5	10	15	
Thr Leu Met Phe Cys Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala				
	20	25	30	
Val Ile Glu Glu Ala Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr				
	35	40	45	
Thr Glu Val Ile Gly Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp				
	50	55	60	
His Ser Ala Thr Tyr Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val				
	65	70	75	80
Thr Thr Gly Ser Ser Gly Gly Phe Val Ala Ser Phe Ile Ala Thr Leu				
	85	90	95	
Asp His Gly Asp Tyr Val Ala Met Pro Thr Pro Gly Tyr Pro Ala Tyr				
	100	105	110	
Arg Asn Ile Leu Glu Ser Leu Gly Ala Lys Val Leu Asn Leu Arg Cys				
	115	120	125	
Thr Ala Glu Thr Arg Phe Gln Pro Thr Ala Gln Met Leu Glu Glu Leu				
	130	135	140	
Pro His Lys Pro Lys Ala Val Ile Val Thr Ser Pro Gly Asn Pro Thr				
	145	150	155	160
Gly Thr Ile Ile Asp Pro Glu Glu Leu Glu Arg Ile Ala Lys Trp Cys				
	165	170	175	
Asp Asp Asn Asp Ala Val Leu Ile Ser Asp Glu Asp Tyr His Gly Met				
	180	185	190	
Ser Phe Gly Arg Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala				
	195	200	205	
Ile Val Val Gly Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg				
	210	215	220	

Val Gly Trp Ile Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn  
 225 230 235 240

Leu Gln Ala Ser Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala  
 245 250 255

Gly Arg Ala Ala Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His  
 260 265 270

Val Glu Ala Tyr Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro  
 275 280 285

Glu Ile Gly Leu Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu  
 290 295 300

Trp Val Asp Val Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu  
 305 310 315 320

Arg Leu Leu Asp Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe  
 325 330 335

Asp Pro Glu Glu Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser  
 340 345 350

Lys Glu Asp Thr Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys  
 355 360 365

Lys

<210> 487  
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 <212> DNA  
 <213> Corynebacterium glutamicum

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 <222> (101)..(634)  
 <223> FRXA00618

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 Met Ser Phe Gly Arg  
 1 5

ccg ctg gca act gcg cat cag ttt tcc aag aac gcc atc gtg gtg ggt 163  
 Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala Ile Val Val Gly  
 10 15 20

acc ttg tcc aag tac ttc tcc atg acg ggt tgg cgc gtg ggt tgg atc 211  
 Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg Val Gly Trp Ile  
 25 30 35

atc gtt cca gat gag ctg gtc aca ccg att gaa aac ctg cag gct tct 259  
 Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn Leu Gln Ala Ser  
 40 45 50

ctt tcc ttg tgt gct cct gcc atc ggg cag gct gcg gga cgc gca gcc 307

Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala Gly Arg Ala Ala  
 55 60 65  
 ttc act ttg gag gct ggg gcc gaa ctt gat gcc cac gtt gaa gcg tat 355  
 Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His Val Glu Ala Tyr  
 70 75 80 85  
 cgc gag gcc cgg gag gtg ttc gtc gat aag ctc cct gaa atc ggg ctt 403  
 Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro Glu Ile Gly Leu  
 90 95 100  
 ggc act ttc gcc gac ccg gat ggc ggc ctg tat ttg tgg gtc gat gtt 451  
 Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu Trp Val Asp Val  
 105 110 115  
 tct gca tac acc gat gat tca gag gaa tgg gca ttg cgt ttg ctc gat 499  
 Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu Arg Leu Leu Asp  
 120 125 130  
 gaa gcg ggc gtg gcc gtc gcg ccg ggt gtt gat ttt gat cct gag gaa 547  
 Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe Asp Pro Glu Glu  
 135 140 145  
 ggc cac aag tgg att cgt ttg agc ctg tgc gcg tca aag gaa gac acc 595  
 Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser Lys Glu Asp Thr  
 150 155 160 165  
 att gaa ggt gtg cgc aaa atc gga gaa ttc atc aaa aaa tagcagcgac 644  
 Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys Lys  
 170 175  
 taggttagtt tcg 657

<210> 488  
 <211> 178  
 <212> PRT  
 <213> Corynebacterium glutamicum

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 Arg Val Gly Trp Ile Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu  
 35 40 45  
 Asn Leu Gln Ala Ser Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala  
 50 55 60  
 Ala Gly Arg Ala Ala Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala  
 65 70 75 80  
 His Val Glu Ala Tyr Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu  
 85 90 95  
 Pro Glu Ile Gly Leu Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr  
 100 105 110

Leu Trp Val Asp Val Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala  
 115 120 125  
 Leu Arg Leu Leu Asp Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp  
 130 135 140  
 Phe Asp Pro Glu Glu Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala  
 145 150 155 160  
 Ser Lys Glu Asp Thr Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile  
 165 170 175  
 Lys Lys

<210> 489  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(385)  
 <223> FRXA00627

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 Met Gln Met Leu Asp  
 1 5  
 cga gtc cac cgt cgc agg cgc gaa ggc aaa gac acc tta atg ttc tgc 163  
 Arg Val His Arg Arg Arg Glu Gly Lys Asp Thr Leu Met Phe Cys  
 10 15 20  
 gct ggc cag cgc tca act ggt gcg cca gaa gca gtc atc gaa gaa gca 211  
 Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala Val Ile Glu Glu Ala  
 25 30 35  
 gag atc gct ctt cgc tcg ggt cct ttg gga tac acc gag gtg att ggt 259  
 Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr Thr Glu Val Ile Gly  
 40 45 50  
 gat cgt gag ttc cgt gaa cgc atc gcc gat tgg cac tct gct act tat 307  
 Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp His Ser Ala Thr Tyr  
 55 60 65  
 gac gta gac acc aac cct gac aat gtt att gtc acc acc ggt tct tca 355  
 Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val Thr Thr Gly Ser Ser  
 70 75 80 85  
 ggt gga ttc gtg gca tcg ttt atc gcc acc 385  
 Gly Gly Phe Val Ala Ser Phe Ile Ala Thr  
 90 95

<210> 490  
 <211> 95  
 <212> PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 490

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Thr Leu Met Phe Cys Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala
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Val Ile Glu Glu Ala Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr
      35             40             45

Thr Glu Val Ile Gly Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp
      50             55             60

His Ser Ala Thr Tyr Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val
      65             70             75             80

Thr Thr Gly Ser Ser Gly Gly Phe Val Ala Ser Phe Ile Ala Thr
      85             90             95

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&lt;210&gt; 491

&lt;211&gt; 1221

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1198)

&lt;223&gt; RXS01105

&lt;400&gt; 491

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gctttgaaaa cctccccacc accgacgagg cctaagaaaa atg acc aaa att act 115
                Met Thr Lys Ile Thr
                1             5

ttg agc gat ttg cca ttg cgt gaa gaa ctg cgc ggt gag cac gct tac 163
Leu Ser Asp Leu Pro Leu Arg Glu Glu Leu Arg Gly Glu His Ala Tyr
                10             15             20

ggc gca ccc cag ctc aac gtt gat att cgc ctc aac acc aac gaa aac 211
Gly Ala Pro Gln Leu Asn Val Asp Ile Arg Leu Asn Thr Asn Glu Asn
                25             30             35

cct tac cca ccg tca gag gca ttg gtc gct gac ttg gtt gcc acc gtg 259
Pro Tyr Pro Pro Ser Glu Ala Leu Val Ala Asp Leu Val Ala Thr Val
                40             45             50

gat aag atc gcc acc gag ctg aac cgc tac cca gag cgc gat gct gtg 307
Asp Lys Ile Ala Thr Glu Leu Asn Arg Tyr Pro Glu Arg Asp Ala Val
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gaa ctg cgt gat gag ttg gct gcg tac atc acc aag caa acc ggc gtg 355
Glu Leu Arg Asp Glu Leu Ala Ala Tyr Ile Thr Lys Gln Thr Gly Val
                70             75             80             85

gct gtc acc agg gat aac ctg tgg gct gcc aat ggt tcc aat gaa att 403
Ala Val Thr Arg Asp Asn Leu Trp Ala Ala Asn Gly Ser Asn Glu Ile

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90						95						100						
ctg	cag	cag	ctg	ctg	cag	gct	ttt	ggg	gga	cct	gga	cgc	acc	gcg	ttg	451		
Leu	Gln	Gln	Leu	Leu	Gln	Ala	Phe	Gly	Gly	Pro	Gly	Arg	Thr	Ala	Leu			
			105						110			115						
gga	ttc	caa	ccc	agc	tat	tcc	atg	cac	cca	att	ttg	gct	aaa	ggc	acc	499		
Gly	Phe	Gln	Pro	Ser	Tyr	Ser	Met	His	Pro	Ile	Leu	Ala	Lys	Gly	Thr			
			120						125			130						
cac	act	gaa	ttc	att	gcg	gtg	tcc	cga	ggg	gct	gat	ttc	cgc	atc	gat	547		
His	Thr	Glu	Phe	Ile	Ala	Val	Ser	Arg	Gly	Ala	Asp	Phe	Arg	Ile	Asp			
			135						140			145						
atg	gat	gtg	gcg	ctg	gaa	gaa	att	cgt	gca	aag	cag	cct	gac	att	gtt	595		
Met	Asp	Val	Ala	Leu	Glu	Glu	Ile	Arg	Ala	Lys	Gln	Pro	Asp	Ile	Val			
			150						155			160			165			
ttt	gtc	acc	acc	ccg	aac	aac	ccg	acc	ggg	gat	gtg	acc	tcg	ctg	gac	643		
Phe	Val	Thr	Thr	Pro	Asn	Asn	Pro	Thr	Gly	Asp	Val	Thr	Ser	Leu	Asp			
			170						175			180						
gat	gtt	gag	cgc	atc	atc	aac	gtt	gcc	cca	ggc	atc	gtg	atc	gtg	gat	691		
Asp	Val	Glu	Arg	Ile	Ile	Asn	Val	Ala	Pro	Gly	Ile	Val	Ile	Val	Asp			
			185						190			195						
gaa	gct	tat	gcg	gaa	ttc	tcc	cca	tca	cct	tca	gca	acc	act	ctt	ctg	739		
Glu	Ala	Tyr	Ala	Glu	Phe	Ser	Pro	Ser	Pro	Ser	Ala	Thr	Thr	Leu	Leu			
			200						205			210						
gag	aag	tac	cca	acc	aag	ctg	gtg	gtg	tcc	cgc	acc	atg	agt	aag	gct	787		
Glu	Lys	Tyr	Pro	Thr	Lys	Leu	Val	Val	Ser	Arg	Thr	Met	Ser	Lys	Ala			
			215						220			225						
ttt	gat	ttc	gca	ggg	gga	cgc	ctc	ggc	tac	ttc	gtg	gcc	aac	cca	gcg	835		
Phe	Asp	Phe	Ala	Gly	Gly	Arg	Leu	Gly	Tyr	Phe	Val	Ala	Asn	Pro	Ala			
			230						235			240			245			
ttt	atc	gac	gcc	gtg	atg	cta	gtc	cgc	ctt	ccg	tat	cat	ctt	tca	gcg	883		
Phe	Ile	Asp	Ala	Val	Met	Leu	Val	Arg	Leu	Pro	Tyr	His	Leu	Ser	Ala			
			250						255			260						
ctg	agc	caa	gca	gcc	gca	atc	gta	gcg	ctg	cgt	cac	tcc	gct	gac	acg	931		
Leu	Ser	Gln	Ala	Ala	Ala	Ile	Val	Ala	Leu	Arg	His	Ser	Ala	Asp	Thr			
			265						270			275						
ctg	gga	acc	gtc	gaa	aag	ctc	tct	gta	gag	cgt	gtt	cgc	gtg	gca	gca	979		
Leu	Gly	Thr	Val	Glu	Lys	Leu	Ser	Val	Glu	Arg	Val	Arg	Val	Ala	Ala			
			280						285			290						
cgc	ttg	gag	gaa	ctg	ggc	tac	gct	gtg	gtt	cca	agt	gag	tcc	aac	ttt	1027		
Arg	Leu	Glu	Glu	Leu	Gly	Tyr	Ala	Val	Val	Pro	Ser	Glu	Ser	Asn	Phe			
			295						300			305						
gtg	ttc	ttt	gga	gat	ttc	tcc	gat	cag	cac	gcg	gca	tgg	cag	gca	ttt	1075		
Val	Phe	Phe	Gly	Asp	Phe	Ser	Asp	Gln	His	Ala	Ala	Trp	Gln</					

cgc act acc att ggt gtg cct gag gaa aat gat gcg ttt ttg gac gca 1171  
 Arg Thr Thr Ile Gly Val Pro Glu Glu Asn Asp Ala Phe Leu Asp Ala  
                   345                                  350                                  355

gct gca gag atc atc aag ctg aac ctg taagagagaa gaatttttca 1218  
 Ala Ala Glu Ile Ile Lys Leu Asn Leu  
                   360                                  365

tga 1221

<210> 492

<211> 366

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 492

Met Thr Lys Ile Thr Leu Ser Asp Leu Pro Leu Arg Glu Glu Leu Arg  
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Gly Glu His Ala Tyr Gly Ala Pro Gln Leu Asn Val Asp Ile Arg Leu  
                   20                                  25                                  30

Asn Thr Asn Glu Asn Pro Tyr Pro Pro Ser Glu Ala Leu Val Ala Asp  
                   35                                  40                                  45

Leu Val Ala Thr Val Asp Lys Ile Ala Thr Glu Leu Asn Arg Tyr Pro  
                   50                                  55                                  60

Glu Arg Asp Ala Val Glu Leu Arg Asp Glu Leu Ala Ala Tyr Ile Thr  
                   65                                  70                                  75                                  80

Lys Gln Thr Gly Val Ala Val Thr Arg Asp Asn Leu Trp Ala Ala Asn  
                                   85                                  90                                  95

Gly Ser Asn Glu Ile Leu Gln Gln Leu Leu Gln Ala Phe Gly Gly Pro  
                   100                                  105                                  110

Gly Arg Thr Ala Leu Gly Phe Gln Pro Ser Tyr Ser Met His Pro Ile  
                   115                                  120                                  125

Leu Ala Lys Gly Thr His Thr Glu Phe Ile Ala Val Ser Arg Gly Ala  
                   130                                  135                                  140

Asp Phe Arg Ile Asp Met Asp Val Ala Leu Glu Glu Ile Arg Ala Lys  
                   145                                  150                                  155                                  160

Gln Pro Asp Ile Val Phe Val Thr Thr Pro Asn Asn Pro Thr Gly Asp  
                   165                                  170                                  175

Val Thr Ser Leu Asp Asp Val Glu Arg Ile Ile Asn Val Ala Pro Gly  
                   180                                  185                                  190

Ile Val Ile Val Asp Glu Ala Tyr Ala Glu Phe Ser Pro Ser Pro Ser  
                   195                                  200                                  205

Ala Thr Thr Leu Leu Glu Lys Tyr Pro Thr Lys Leu Val Val Ser Arg  
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Thr Met Ser Lys Ala Phe Asp Phe Ala Gly Gly Arg Leu Gly Tyr Phe



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<211> 1752
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1729)
<223> RXS02315
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cct	gct	gtt	gct	gaa	gct	gcg	cat	gcc	cat	atc	ccg	ttg	att	gtg	ctc	403	
Pro	Ala	Val	Ala	Glu	Ala	Ala	His	Ala	His	Ile	Pro	Leu	Ile	Val	Leu		
				90					95					100			
tct	gct	gac	cgt	cct	gca	cat	ttg	gtg	gga	acg	ggg	gcg	agc	caa	acg	451	
Ser	Ala	Asp	Arg	Pro	Ala	His	Leu	Val	Gly	Thr	Gly	Ala	Ser	Gln	Thr		
			105					110						115			
att	aac	cag	acc	ggc	att	ttt	ggc	gat	ctt	gca	ccg	acg	gtc	ggc	atc	499	
Ile	Asn	Gln	Thr	Gly	Ile	Phe	Gly	Asp	Leu	Ala	Pro	Thr	Val	Gly	Ile		
			120				125						130				
act	gag	ctg	gat	cag	gta	gcg	cag	att	gct	gaa	agc	ctt	gct	cag	ggg	547	
Thr	Glu	Leu	Asp	Gln	Val	Ala	Gln	Ile	Ala	Glu	Ser	Leu	Ala	Gln	Gly		
			135				140						145				
gct	tcc	cag	att	ccg	cgt	cat	ttc	aat	ctt	gca	ctt	gat	gtt	cct	ttg	595	
Ala	Ser	Gln	Ile	Pro	Arg	His	Phe	Asn	Leu	Ala	Leu	Asp	Val	Pro	Leu		
					155					160					165		
gtt	gct	cct	gaa	ctg	cca	gag	ctt	cat	ggc	gag	gca	gtt	gga	gca	tca	643	
Val	Ala	Pro	Glu	Leu	Pro	Glu	Leu	His	Gly	Glu	Ala	Val	Gly	Ala	Ser		
				170					175					180			
tgg	acg	cat	cgc	tgg	atc	aac	cac	ggc	gag	gtg	acc	gtg	gac	ctg	ggg	691	
Trp	Thr	His	Arg	Trp	Ile	Asn	His	Gly	Glu	Val	Thr	Val	Asp	Leu	Gly		
			185					190						195			
gag	cac	acc	ctc	gtg	att	gcc	ggc	gat	gaa	gca	tgg	gaa	gtg	gaa	ggg	739	
Glu	His	Thr	Leu	Val	Ile	Ala	Gly	Asp	Glu	Ala	Trp	Glu	Val	Glu	Gly		
			200				205						210				
ctg	gaa	gat	gtg	ccc	acc	atc	gct	gaa	cct	act	gca	cca	aag	cct	tat	787	
Leu	Glu	Asp	Val	Pro	Thr	Ile	Ala	Glu	Pro	Thr	Ala	Pro	Lys	Pro	Tyr		
			215				220										
aat	ccg	gtg	cac	cca	ctg	gct	gct	gaa	atc	ttg	ctg	aag	gag	cag	gtc	835	
Asn	Pro	Val	His	Pro	Leu	Ala	Ala	Glu	Ile	Leu	Leu	Lys	Glu	Gln	Val		
					235					240					245		
tcc	gcg	gaa	ggc	tat	gtg	gta	aac	acc	agg	cct	gat	cat	gtg	atc	gtg	883	
Ser	Ala	Glu	Gly	Tyr	Val	Val	Asn	Thr	Arg	Pro	Asp	His	Val	Ile	Val		
				250					255					260			
gtg	gga	cac	ccc	acg	ctg	cac	cgc	gga	gtg	ttg	aag	ttg	atg	tca	gat	931	
Val	Gly	His	Pro	Thr	Leu	His	Arg	Gly	Val	Leu	Lys	Leu	Met	Ser	Asp		
				265				270						275			
cct	ggc	att	aaa	tta	act	gtg	ctt	tca	cgc	acc	gat	atc	atc	act	gat	979	
Pro	Gly	Ile	Lys	Leu	Thr	Val	Leu	Ser	Arg	Thr	Asp	Ile	Ile	Thr	Asp		
				280				285					290				
ccc	ggc	cgc	cat	gcc	gat	cag	gtg	ggc	agc	aca	gtg	aaa	gtc	acc	ggc	1027	
Pro	Gly	Arg	His	Ala	Asp	Gln	Val	Gly	Ser	Thr	Val	Lys	Val	Thr	Gly		
				295			300					305					
acc	cag	gaa	aag	cag	tgg	cta	aag	atc	tgt	tcg	gca	gca	tca	gaa	ctt	1075	
Thr	Gln	Glu	Lys	Gln	Trp	Leu	Lys	Ile	Cys	Ser	Ala	Ala	Ser	Glu	Leu		

310	315	320	325	
gcg gcc gat ggt gtg cgt gac gtc ctg gac aac caa gaa ttc ggt ttc				1123
Ala Ala Asp Gly Val Arg Asp Val Leu Asp Asn Gln Glu Phe Gly Phe				
	330	335	340	
acc ggc ctc cat gtt gcc gca gcc gtg gcg gat acc tta ggc acc ggc				1171
Thr Gly Leu His Val Ala Ala Ala Val Ala Asp Thr Leu Gly Thr Gly				
	345	350	355	
gat act ctc ttt gct gca gca tcc aac tca atc cgt gac ctc tcc ctg				1219
Asp Thr Leu Phe Ala Ala Ala Ser Asn Ser Ile Arg Asp Leu Ser Leu				
	360	365	370	
gtg ggt atg cct ttt gat ggc gtg gat acc ttc tcc cca cga ggt gtc				1267
Val Gly Met Pro Phe Asp Gly Val Asp Thr Phe Ser Pro Arg Gly Val				
	375	380	385	
gca ggc att gat ggt tct gtt gct caa gca atc ggc act tca ctt gct				1315
Ala Gly Ile Asp Gly Ser Val Ala Gln Ala Ile Gly Thr Ser Leu Ala				
	390	395	400	405
gtg cag tcc cgc cac ccc gat gaa atc cgc gcg cca cgc act gtg gcc				1363
Val Gln Ser Arg His Pro Asp Glu Ile Arg Ala Pro Arg Thr Val Ala				
	410	415	420	
ctt ctg ggc gat ctg tcg ttc ctt cac gat att ggc gga ctg ctc atc				1411
Leu Leu Gly Asp Leu Ser Phe Leu His Asp Ile Gly Gly Leu Leu Ile				
	425	430	435	
ggc cct gat gaa cca cgc cca gaa aac ctc acc atc gtg gtc tcc aac				1459
Gly Pro Asp Glu Pro Arg Pro Glu Asn Leu Thr Ile Val Val Ser Asn				
	440	445	450	
gac aac ggt ggc gga atc ttc gaa ctc cta gaa acc ggc gca gat ggt				1507
Asp Asn Gly Gly Gly Ile Phe Glu Leu Leu Glu Thr Gly Ala Asp Gly				
	455	460	465	
ctc cgc ccc aac ttc gag cgt gct ttc ggt acc cca cac gac gcg tcc				1555
Leu Arg Pro Asn Phe Glu Arg Ala Phe Gly Thr Pro His Asp Ala Ser				
	470	475	480	485
atc gcg gat ctc tgc gca ggc tac ggc att gaa cac caa gtg gta gac				1603
Ile Ala Asp Leu Cys Ala Gly Tyr Gly Ile Glu His Gln Val Val Asp				
	490	495	500	
aac ctc caa gac ctc atc atc gcg cta gtt gat acc acc gaa gta tcc				1651
Asn Leu Gln Asp Leu Ile Ile Ala Leu Val Asp Thr Thr Glu Val Ser				
	505	510	515	
gga ttc acc att att gaa gct tcg acc gtc cga gat acc cgc cgt gca				1699
Gly Phe Thr Ile Ile Glu Ala Ser Thr Val Arg Asp Thr Arg Arg Ala				
	520	525	530	
caa cag caa gct ctc atg gac acg gtg cac taaatggagt ggtaccaagt				1749
Gln Gln Gln Ala Leu Met Asp Thr Val His				
	535	540		
gcg				1752

&lt;210&gt; 494

&lt;211&gt; 543

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 494

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Met Ser Ser Thr Pro Ala Gln Asp Leu Ala Arg Ala Val Ile Asp Ser
  1           5           10           15

Leu Ala Pro His Val Thr Asp Val Val Leu Cys Pro Gly Ser Arg Asn
          20           25           30

Ser Pro Leu Ser Leu Glu Leu Leu Ala Arg Gln Asp Leu Arg Val His
          35           40           45

Val Arg Ile Asp Glu Arg Ser Ala Ser Phe Leu Ala Leu Ser Leu Ala
          50           55           60

Arg Thr Gln Ala Arg Pro Val Ala Val Val Met Thr Ser Gly Thr Ala
          65           70           75           80

Val Ala Asn Cys Leu Pro Ala Val Ala Glu Ala Ala His Ala His Ile
          85           90           95

Pro Leu Ile Val Leu Ser Ala Asp Arg Pro Ala His Leu Val Gly Thr
          100          105          110

Gly Ala Ser Gln Thr Ile Asn Gln Thr Gly Ile Phe Gly Asp Leu Ala
          115          120          125

Pro Thr Val Gly Ile Thr Glu Leu Asp Gln Val Ala Gln Ile Ala Glu
          130          135          140

Ser Leu Ala Gln Gly Ala Ser Gln Ile Pro Arg His Phe Asn Leu Ala
          145          150          155          160

Leu Asp Val Pro Leu Val Ala Pro Glu Leu Pro Glu Leu His Gly Glu
          165          170          175

Ala Val Gly Ala Ser Trp Thr His Arg Trp Ile Asn His Gly Glu Val
          180          185          190

Thr Val Asp Leu Gly Glu His Thr Leu Val Ile Ala Gly Asp Glu Ala
          195          200          205

Trp Glu Val Glu Gly Leu Glu Asp Val Pro Thr Ile Ala Glu Pro Thr
          210          215          220

Ala Pro Lys Pro Tyr Asn Pro Val His Pro Leu Ala Ala Glu Ile Leu
          225          230          235          240

Leu Lys Glu Gln Val Ser Ala Glu Gly Tyr Val Val Asn Thr Arg Pro
          245          250          255

Asp His Val Ile Val Val Gly His Pro Thr Leu His Arg Gly Val Leu
          260          265          270

Lys Leu Met Ser Asp Pro Gly Ile Lys Leu Thr Val Leu Ser Arg Thr
          275          280          285

Asp Ile Ile Thr Asp Pro Gly Arg His Ala Asp Gln Val Gly Ser Thr

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290	295	300
Val Lys Val Thr Gly Thr Gln Glu Lys Gln Trp Leu Lys Ile Cys Ser		
305	310	315 320
Ala Ala Ser Glu Leu Ala Ala Asp Gly Val Arg Asp Val Leu Asp Asn		
	325	330 335
Gln Glu Phe Gly Phe Thr Gly Leu His Val Ala Ala Ala Val Ala Asp		
	340	345 350
Thr Leu Gly Thr Gly Asp Thr Leu Phe Ala Ala Ala Ser Asn Ser Ile		
	355	360 365
Arg Asp Leu Ser Leu Val Gly Met Pro Phe Asp Gly Val Asp Thr Phe		
	370	375 380
Ser Pro Arg Gly Val Ala Gly Ile Asp Gly Ser Val Ala Gln Ala Ile		
	385	390 395 400
Gly Thr Ser Leu Ala Val Gln Ser Arg His Pro Asp Glu Ile Arg Ala		
	405	410 415
Pro Arg Thr Val Ala Leu Leu Gly Asp Leu Ser Phe Leu His Asp Ile		
	420	425 430
Gly Gly Leu Leu Ile Gly Pro Asp Glu Pro Arg Pro Glu Asn Leu Thr		
	435	440 445
Ile Val Val Ser Asn Asp Asn Gly Gly Gly Ile Phe Glu Leu Leu Glu		
	450	455 460
Thr Gly Ala Asp Gly Leu Arg Pro Asn Phe Glu Arg Ala Phe Gly Thr		
	465	470 475 480
Pro His Asp Ala Ser Ile Ala Asp Leu Cys Ala Gly Tyr Gly Ile Glu		
	485	490 495
His Gln Val Val Asp Asn Leu Gln Asp Leu Ile Ile Ala Leu Val Asp		
	500	505 510
Thr Thr Glu Val Ser Gly Phe Thr Ile Ile Glu Ala Ser Thr Val Arg		
	515	520 525
Asp Thr Arg Arg Ala Gln Gln Gln Ala Leu Met Asp Thr Val His		
	530	535 540

&lt;210&gt; 495

&lt;211&gt; 1434

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1411)

&lt;223&gt; RXS02550

&lt;400&gt; 495

gatcttaggc agccgtggga ttacaccctt ttagagctag aacagtaaaa attcacccaa 60

tagctttcaa	ctacgcacac	aaagtggcaa	cattgagcgg	gtg	act	aca	gac	aag	115
				Val	Thr	Thr	Asp	Lys	
				1				5	
cgc aaa acc tct aag acc acc gac acc gcc aac aag gct gtg ggc gcg	163								
Arg Lys Thr Ser Lys Thr Thr Asp Thr Ala Asn Lys Ala Val Gly Ala									
	10	15	20						
gat cag gca gcg cgt ccc act cgg cga aca act cgc cgc atc ttc gat	211								
Asp Gln Ala Ala Arg Pro Thr Arg Thr Thr Arg Arg Ile Phe Asp									
	25	30	35						
cag tcg gag aag atg aag gac gtg ctg tac gag atc cgt ggc ccg gtg	259								
Gln Ser Glu Lys Met Lys Asp Val Leu Tyr Glu Ile Arg Gly Pro Val									
	40	45	50						
gcc gcg gag gcg gaa cgc atg gag ctt gat ggg cat aac atc tta aag	307								
Ala Ala Glu Ala Glu Arg Met Glu Leu Asp Gly His Asn Ile Leu Lys									
	55	60	65						
ctc aac acg gga aat cca gcc gtg ttc gga ttc gat gcc ccc gac gtg	355								
Leu Asn Thr Gly Asn Pro Ala Val Phe Gly Phe Asp Ala Pro Asp Val									
	70	75	80	85					
att atg cgt gac atg atc gcc aac ctt cca act tcc caa ggg tat tcc	403								
Ile Met Arg Asp Met Ile Ala Asn Leu Pro Thr Ser Gln Gly Tyr Ser									
	90	95	100						
acc tcc aaa ggc att att ccg gcc cgg cga gca gtg gtc acc cgc tac	451								
Thr Ser Lys Gly Ile Ile Pro Ala Arg Arg Ala Val Val Thr Arg Tyr									
	105	110	115						
gaa gtt gtg ccc gga ttc ccc cac ttc gat gtt gat gat gtg ttc tta	499								
Glu Val Val Pro Gly Phe Pro His Phe Asp Val Asp Asp Val Phe Leu									
	120	125	130						
ggc aac ggt gtc tca gaa cta atc acc atg acc acc caa gca ctc ctc	547								
Gly Asn Gly Val Ser Glu Leu Ile Thr Met Thr Thr Gln Ala Leu Leu									
	135	140	145						
aac gac ggc gat gaa gtt ctt atc ccc gca ccg gac tac cca ctg tgg	595								
Asn Asp Gly Asp Glu Val Leu Ile Pro Ala Pro Asp Tyr Pro Leu Trp									
	150	155	160	165					
act gcc gca acc tcc ctg gct ggt ggt aag cct gtg cac tac ctc tgt	643								
Thr Ala Ala Thr Ser Leu Ala Gly Gly Lys Pro Val His Tyr Leu Cys									
	170	175	180						
gat gag gaa gat gac tgg aac cca tcc atc gaa gac atc aag tcc aaa	691								
Asp Glu Glu Asp Asp Trp Asn Pro Ser Ile Glu Asp Ile Lys Ser Lys									
	185	190	195						
atc tca gag aaa acc aaa gct att gtg gtg atc aac ccc aac aac ccc	739								
Ile Ser Glu Lys Thr Lys Ala Ile Val Val Ile Asn Pro Asn Asn Pro									
	200	205	210						
acg gga gct gtc tac ccg cgc cgg gtg ttg gaa caa atc gtc gag att	787								
Thr Gly Ala Val Tyr Pro Arg Arg Val Leu Glu Gln Ile Val Glu Ile									
	215	220	225						
gca cgc gag cat gac ctg ctg att ttg gcc gat gaa atc tac gac cgc	835								

Ala Arg Glu His Asp Leu Leu Ile Leu Ala Asp Glu Ile Tyr Asp Arg  
 230 235 240 245  
 att ctc tac gat gat gcc gag cac atc agc ctg gca acc ctt gca cca 883  
 Ile Leu Tyr Asp Asp Ala Glu His Ile Ser Leu Ala Thr Leu Ala Pro  
 250 255 260  
 gat ctc ctt tgc atc aca tac aac ggt cta tcc aag gca tac cgc gtc 931  
 Asp Leu Leu Cys Ile Thr Tyr Asn Gly Leu Ser Lys Ala Tyr Arg Val  
 265 270 275  
 gca gga tac cga gct ggc tgg atg gta ttg act gga cca aag caa tac 979  
 Ala Gly Tyr Arg Ala Gly Trp Met Val Leu Thr Gly Pro Lys Gln Tyr  
 280 285 290  
 gca cgt gga ttt att gag ggc ctc gaa ctc ctc gca ggc act cga ctc 1027  
 Ala Arg Gly Phe Ile Glu Gly Leu Glu Leu Leu Ala Gly Thr Arg Leu  
 295 300 305  
 tgc cca aat gtc cca gct cag cac gct att cag gta gct ctg ggt gga 1075  
 Cys Pro Asn Val Pro Ala Gln His Ala Ile Gln Val Ala Leu Gly Gly  
 310 315 320 325  
 cgc cag tcc atc tac gac ctc act ggc gaa cac ggc cga ctc ctg gaa 1123  
 Arg Gln Ser Ile Tyr Asp Leu Thr Gly Glu His Gly Arg Leu Leu Glu  
 330 335 340  
 cag cgc aac atg gca tgg acg aaa ctc aac gaa atc cca ggt gtc agc 1171  
 Gln Arg Asn Met Ala Trp Thr Lys Leu Asn Glu Ile Pro Gly Val Ser  
 345 350 355  
 tgt gtg aaa cca atg gga gct cta tac gcg ttc ccc aag ctc gac ccc 1219  
 Cys Val Lys Pro Met Gly Ala Leu Tyr Ala Phe Pro Lys Leu Asp Pro  
 360 365 370  
 aac gtg tac gaa atc cac gac gac acc caa ctc atg ctg gat ctt ctc 1267  
 Asn Val Tyr Glu Ile His Asp Asp Thr Gln Leu Met Leu Asp Leu Leu  
 375 380 385  
 cgt gcc gag aaa atc ctc atg gtt cag ggc act ggc ttc aac tgg cca 1315  
 Arg Ala Glu Lys Ile Leu Met Val Gln Gly Thr Gly Phe Asn Trp Pro  
 390 395 400 405  
 cat cac gat cac ttc cga gtg gtc acc ctg cca tgg gca tcc cag ttg 1363  
 His His Asp His Phe Arg Val Val Thr Leu Pro Trp Ala Ser Gln Leu  
 410 415 420  
 gaa aac gca att gag cgc ctg ggt aac ttc ctg tcc act tac aag cag 1411  
 Glu Asn Ala Ile Glu Arg Leu Gly Asn Phe Leu Ser Thr Tyr Lys Gln  
 425 430 435  
 tagtagttgt taggattcac cac 1434

&lt;210&gt; 496

&lt;211&gt; 437

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 496

Val Thr Thr Asp Lys Arg Lys Thr Ser Lys Thr Thr Asp Thr Ala Asn

1	5	10	15
Lys Ala Val Gly	Ala Asp Gln Ala	Ala Arg Pro Thr	Arg Arg Thr Thr
20	25	30	
Arg Arg Ile Phe	Asp Gln Ser Glu	Lys Met Lys Asp	Val Leu Tyr Glu
35	40	45	
Ile Arg Gly Pro	Val Ala Ala Glu	Ala Glu Arg Met	Glu Leu Asp Gly
50	55	60	
His Asn Ile Leu	Lys Leu Asn Thr	Gly Asn Pro Ala	Val Phe Gly Phe
65	70	75	80
Asp Ala Pro Asp	Val Ile Met Arg	Asp Met Ile Ala	Asn Leu Pro Thr
85	90	95	
Ser Gln Gly Tyr	Ser Thr Ser Lys	Gly Ile Ile Pro	Ala Arg Arg Ala
100	105	110	
Val Val Thr Arg	Tyr Glu Val Val	Pro Gly Phe Pro	His Phe Asp Val
115	120	125	
Asp Asp Val Phe	Leu Gly Asn Gly	Val Ser Glu Leu	Ile Thr Met Thr
130	135	140	
Thr Gln Ala Leu	Leu Asn Asp Gly	Asp Glu Val Leu	Ile Pro Ala Pro
145	150	155	160
Asp Tyr Pro Leu	Trp Thr Ala Ala	Thr Ser Leu Ala	Gly Gly Lys Pro
165	170	175	
Val His Tyr Leu	Cys Asp Glu Glu	Asp Asp Trp Asn	Pro Ser Ile Glu
180	185	190	
Asp Ile Lys Ser	Lys Ile Ser Glu	Lys Thr Lys Ala	Ile Val Val Ile
195	200	205	
Asn Pro Asn Asn	Pro Thr Gly Ala	Val Tyr Pro Arg	Arg Val Leu Glu
210	215	220	
Gln Ile Val Glu	Ile Ala Arg Glu	His Asp Leu Leu	Ile Leu Ala Asp
225	230	235	240
Glu Ile Tyr Asp	Arg Ile Leu Tyr	Asp Asp Ala Glu	His Ile Ser Leu
245	250	255	
Ala Thr Leu Ala	Pro Asp Leu Leu	Cys Ile Thr Tyr	Asn Gly Leu Ser
260	265	270	
Lys Ala Tyr Arg	Val Ala Gly Tyr	Arg Ala Gly Trp	Met Val Leu Thr
275	280	285	
Gly Pro Lys Gln	Tyr Ala Arg Gly	Phe Ile Glu Gly	Leu Glu Leu Leu
290	295	300	
Ala Gly Thr Arg	Leu Cys Pro Asn	Val Pro Ala Gln	His Ala Ile Gln
305	310	315	320
Val Ala Leu Gly	Gly Arg Gln Ser	Ile Tyr Asp Leu	Thr Gly Glu His
325	330	335	



Gly Arg Leu Leu Glu Gln Arg Asn Met Ala Trp Thr Lys Leu Asn Glu  
                   340                                  345                                  350  
 Ile Pro Gly Val Ser Cys Val Lys Pro Met Gly Ala Leu Tyr Ala Phe  
                   355                                  360                                  365  
 Pro Lys Leu Asp Pro Asn Val Tyr Glu Ile His Asp Asp Thr Gln Leu  
                   370                                  375                                  380  
 Met Leu Asp Leu Leu Arg Ala Glu Lys Ile Leu Met Val Gln Gly Thr  
                   385                                  390                                  395                                  400  
 Gly Phe Asn Trp Pro His His Asp His Phe Arg Val Val Thr Leu Pro  
                                   405                                  410                                  415  
 Trp Ala Ser Gln Leu Glu Asn Ala Ile Glu Arg Leu Gly Asn Phe Leu  
                                   420                                  425                                  430  
 Ser Thr Tyr Lys Gln  
                   435

<210> 497  
 <211> 1080  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1057)  
 <223> RXS02319

<400> 497  
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 agaccttggc catttcggca gaggcttaag gttaaagatt atg agc aac tac agc 115  
   Met Ser Asn Tyr Ser  
   1                                  5  
 acc gac aac cct ttt gat ccc acc caa tgg gcc acc gtt cca ggt ttt 163  
 Thr Asp Asn Pro Phe Asp Pro Thr Gln Trp Ala Thr Val Pro Gly Phe  
                                   10                                  15                                  20  
 gaa gaa ttc acc gac atc acc tac cac cgc cac gtg ggc acc acc cgc 211  
 Glu Glu Phe Thr Asp Ile Thr Tyr His Arg His Val Gly Thr Thr Arg  
                                   25                                  30                                  35  
 gcc gat ggc atc gtg cgc atc gcc ttc gac cgc ccc gaa gtt cgc aat 259  
 Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg Pro Glu Val Arg Asn  
                                   40                                  45                                  50  
 gct ttc cgc ccc cac acc gtc gac gag ctt tac caa gcc ctc gac cac 307  
 Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr Gln Ala Leu Asp His  
                                   55                                  60                                  65  
 gcg cgc cgg acc cca gat gtt gga acc atc ctg ctc acc ggc aac ggc 355  
 Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu Leu Thr Gly Asn Gly  
                   70                                  75                                  80                                  85  
 ccc agc gaa aaa gac ggt ggc tgg gcg ttc tgc tcc ggc ggc gac caa 403

Pro	Ser	Glu	Lys	Asp	Gly	Gly	Trp	Ala	Phe	Cys	Ser	Gly	Gly	Asp	Gln	
				90					95					100		
cgc	atc	cgc	ggg	cgc	tcc	ggc	tac	caa	tac	gcc	acc	gaa	cac	gcg	cgc	451
Arg	Ile	Arg	Gly	Arg	Ser	Gly	Tyr	Gln	Tyr	Ala	Thr	Glu	His	Ala	Arg	
			105					110					115			
gac	gat	gcc	acc	gct	gat	gtc	ttc	acg	gta	gat	att	gcc	cgc	acc	aaa	499
Asp	Asp	Ala	Thr	Ala	Asp	Val	Phe	Thr	Val	Asp	Ile	Ala	Arg	Thr	Lys	
		120					125					130				
gtt	gaa	ggc	gga	cgc	ctc	cac	att	ttg	gaa	gtc	caa	cgc	ctc	atc	cgc	547
Val	Glu	Gly	Gly	Arg	Leu	His	Ile	Leu	Glu	Val	Gln	Arg	Leu	Ile	Arg	
	135					140					145					
acc	atg	cct	aaa	gtt	gtc	atc	gca	gta	gtc	aac	ggc	tgg	gca	gcc	ggc	595
Thr	Met	Pro	Lys	Val	Val	Ile	Ala	Val	Val	Asn	Gly	Trp	Ala	Ala	Gly	
150					155					160					165	
ggg	ggg	cac	tcc	ctc	cat	gtc	gtt	tgc	gac	ctc	acc	atc	gct	tcc	cgc	643
Gly	Gly	His	Ser	Leu	His	Val	Val	Cys	Asp	Leu	Thr	Ile	Ala	Ser	Arg	
			170					175						180		
caa	gaa	gca	cgc	ttc	aag	caa	acc	gac	gct	gac	gtg	gga	tcc	ttc	gac	691
Gln	Glu	Ala	Arg	Phe	Lys	Gln	Thr	Asp	Ala	Asp	Val	Gly	Ser	Phe	Asp	
		185						190				195				
gct	ggc	tac	ggc	tcc	gcc	tac	cta	gcg	aaa	atg	gtc	gga	cag	aaa	aac	739
Ala	Gly	Tyr	Gly	Ser	Ala	Tyr	Leu	Ala	Lys	Met	Val	Gly	Gln	Lys	Asn	
		200					205					210				
gcc	cgc	gaa	atc	ttc	ttc	ctc	gga	cgc	acc	tac	gac	gcc	gaa	cgc	atg	787
Ala	Arg	Glu	Ile	Phe	Phe	Leu	Gly	Arg	Thr	Tyr	Asp	Ala	Glu	Arg	Met	
	215					220					225					
caa	caa	atg	ggc	gca	gtc	aac	atc	gtg	gcc	gac	cac	ggc	gac	cta	gaa	835
Gln	Gln	Met	Gly	Ala	Val	Asn	Ile	Val	Ala	Asp	His	Gly	Asp	Leu	Glu	
230					235				240					245		
aaa	gaa	gcc	atc	caa	gca	gcc	cgc	gaa	atc	aac	acc	aaa	tcc	ccc	acc	883
Lys	Glu	Ala	Ile	Gln	Ala	Ala	Arg	Glu	Ile	Asn	Thr	Lys	Ser	Pro	Thr	
			250					255					260			
ggg	caa	cgc	atg	ctg	aaa	ttc	gcc	ttc	aat	ctc	acc	gac	gat	ggc	ctc	931
Gly	Gln	Arg	Met	Leu	Lys	Phe	Ala	Phe	Asn	Leu	Thr	Asp	Asp	Gly	Leu	
		265						270				275				
atg	gga	caa	caa	gtc	ttc	gcc	ggc	gaa	gcc	acc	cgc	ctg	gcc	tac	atg	979
Met	Gly	Gln	Gln	Val	Phe	Ala	Gly	Glu	Ala	Thr	Arg	Leu	Ala	Tyr	Met	
	280					285						290				
acg	gat	gaa	gcc	gta	gag	ggg	aag	gaa	gca	ttc	cta	gaa	aag	cgc	gaa	1027
Thr	Asp	Glu	Ala	Val	Glu	Gly	Lys	Glu	Ala	Phe						

&lt;210&gt; 498

&lt;211&gt; 319

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 498

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Val Gly Thr Thr Arg Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg
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Pro Glu Val Arg Asn Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr
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Gln Ala Leu Asp His Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu
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Leu Thr Gly Asn Gly Pro Ser Glu Lys Asp Gly Gly Trp Ala Phe Cys
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Ser Gly Gly Asp Gln Arg Ile Arg Gly Arg Ser Gly Tyr Gln Tyr Ala
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Thr Glu His Ala Arg Asp Asp Ala Thr Ala Asp Val Phe Thr Val Asp
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Ile Ala Arg Thr Lys Val Glu Gly Gly Arg Leu His Ile Leu Glu Val
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Gln Arg Leu Ile Arg Thr Met Pro Lys Val Val Ile Ala Val Val Asn
 145          150          155          160

Gly Trp Ala Ala Gly Gly Gly His Ser Leu His Val Val Cys Asp Leu
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Thr Ile Ala Ser Arg Gln Glu Ala Arg Phe Lys Gln Thr Asp Ala Asp
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Val Gly Ser Phe Asp Ala Gly Tyr Gly Ser Ala Tyr Leu Ala Lys Met
          195          200          205

Val Gly Gln Lys Asn Ala Arg Glu Ile Phe Phe Leu Gly Arg Thr Tyr
 210          215          220

Asp Ala Glu Arg Met Gln Gln Met Gly Ala Val Asn Ile Val Ala Asp
 225          230          235          240

His Gly Asp Leu Glu Lys Glu Ala Ile Gln Ala Ala Arg Glu Ile Asn
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Thr Lys Ser Pro Thr Gly Gln Arg Met Leu Lys Phe Ala Phe Asn Leu
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Thr Asp Asp Gly Leu Met Gly Gln Gln Val Phe Ala Gly Glu Ala Thr
 275          280          285

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<220>

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<222> (101)..(361)

<223> RXS02908

<400> 499

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 Leu Lys Leu His Pro  
 1 5  
 gag gta ctg gaa cgt gcc atc gca gat att aaa ggt gtc acc gcg gcg 163  
 Glu Val Leu Glu Arg Ala Ile Ala Asp Ile Lys Gly Val Thr Ala Ala  
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 Cys Val Val Gly Ile Pro Asp Pro Arg Leu Gly Gln Ala Ile Val Ala  
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 gcg tac tcc gga tcg atc agt ccg tct gaa gtt att gaa ggc ctc gac 259  
 Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu Val Ile Glu Gly Leu Asp  
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 gat cta cct cgt tgg cag ctt ccc aaa cgg ctg aag cat ctg gaa tct 307  
 Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg Leu Lys His Leu Glu Ser  
 55 60 65  
 ttg ccc agc att ggt cct gga aaa gct gat cga cgt gct atc gcg aag 355  
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 Leu Phe

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<212> PRT

<213> Corynebacterium glutamicum

<400> 500

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gca	aaa	gcc	aaa	gct	gcg	tct	cac	cgc	gat	ggg	atc	gtg	aat	ctt	tct	211	
Ala	Lys	Ala	Lys	Ala	Ala	Ser	His	Pro	Asp	Gly	Ile	Val	Asn	Leu	Ser		
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Val	Gly	Thr	Pro	Val	Asp	Pro	Val	Ala	Pro	Ser	Ile	Gln	Ile	Ala	Leu		
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Ala	Glu	Ala	Ala	Gly	Phe	Ser	Gly	Tyr	Pro	Gln	Thr	Ile	Gly	Thr	Pro		
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gaa	ctc	cgc	gca	gcc	atc	agg	ggc	gcg	ctt	gag	cgg	cgc	tac	aac	atg	355	
Glu	Leu	Arg	Ala	Ala	Ile	Arg	Gly	Ala	Leu	Glu	Arg	Arg	Tyr	Asn	Met		
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Thr	Lys	Leu	Val	Asp	Ala	Ser	Leu	Leu	Pro	Val	Val	Gly	Thr	Lys	Glu		
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Ala	Ile	Ala	Leu	Leu	Pro	Phe	Ala	Leu	Gly	Ile	Ser	Gly	Thr	Val	Val		
			105					110					115				
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 Gly Cys Thr Val Leu Arg Ser Asp Ser Leu Phe Lys Leu Gly Pro Gln  
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atc ccg tcg atg atg ttt atc aac tca cca tcc aac ccc aca ggc aag 595  
 Ile Pro Ser Met Met Phe Ile Asn Ser Pro Ser Asn Pro Thr Gly Lys  
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gtt ctg ggc atc cca cac ttg cgc aag gtt gtg aag tgg gcg cag gaa 643  
 Val Leu Gly Ile Pro His Leu Arg Lys Val Val Lys Trp Ala Gln Glu  
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aac aac gtg atc ctc gca gct gat gaa tgc tac ttg ggt ctt ggc tgg 691  
 Asn Asn Val Ile Leu Ala Ala Asp Glu Cys Tyr Leu Gly Leu Gly Trp  
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<210> 502  
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 <212> PRT  
 <213> Corynebacterium glutamicum

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 35 40 45

Ile Gln Ile Ala Leu Ala Glu Ala Ala Gly Phe Ser Gly Tyr Pro Gln  
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Thr Ile Gly Thr Pro Glu Leu Arg Ala Ala Ile Arg Gly Ala Leu Glu  
 65 70 75 80

Arg Arg Tyr Asn Met Thr Lys Leu Val Asp Ala Ser Leu Leu Pro Val  
 85 90 95

Val Gly Thr Lys Glu Ala Ile Ala Leu Leu Pro Phe Ala Leu Gly Ile  
 100 105 110

Ser Gly Thr Val Val Ile Pro Glu Ile Ala Tyr Pro Thr Tyr Glu Val  
 115 120 125

Ala Val Val Ala Ala Gly Cys Thr Val Leu Arg Ser Asp Ser Leu Phe  
 130 135 140

Lys Leu Gly Pro Gln Ile Pro Ser Met Met Phe Ile Asn Ser Pro Ser  
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Asn Pro Thr Gly Lys Val Leu Gly Ile Pro His Leu Arg Lys Val Val  
 165 170 175  
 Lys Trp Ala Gln Glu Asn Asn Val Ile Leu Ala Ala Asp Glu Cys Tyr  
 180 185 190  
 Leu Gly Leu Gly Trp Asp Asp Glu Asn Pro Pro Ile Ser Ile Leu Asp  
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 Leu  
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 Met Pro Gly Lys Ile  
 1 5  
 ctc ctt ctc aac ggc cca aac ctg aac atg ctg ggc aaa cgc gag cct 163  
 Leu Leu Leu Asn Gly Pro Asn Leu Asn Met Leu Gly Lys Arg Glu Pro  
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 Asp Ile Tyr Gly His Asp Thr Leu Glu Asp Val Val Ala Leu Ala Thr  
 25 30 35  
 gct gag gct gcg aaa cac ggc ctt gag gtt gag gcg ctg cag agc aat 259  
 Ala Glu Ala Ala Lys His Gly Leu Glu Val Glu Ala Leu Gln Ser Asn  
 40 45 50  
 cac caa ggt gag cta atc gat gcg ctg cac aac gct cgc ggg acc cac 307  
 His Gln Gly Glu Leu Ile Asp Ala Leu His Asn Ala Arg Gly Thr His  
 55 60 65  
 atc ggt tgc gtg att aac ccc ggc ggc ctg act aca ctt cgg tgg cgc 355  
 Ile Gly Cys Val Ile Asn Pro Gly Gly Leu Thr Thr Leu Arg Trp Arg  
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<210> 504  
 <211> 89

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 504

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Gly Lys Arg Glu Pro Asp Ile Tyr Gly His Asp Thr Leu Glu Asp Val
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Val Ala Leu Ala Thr Ala Glu Ala Ala Lys His Gly Leu Glu Val Glu
          35             40             45

Ala Leu Gln Ser Asn His Gln Gly Glu Leu Ile Asp Ala Leu His Asn
          50             55             60

Ala Arg Gly Thr His Ile Gly Cys Val Ile Asn Pro Gly Gly Leu Thr
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Thr Leu Arg Trp Arg Phe Trp Met Leu
          85

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&lt;210&gt; 505

&lt;211&gt; 621

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(598)

&lt;223&gt; RXS03074

&lt;400&gt; 505

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                               Met Thr Gln Ser Ala
                               1             5

cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163
Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn
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gcg caa tca tgc gac act. cag ttt caa aac ctt gga ggt gcc aca gaa 211
Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu
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Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu
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ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307
Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile
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gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355
Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala
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gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403

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 105 110 115  
 ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499  
 Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg  
 120 125 130  
 gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547  
 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr  
 135 140 145  
 gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595  
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys  
 150 155 160 165  
 cag taatttgttt tgacgacgca gta 621  
 Gln

&lt;210&gt; 506

&lt;211&gt; 166

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 506

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 Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe  
 35 40 45  
 Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly  
 50 55 60  
 Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val  
 65 70 75 80  
 Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val  
 85 90 95  
 Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr  
 100 105 110  
 Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr  
 115 120 125  
 Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe  
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 Glu Ala Pro Ile Lys Gln

165

<210> 507  
 <211> 3075  
 <212> DNA  
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 Ala Asp Gly Gly Ser Gly Phe Phe Arg Arg Leu Leu Thr Leu Ser Val  
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 Thr Leu Leu Gly Gly Val Thr Ile Leu Ser Ile Ile Gly Ala Pro Leu  
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 Leu Gly Val Tyr Met Val Leu Pro Ala Arg Leu His Pro His Glu Gln  
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 Val Gly Ile Phe Asp Pro Gln Ile Ile Phe Leu Gly Val Gly Thr Thr  
 135 140 145  
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 Leu Gly Val Val Ala Gln Cys Leu Ile Met Ile Pro Tyr Leu Arg Arg  
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Gln Phe Gly Gly Met Ala Met Ala Ile Ile Val Tyr Val Ala Ile Ser	
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Gln Phe Gly Tyr Ile Ile Thr Arg Ile Ala Ser Ile Ala Asp Asp	
200 205 210	
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Ala Ala Pro Phe Ile Tyr Gln Gln His Trp Met Leu Leu Gln Val Pro	
215 220 225	
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Tyr Gly Ile Ile Gly Val Thr Leu Leu Thr Ala Ile Met Pro Arg Leu	
230 235 240 245	
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Ser Arg Asn Ala Ala Asp Gly Asp Asp Arg Ala Val Val Ser Asp Leu	
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Gln Leu Gly Ser Lys Leu Thr Phe Ile Ala Leu Ile Pro Ile Val Val	
265 270 275	
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Phe Phe Thr Ala Phe Gly Val Pro Ile Ala Asn Gly Leu Phe Ala Tyr	
280 285 290	
ggc caa ttc gat gcc aac gcc gcc aac atc ctt ggt tgg act ctg agc	1027
Gly Gln Phe Asp Ala Asn Ala Ala Asn Ile Leu Gly Trp Thr Leu Ser	
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Phe Ser Ala Phe Thr Leu Ile Pro Tyr Ala Leu Val Leu Leu His Leu	
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Leu Ser Ser Ser Pro Glu Arg Val Val Val Leu Leu Gly Ala Ala Asn	
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Gly Phe Ser Phe Ile Thr Gly Ala Val Ile Gly Ala Tyr Leu Leu Arg	
375 380 385	
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Asn Lys Leu Gly Leu Leu Gly Met Arg Ser Leu Ala Lys Thr Ser Leu	
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Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala Ala Ala Trp Ala Leu	

410										415					420					
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Ser	Ser	Val	Gly	Tyr	Leu	Leu	Asn	Leu	Ala	Val	Leu	Gly	Val	Phe	Phe					
440				445				450												
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470				475				480				485								
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490				495				500												
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Val	Pro	Gly	Ala	Pro	Val	Gly	Asp	Gly	Arg	Phe	Arg	Leu	Leu	Ala	Asp					
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550				555				560				565								
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Thr	Gly	Lys	Glu	Val	Ala	Leu	Ile	Phe	Val	Asp	Thr	Ser	Gly	Asn	Ala					
570				575				580												
cca	ttt	gcg	cca	ctg	tct	tcg	gca	gcc	gca	gcg	ggc	atc	gcc	tac	gag	1891				
Pro	Phe	Ala	Pro	Leu	Ser	Ser	Ala	Ala	Ala	Ala	Gly	Ile	Ala	Tyr	Glu					
585				590				595												
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Val	Gln	Arg	Arg	Thr	Lys	Lys	Leu	Ala	Ser	Leu	Gly	Ser	Leu	Ala	Val					
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Ala	Pro	Asn	Ile	His	Ser	Glu	Ala	Tyr	Arg	Asn	Gly	Cys	Leu	Ile	Val					
615				620				625												
gcc	gat	tgg	gtg	cct	ggc	tcc	agc	ttg	agc	gcc	gtc	gcg	gaa	tcc	ggg	2035				
Ala	Asp	Trp	Val	Pro	Gly	Ser	Ser	Leu	Ser	Ala	Val	Ala	Glu	Ser	Gly					
630				635				640				645								
gcc	gat	ccc	cgc	gcc	gcc	gcg	ttc	gcg	ctc	gcg	gaa	cta	act	gaa	acc	2083				
Ala	Asp	Pro	Arg	Ala	Ala	Ala	Phe	Ala	Leu	Ala	Glu	Leu	Thr	Glu	Thr					
650				655				660												

atc ggc gag gcc cac gag atg ggt atc ccg gcc ggc ttg gac aac aag	2131
Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala Gly Leu Asp Asn Lys	
665 670 675	
tgc cga att cgt atc aac acc gac ggc cat gcc gtc ctc gcc ttg ccg	2179
Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala Val Leu Ala Leu Pro	
680 685 690	
gcg att ttg ccc gat gcc tca gag ctc cgc gac gcc aag tcc ctg gcc	2227
Ala Ile Leu Pro Asp Ala Ser Glu Leu Arg Asp Ala Lys Ser Leu Ala	
695 700 705	
tcg gcc gcc gag atg ctt atc gac gcg acc ctc gct ccc agc gac gtc	2275
Ser Ala Ala Glu Met Leu Ile Asp Ala Thr Leu Ala Pro Ser Asp Val	
710 715 720 725	
aag gca atg gtc act gaa gcc cag ggg cta gct aca gaa gac aat ccc	2323
Lys Ala Met Val Thr Glu Ala Gln Gly Leu Ala Thr Glu Asp Asn Pro	
730 735 740	
gat tac gca tca ctt gcc atg gcg atg cgc acc tgc gga ctg ttc acc	2371
Asp Tyr Ala Ser Leu Ala Met Ala Met Arg Thr Cys Gly Leu Phe Thr	
745 750 755	
gag gaa cca acc cac ctt gtg gtg aag aag gaa aag aca cca aag cct	2419
Glu Glu Pro Thr His Leu Val Val Lys Lys Glu Lys Thr Pro Lys Pro	
760 765 770	
gcg aca cgt gat ggt ttc ggt gcc tcc gac tac acc gtc aag ggc atg	2467
Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr Thr Val Lys Gly Met	
775 780 785	
gca gcc atc gcc gct gtg gtg atc atc ttg gtt tcc ctg gtg gcc gcc	2515
Ala Ala Ile Ala Ala Val Val Ile Ile Leu Val Ser Leu Val Ala Ala	
790 795 800 805	
ggt acc gcg ttc ctc acc agc ttc ttc ggc agc agc acc aac gaa caa	2563
Gly Thr Ala Phe Leu Thr Ser Phe Phe Gly Ser Ser Thr Asn Glu Gln	
810 815 820	
tcc ccg ttg gcc tct gtt gaa gcc acc acc tct gca aca cca gaa cct	2611
Ser Pro Leu Ala Ser Val Glu Ala Thr Thr Ser Ala Thr Pro Glu Pro	
825 830 835	
gtg ggg cca ccg gtc tac ctg gat ctg gat caa gcc cgc acg tgg gat	2659
Val Gly Pro Pro Val Tyr Leu Asp Leu Asp Gln Ala Arg Thr Trp Asp	
840 845 850	
gac ggt gca gga aca gat gtc acc gac gtc acc gac ggc aac acc tcc	2707
Asp Gly Ala Gly Thr Asp Val Thr Asp Val Thr Asp Gly Asn Thr Ser	
855 860 865	
acc gca tgg acc tcc acc ggc ggc gac ggc ctc cta gtt gac ctg tcc	2755
Thr Ala Trp Thr Ser Thr Gly Gly Asp Gly Leu Leu Val Asp Leu Ser	
870 875 880 885	
acg cct gcc cgc ctc gac cgc gtc atc ttg acc acc ggc acc ggc tcc	2803
Thr Pro Ala Arg Leu Asp Arg Val Ile Leu Thr Thr Gly Thr Gly Ser	
890 895 900	

gac agc aac gtg acc tcg acc gtg aag atc tac gca ttc aac gac gcc 2851  
 Asp Ser Asn Val Thr Ser Thr Val Lys Ile Tyr Ala Phe Asn Asp Ala  
 905 910 915

tca cca cac tcc ctg tcg gaa ggc atc gag atc ggc acc gtg gat tat 2899  
 Ser Pro His Ser Leu Ser Glu Gly Ile Glu Ile Gly Thr Val Asp Tyr  
 920 925 930

tcc ggc cgc agt ctc agc cac agc atc cgc gat tcc tcc aag ctt ccg 2947  
 Ser Gly Arg Ser Leu Ser His Ser Ile Arg Asp Ser Ser Lys Leu Pro  
 935 940 945

ggt cag gtg gaa tcc gtg gtg att ctg gtc gat gag gtt cgt tcc tca 2995  
 Gly Gln Val Glu Ser Val Val Ile Leu Val Asp Glu Val Arg Ser Ser  
 950 955 960 965

caa acc tca gac acc aat cca cag atg cag atc gct gaa gta caa ctt 3043  
 Gln Thr Ser Asp Thr Asn Pro Gln Met Gln Ile Ala Glu Val Gln Leu  
 970 975 980

gtt ggt tgg taaattacgc gtttgtgatt gac 3075  
 Val Gly Trp

&lt;210&gt; 508

&lt;211&gt; 984

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 508

Val Leu Gly Ala Val Leu Thr Ser Leu Val Ile Pro Val Leu Thr Arg  
 1 5 10 15

Ala Glu Lys Glu Asp Ala Asp Gly Gly Ser Gly Phe Phe Arg Arg Leu  
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Leu Thr Leu Ser Val Thr Leu Leu Gly Gly Val Thr Ile Leu Ser Ile  
 35 40 45

Ile Gly Ala Pro Leu Leu Thr Arg Met Met Leu Ser Ser Glu Gly Gln  
 50 55 60

Val Asn Val Val Met Ser Thr Ala Phe Ala Tyr Trp Leu Leu Pro Gln  
 65 70 75 80

Ile Phe Phe Tyr Gly Leu Phe Ala Leu Phe Met Ala Val Leu Asn Thr  
 85 90 95

Arg Glu Val Phe Lys Pro Gly Ala Trp Ala Pro Val Val Asn Asn Val  
 100 105 110

Ile Thr Leu Thr Val Leu Gly Val Tyr Met Val Leu Pro Ala Arg Leu  
 115 120 125

His Pro His Glu Gln Val Gly Ile Phe Asp Pro Gln Ile Ile Phe Leu  
 130 135 140

Gly Val Gly Thr Thr Leu Gly Val Val Ala Gln Cys Leu Ile Met Ile  
 145 150 155 160

Pro Tyr Leu Arg Arg Ala Gly Ile Asp Met Arg Pro Leu Trp Gly Ile  
 165 170 175  
 Asp Ala Arg Leu Lys Gln Phe Gly Gly Met Ala Met Ala Ile Ile Val  
 180 185 190  
 Tyr Val Ala Ile Ser Gln Phe Gly Tyr Ile Ile Thr Thr Arg Ile Ala  
 195 200 205  
 Ser Ile Ala Asp Asp Ala Ala Pro Phe Ile Tyr Gln Gln His Trp Met  
 210 215 220  
 Leu Leu Gln Val Pro Tyr Gly Ile Ile Gly Val Thr Leu Leu Thr Ala  
 225 230 235 240  
 Ile Met Pro Arg Leu Ser Arg Asn Ala Ala Asp Gly Asp Asp Arg Ala  
 245 250 255  
 Val Val Ser Asp Leu Gln Leu Gly Ser Lys Leu Thr Phe Ile Ala Leu  
 260 265 270  
 Ile Pro Ile Val Val Phe Phe Thr Ala Phe Gly Val Pro Ile Ala Asn  
 275 280 285  
 Gly Leu Phe Ala Tyr Gly Gln Phe Asp Ala Asn Ala Ala Asn Ile Leu  
 290 295 300  
 Gly Trp Thr Leu Ser Phe Ser Ala Phe Thr Leu Ile Pro Tyr Ala Leu  
 305 310 315 320  
 Val Leu Leu His Leu Arg Val Phe Tyr Ala Arg Glu Glu Val Trp Thr  
 325 330 335  
 Pro Thr Phe Ile Ile Ala Gly Ile Thr Ala Thr Lys Val Val Leu Ser  
 340 345 350  
 Leu Leu Ala Pro Leu Leu Ser Ser Ser Pro Glu Arg Val Val Val Leu  
 355 360 365  
 Leu Gly Ala Ala Asn Gly Phe Ser Phe Ile Thr Gly Ala Val Ile Gly  
 370 375 380  
 Ala Tyr Leu Leu Arg Asn Lys Leu Gly Leu Leu Gly Met Arg Ser Leu  
 385 390 395 400  
 Ala Lys Thr Ser Leu Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala  
 405 410 415  
 Ala Ala Trp Ala Leu Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe  
 420 425 430  
 Leu Leu Gly Thr Leu Ser Ser Val Gly Tyr Leu Leu Asn Leu Ala Val  
 435 440 445  
 Leu Gly Val Phe Phe Ile Phe Val Thr Gly Ile Val Leu Ser Arg Ser  
 450 455 460  
 Gly Leu Pro Glu Val Gln Asn Leu Gly Gln Ala Leu Thr Arg Ile Pro  
 465 470 475 480  
 Gly Leu Ser Arg Phe Ile Arg Pro Asn Thr Lys Ile Ser Leu Asp Val

485										490					495				
Gly	Glu	Val	Ser	Glu	Gln	Asp	Phe	Ser	Thr	Gln	Leu	Val	Ala	Pro	Ser				
			500					505					510						
Glu	Phe	Ala	Ala	Thr	Pro	Val	Pro	Pro	Pro	Met	Ser	Ala	Gly	Ile	Val				
		515					520					525							
Arg	Gly	Pro	Arg	Leu	Val	Pro	Gly	Ala	Pro	Val	Gly	Asp	Gly	Arg	Phe				
	530					535					540								
Arg	Leu	Leu	Ala	Asp	His	Gly	Gly	Val	Gln	Gly	Ala	Arg	Phe	Trp	Gln				
	545				550					555					560				
Ala	Arg	Glu	Ile	Ala	Thr	Gly	Lys	Glu	Val	Ala	Leu	Ile	Phe	Val	Asp				
				565				570						575					
Thr	Ser	Gly	Asn	Ala	Pro	Phe	Ala	Pro	Leu	Ser	Ser	Ala	Ala	Ala	Ala				
			580					585					590						
Gly	Ile	Ala	Tyr	Glu	Val	Gln	Arg	Arg	Thr	Lys	Lys	Leu	Ala	Ser	Leu				
		595					600					605							
Gly	Ser	Leu	Ala	Val	Ala	Pro	Asn	Ile	His	Ser	Glu	Ala	Tyr	Arg	Asn				
	610					615					620								
Gly	Cys	Leu	Ile	Val	Ala	Asp	Trp	Val	Pro	Gly	Ser	Ser	Leu	Ser	Ala				
	625				630					635					640				
Val	Ala	Glu	Ser	Gly	Ala	Asp	Pro	Arg	Ala	Ala	Ala	Phe	Ala	Leu	Ala				
				645				650						655					
Glu	Leu	Thr	Glu	Thr	Ile	Gly	Glu	Ala	His	Glu	Met	Gly	Ile	Pro	Ala				
			660				665						670						
Gly	Leu	Asp	Asn	Lys	Cys	Arg	Ile	Arg	Ile	Asn	Thr	Asp	Gly	His	Ala				
		675					680					685							
Val	Leu	Ala	Leu	Pro	Ala	Ile	Leu	Pro	Asp	Ala	Ser	Glu	Leu	Arg	Asp				
	690					695					700								
Ala	Lys	Ser	Leu	Ala	Ser	Ala	Ala	Glu	Met	Leu	Ile	Asp	Ala	Thr	Leu				
	705				710					715					720				
Ala	Pro	Ser	Asp	Val	Lys	Ala	Met	Val	Thr	Glu	Ala	Gln	Gly	Leu	Ala				
				725					730					735					
Thr	Glu	Asp	Asn	Pro	Asp	Tyr	Ala	Ser	Leu	Ala	Met	Ala	Met	Arg	Thr				
			740					745					750						
Cys	Gly	Leu	Phe	Thr	Glu	Glu	Pro	Thr	His	Leu	Val	Val	Lys	Lys	Glu				
		755					760					765							
Lys	Thr	Pro	Lys	Pro	Ala	Thr	Arg	Asp	Gly	Phe	Gly	Ala	Ser	Asp	Tyr				
	770					775					780								
Thr	Val	Lys	Gly	Met	Ala	Ala	Ile	Ala	Ala	Val	Val	Ile	Ile	Leu	Val				
	785				790					795				800					
Ser	Leu	Val	Ala	Ala	Gly	Thr	Ala	Phe	Leu	Thr	Ser	Phe	Phe	Gly	Ser				
				805					810					815					



Ser Thr Asn Glu Gln Ser Pro Leu Ala Ser Val Glu Ala Thr Thr Ser  
 820 825 830  
 Ala Thr Pro Glu Pro Val Gly Pro Pro Val Tyr Leu Asp Leu Asp Gln  
 835 840 845  
 Ala Arg Thr Trp Asp Asp Gly Ala Gly Thr Asp Val Thr Asp Val Thr  
 850 855 860  
 Asp Gly Asn Thr Ser Thr Ala Trp Thr Ser Thr Gly Gly Asp Gly Leu  
 865 870 875 880  
 Leu Val Asp Leu Ser Thr Pro Ala Arg Leu Asp Arg Val Ile Leu Thr  
 885 890 895  
 Thr Gly Thr Gly Ser Asp Ser Asn Val Thr Ser Thr Val Lys Ile Tyr  
 900 905 910  
 Ala Phe Asn Asp Ala Ser Pro His Ser Leu Ser Glu Gly Ile Glu Ile  
 915 920 925  
 Gly Thr Val Asp Tyr Ser Gly Arg Ser Leu Ser His Ser Ile Arg Asp  
 930 935 940  
 Ser Ser Lys Leu Pro Gly Gln Val Glu Ser Val Val Ile Leu Val Asp  
 945 950 955 960  
 Glu Val Arg Ser Ser Gln Thr Ser Asp Thr Asn Pro Gln Met Gln Ile  
 965 970 975  
 Ala Glu Val Gln Leu Val Gly Trp  
 980

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 <212> DNA  
 <213> Corynebacterium glutamicum

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 <222> (101)..(907)  
 <223> RXC02080

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 Met Ser Ile Glu Trp  
 1 5  
 tta caa att gtt gaa tta gga gcg atc ttt ggt gca ggt ttc ctc gca 163  
 Leu Gln Ile Val Glu Leu Gly Ala Ile Phe Gly Ala Gly Phe Leu Ala  
 10 15 20  
 gga agc atc aat gta att gtc gga gca gga aca tta gtg tcg ttt cct 211  
 Gly Ser Ile Asn Val Ile Val Gly Ala Gly Thr Leu Val Ser Phe Pro  
 25 30 35  
 att ctc gtg ttc ctg ggc ctt cca ccg ttg act gcc acc atc gcc aac 259

Ile Leu Val	Phe Leu Gly	Leu Pro Pro	Leu Thr Ala	Thr Ile Ala	Asn	
40		45		50		
acc atc ggc	atc gtt cct	gga agt att	tcg ggt gtg	gtt gct tat	aga	307
Thr Ile Gly	Ile Val Pro	Gly Ser Ile	Ser Gly Val	Val Ala Tyr	Arg	
55		60		65		
cgt gaa cta	cac gcc cat	gta aaa acc	atc aga ttt	ctg ctg cca	gca	355
Arg Glu Leu	His Ala His	Val Lys Thr	Ile Arg Phe	Leu Leu Pro	Ala	
70		75		80	85	
tca atc ctc	gga ggg atc	acc ggc gcc	tcg ctc ttg	ctg cat ttc	tcc	403
Ser Ile Leu	Gly Gly Ile	Thr Gly Ala	Ser Leu Leu	Leu Leu His	Phe Ser	
	90		95		100	
gca gat gtt	ttt aca gca	gta att ccc	tgg ctg att	gga ttc ggc	acg	451
Ala Asp Val	Phe Thr Ala	Val Ile Pro	Trp Leu Ile	Gly Phe Gly	Thr	
	105		110		115	
ctg ttg gtt	atc gca ggt	cca tca att	aag aag cat	gtt ggc gct	cat	499
Leu Leu Val	Ile Ala Gly	Pro Ser Ile	Lys Lys His	Val Gly Ala	His	
	120		125		130	
act tca ggt	ggc atc tct	gct ggg ttt	agg caa ttg	cct ttc ccg	agc	547
Thr Ser Gly	Gly Ile Ser	Ala Gly Phe	Arg Gln Leu	Pro Phe Pro	Ser	
	135		140		145	
cga acc acc	ttc atc gtc	tca gta tgt	ggg gcc ctg	ttg ctg ggc	atg	595
Arg Thr Thr	Phe Ile Val	Ser Val Cys	Gly Ala Leu	Leu Leu Leu	Gly Met	
150		155		160	165	
tat gga ggg	tac ttc agc	gca gct caa	ggc att ctt	ctc atc gca	ttg	643
Tyr Gly Gly	Tyr Phe Ser	Ala Ala Gln	Gly Ile Leu	Leu Leu Ile	Ala Leu	
	170		175		180	
ctt ggc atc	aca tca acg	ctg cag atg	cag gaa ctc	aac gcc atc	aaa	691
Leu Gly Ile	Thr Ser Thr	Leu Gln Met	Gln Glu Leu	Asn Ala Ile	Lys	
	185		190		195	
aac ctc aca	gtg gcg gca	gtt aat ctc	atc gca gcc	agt gtt ttt	ata	739
Asn Leu Thr	Val Ala Ala	Val Asn Leu	Ile Ala Ala	Ser Val Phe	Ile	
	200		205		210	
atc atc tcc	cct gag ttg	atc tcc tgg	ccg acc gtt	gcc tta atc	gcg	787
Ile Ile Ser	Pro Glu Leu	Ile Ser Trp	Pro Thr Val	Ala Leu Ile	Ala	
	215		220		225	
ctt ggc tca	gct tta ggt	gga tac atc	ggc gga cgg	tac gcc cgc	cga	835
Leu Gly Ser	Ala Leu Gly	Gly Tyr Ile	Gly Gly Arg	Tyr Ala Arg	Arg	
230		235		240	245	
ctt cgc ccc	agt gtt ttt	aga gca ttt	gtg gtc atc	gtc gga atc	acc	883
Leu Arg Pro	Ser Val Phe	Arg Ala Phe	Val Val Ile	Val Gly Ile	Thr	
	250		255		260	
acg gtc atc	gtt atg acg	atc ggt taatgcagca	gactagtaac ccc			930
Thr Val Ile	Val Met Thr	Ile Gly				
	265					

&lt;210&gt; 510

&lt;211&gt; 269

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 510

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Met Ser Ile Glu Trp Leu Gln Ile Val Glu Leu Gly Ala Ile Phe Gly
  1           5           10           15

Ala Gly Phe Leu Ala Gly Ser Ile Asn Val Ile Val Gly Ala Gly Thr
      20           25           30

Leu Val Ser Phe Pro Ile Leu Val Phe Leu Gly Leu Pro Pro Leu Thr
      35           40           45

Ala Thr Ile Ala Asn Thr Ile Gly Ile Val Pro Gly Ser Ile Ser Gly
      50           55           60

Val Val Ala Tyr Arg Arg Glu Leu His Ala His Val Lys Thr Ile Arg
      65           70           75           80

Phe Leu Leu Pro Ala Ser Ile Leu Gly Gly Ile Thr Gly Ala Ser Leu
      85           90           95

Leu Leu His Phe Ser Ala Asp Val Phe Thr Ala Val Ile Pro Trp Leu
      100          105          110

Ile Gly Phe Gly Thr Leu Leu Val Ile Ala Gly Pro Ser Ile Lys Lys
      115          120          125

His Val Gly Ala His Thr Ser Gly Gly Ile Ser Ala Gly Phe Arg Gln
      130          135          140

Leu Pro Phe Pro Ser Arg Thr Thr Phe Ile Val Ser Val Cys Gly Ala
      145          150          155          160

Leu Leu Leu Gly Met Tyr Gly Gly Tyr Phe Ser Ala Ala Gln Gly Ile
      165          170          175

Leu Leu Ile Ala Leu Leu Gly Ile Thr Ser Thr Leu Gln Met Gln Glu
      180          185          190

Leu Asn Ala Ile Lys Asn Leu Thr Val Ala Ala Val Asn Leu Ile Ala
      195          200          205

Ala Ser Val Phe Ile Ile Ile Ser Pro Glu Leu Ile Ser Trp Pro Thr
      210          215          220

Val Ala Leu Ile Ala Leu Gly Ser Ala Leu Gly Gly Tyr Ile Gly Gly
      225          230          235          240

Arg Tyr Ala Arg Arg Leu Arg Pro Ser Val Phe Arg Ala Phe Val Val
      245          250          255

Ile Val Gly Ile Thr Thr Val Ile Val Met Thr Ile Gly
      260          265

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&lt;210&gt; 511

&lt;211&gt; 669

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(646)

&lt;223&gt; RXC02789

&lt;400&gt; 511

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ttcttaacac taaacaatgg aaaggtaagc gggtttttct atg aag gtt tcc gcc 115
                                         Met Lys Val Ser Ala
                                         1                               5

gat aca ccc ggt cac gat gat cca ggc cca ggc cgg cgc ctt ggc tta 163
Asp Thr Pro Gly His Asp Asp Pro Gly Pro Gly Arg Arg Leu Gly Leu
                               10                               15                               20

gat gtc ggc acc gtg cgc atc gga gtg gca gcc tct gac cgc gat gcc 211
Asp Val Gly Thr Val Arg Ile Gly Val Ala Ala Ser Asp Arg Asp Ala
                               25                               30                               35

aag ctt gcc atg cct gtg gaa acc gtt ccg cgg gaa act gga ttc aaa 259
Lys Leu Ala Met Pro Val Glu Thr Val Pro Arg Glu Thr Gly Phe Lys
                               40                               45                               50

ggg cca gac ctg gcc gat att gat cgg ttg gtc gcc atc gtt gag gaa 307
Gly Pro Asp Leu Ala Asp Ile Asp Arg Leu Val Ala Ile Val Glu Glu
                               55                               60                               65

tac aac gcc gtg gaa gtc att gtt ggt cta ccc aca gat ctg cag gga 355
Tyr Asn Ala Val Glu Val Ile Val Gly Leu Pro Thr Asp Leu Gln Gly
                               70                               75                               80                               85

aat ggc tcc gcc agt gtg aag cat gca aag gaa att gct ttc cgc gtc 403
Asn Gly Ser Ala Ser Val Lys His Ala Lys Glu Ile Ala Phe Arg Val
                               90                               95                               100

cgt cgg cgc ctc acc aat gct gga aag aac att ccg gta cgg ctt ggc 451
Arg Arg Arg Leu Thr Asn Ala Gly Lys Asn Ile Pro Val Arg Leu Gly
                               105                               110                               115

gac gaa cgc ctc acc acc gtc gtg gcc acc caa gcc ttg cgg gcc tca 499
Asp Glu Arg Leu Thr Thr Val Val Ala Thr Gln Ala Leu Arg Ala Ser
                               120                               125                               130

gga gtc agc gaa aaa gcg gga cgt aaa gtt att gat caa gct gcc gca 547
Gly Val Ser Glu Lys Ala Gly Arg Lys Val Ile Asp Gln Ala Ala Ala
                               135                               140                               145

gta gaa atc ctt caa acc tgg ttg gat gct cgc acc cga gcc ctt gaa 595
Val Glu Ile Leu Gln Thr Trp Leu Asp Ala Arg Thr Arg Ala Leu Glu
                               150                               155                               160                               165

cca caa tcc aca gac acc caa gat ttc gac gag aag gga aat ttc cca 643
Pro Gln Ser Thr Asp Thr Gln Asp Phe Asp Glu Lys Gly Asn Phe Pro
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gga tgaaccaaat ccgaaaccgc cgg 669
Gly

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[illegible]

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<222> (101)..(880)  
<223> RXC02295
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                Met Gly Leu Glu Leu
                1           5

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gca gct agc ggg tgg ggc atc ctc atc gca ggc gcc gcc gta gcc gga	163
Ala Ala Ser Gly Trp Gly Ile Leu Ile Ala Gly Ala Ala Val Ala Gly	
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tgg atc gac gca gta atc ggc ggt ggc gga ctc gtc ctc atc ccg ctg	211
Trp Ile Asp Ala Val Ile Gly Gly Gly Gly Leu Val Leu Ile Pro Leu	
25 30 35	
atc ctc gcg gtc atg ccg caa ctc gca cct gtg aca gcg ctg gcc tcc	259
Ile Leu Ala Val Met Pro Gln Leu Ala Pro Val Thr Ala Leu Ala Ser	
40 45 50	
aac aaa ctg gca gcc gtc acc ggc acg gca tcg gcg gca ttc acc ctg	307
Asn Lys Leu Ala Ala Val Thr Gly Thr Ala Ser Ala Ala Phe Thr Leu	
55 60 65	
gtc agg cgc gtc aaa ccc gac aaa aaa ctg ctt gcg ctc tac gtt ctg	355
Val Arg Arg Val Lys Pro Asp Lys Lys Leu Leu Ala Leu Tyr Val Leu	
70 75 80 85	
gtg gca gct gtg tgc tcc ggt gca ggc gcc ctg gct gcg agt ctc att	403
Val Ala Ala Val Cys Ser Gly Ala Gly Ala Leu Ala Ala Ser Leu Ile	
90 95 100	
gac aaa caa atc atg cga ccg ctg atc atc gtg ttg atg ctg gtc gtt	451
Asp Lys Gln Ile Met Arg Pro Leu Ile Ile Val Leu Met Leu Val Val	
105 110 115	
ggc ctg atc gtg gtg ttc aaa cca aac ttc gga acc ggc gaa agc aaa	499
Gly Leu Ile Val Val Phe Lys Pro Asn Phe Gly Thr Gly Glu Ser Lys	
120 125 130	
gcc ctg ccc acc gga tgg aaa cgc tgg gcc gcc atc gtt gca gtc gga	547
Ala Leu Pro Thr Gly Trp Lys Arg Trp Ala Ala Ile Val Ala Val Gly	
135 140 145	
ctc atc gca gcc tac gac ggc atc ttc gga ccc gga acc ggc atg ttc	595
Leu Ile Ala Ala Tyr Asp Gly Ile Phe Gly Pro Gly Thr Gly Met Phe	
150 155 160 165	
ctc atc atg gcg ttc acc gca ctg ctc tcc caa aat ttc ctg tcc tcc	643
Leu Ile Met Ala Phe Thr Ala Leu Leu Ser Gln Asn Phe Leu Ser Ser	
170 175 180	
gca gcc atg gcg aag gtc gta aac acc gca aca aac ctg ggt gcg cta	691
Ala Ala Met Ala Lys Val Val Asn Thr Ala Thr Asn Leu Gly Ala Leu	
185 190 195	
att gta ttc atc atc ggc ggc cac atg tgg tgg acc cta gga ctc gtg	739
Ile Val Phe Ile Ile Gly Gly His Met Trp Trp Thr Leu Gly Leu Val	
200 205 210	
ctg gca gtc gcc aat gtc gca ggc gca caa ctc ggt gcc cga acg gtg	787
Leu Ala Val Ala Asn Val Ala Gly Ala Gln Leu Gly Ala Arg Thr Val	
215 220 225	
ctt ggt ggc ggt acc agg cta att aga tac gca cta cta acc ctg gtt	835
Leu Gly Gly Gly Thr Arg Leu Ile Arg Tyr Ala Leu Leu Thr Leu Val	
230 235 240 245	
gtc gtc atg agc gtc tac ctc acc tgg caa caa atc caa gga atg	880

Val Val Met Ser Val Tyr Leu Thr Trp Gln Gln Ile Gln Gly Met  
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tagataagtc ggggcaaact cta

903

<210> 514

<211> 260

<212> PRT

<213> Corynebacterium glutamicum

<400> 514

Met Gly Leu Glu Leu Ala Ala Ser Gly Trp Gly Ile Leu Ile Ala Gly  
 1 5 10 15

Ala Ala Val Ala Gly Trp Ile Asp Ala Val Ile Gly Gly Gly Gly Leu  
 20 25 30

Val Leu Ile Pro Leu Ile Leu Ala Val Met Pro Gln Leu Ala Pro Val  
 35 40 45

Thr Ala Leu Ala Ser Asn Lys Leu Ala Ala Val Thr Gly Thr Ala Ser  
 50 55 60

Ala Ala Phe Thr Leu Val Arg Arg Val Lys Pro Asp Lys Lys Leu Leu  
 65 70 75 80

Ala Leu Tyr Val Leu Val Ala Ala Val Cys Ser Gly Ala Gly Ala Leu  
 85 90 95

Ala Ala Ser Leu Ile Asp Lys Gln Ile Met Arg Pro Leu Ile Ile Val  
 100 105 110

Leu Met Leu Val Val Gly Leu Ile Val Val Phe Lys Pro Asn Phe Gly  
 115 120 125

Thr Gly Glu Ser Lys Ala Leu Pro Thr Gly Trp Lys Arg Trp Ala Ala  
 130 135 140

Ile Val Ala Val Gly Leu Ile Ala Ala Tyr Asp Gly Ile Phe Gly Pro  
 145 150 155 160

Gly Thr Gly Met Phe Leu Ile Met Ala Phe Thr Ala Leu Leu Ser Gln  
 165 170 175

Asn Phe Leu Ser Ser Ala Ala Met Ala Lys Val Val Asn Thr Ala Thr  
 180 185 190

Asn Leu Gly Ala Leu Ile Val Phe Ile Ile Gly Gly His Met Trp Trp  
 195 200 205

Thr Leu Gly Leu Val Leu Ala Val Ala Asn Val Ala Gly Ala Gln Leu  
 210 215 220

Gly Ala Arg Thr Val Leu Gly Gly Gly Thr Arg Leu Ile Arg Tyr Ala  
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Leu Leu Thr Leu Val Val Val Met Ser Val Tyr Leu Thr Trp Gln Gln  
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Ile Gln Gly Met

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<211> 1132
<212> DNA
<213> Corynebacterium glutamicum
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<223> RXN03063
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acctagacaa cagtttgtat ctcacctcac aggaggaacc																115
Val Glu Asp Leu Ser																5
1																
tac cgc atc ccg cag tcg cgc acc gtg gcc gag cag gtg cca ggg ccg																163
Tyr Arg Ile Pro Gln Ser Arg Thr Val Ala Glu Gln Val Pro Gly Pro																20
10 15																
aag tcg aaa gcg ctg gat gag cgt cga caa gca gca gta gca cga gca																211
Lys Ser Lys Ala Leu Asp Glu Arg Arg Gln Ala Ala Val Ala Arg Ala																35
25 30																
ctt gca ccg ggt ctg cct gga tac gtg gtg gac gca gac ggt ggc atc																259
Leu Ala Pro Gly Leu Pro Gly Tyr Val Val Asp Ala Asp Gly Gly Ile																50
40 45																
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Leu Ala Asp Ala Asp Gly Asn Arg Phe Ile Asp Leu Ala Ser Gly Ile																65
55 60																
gcc gtg acc acg gtc ggc gga tcc aac gcg gcc gtc gcg aaa gcc gtc																355
Ala Val Thr Thr Val Gly Gly Ser Asn Ala Ala Val Ala Lys Ala Val																85
70 75																
ggc gcc gca gct gcc cgc ttc acc cac acc tgc ttc atg gtc tca cct																403
Gly Ala Ala Ala Ala Arg Phe Thr His Thr Cys Phe Met Val Ser Pro																100
90 95																
tat gaa act tac gtg gcc atg gcg gag aga ctc aac gcc ttg act cca																451
Tyr Glu Thr Tyr Val Ala Met Ala Glu Arg Leu Asn Ala Leu Thr Pro																115
105 110																
ggc gat cac gac aag aag agc gcg ctg ttt aac tct ggc gcc gaa gcc																499
Gly Asp His Asp Lys Lys Ser Ala Leu Phe Asn Ser Gly Ala Glu Ala																130
120 125																
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Val Glu Asn Ala Val Lys Val Ala Arg Ala Tyr Thr Gly Lys Gly Ala																145
135 140																
gtc gtg gtg ttc gac aac gcg tac cac gga cgg acc aac ctc acc atg																595
Val Val Val Phe Asp Asn Ala Tyr His Gly Arg Thr Asn Leu Thr Met																165
150 155 160																
gcg atg acc gcg aag aac cgc cca tac aag tcc gga ttc gga cca cta																643



Ala Met Thr	Ala Lys Asn Arg Pro Tyr	Lys Ser Gly Phe Gly Pro Leu	
	170	175	180
gcc gca gac gtc	tac cgt gca cca atg tct	tac cca ctg cgc gac gga	691
Ala Ala Asp Val	Tyr Arg Ala Pro Met Ser	Tyr Pro Leu Arg Asp Gly	
	185	190	195
ctg tcc ggc ccg	gaa gcc gca gag cgc gcg	atc tcc gtg atc gaa tcc	739
Leu Ser Gly Pro	Glu Ala Ala Glu Arg Ala	Ile Ser Val Ile Glu Ser	
	200	205	210
cag gtc gga gcc	gaa aac ctc gcc tgc gtg	gtc att gaa ccg atc cag	787
Gln Val Gly Ala	Glu Asn Leu Ala Cys Val	Val Ile Glu Pro Ile Gln	
	215	220	225
ggc gaa ggc gga	ttc atc gtc ccc gca cca	gga ttc ctc gca gcc att	835
Gly Glu Gly Gly	Phe Ile Val Pro Ala Pro	Gly Phe Leu Ala Ala Ile	
	230	235	240
tcc acc tgg tgc	cgc gag aac gac gtg gtg	ttc atc gcc gat gaa atc	883
Ser Thr Trp Cys	Arg Glu Asn Asp Val Val	Phe Ile Ala Asp Glu Ile	
	250	255	260
caa tct ggc ttc	ctg cgc acc ggc gac tgg	ttc gcc agc gac gca gaa	931
Gln Ser Gly Phe	Leu Arg Thr Gly Asp Trp	Phe Ala Ser Asp Ala Glu	
	265	270	275
ggt gtg atc ccc	gac gtc atc acc acc gca	aaa ggc atc gcc ggc ggc	979
Gly Val Ile Pro	Asp Val Ile Thr Thr Ala	Lys Gly Ile Ala Gly Gly	
	280	285	290
atg cca cta tcc	gca gtg acc ggc cgc gca	gaa atc atg gac gca ccc	1027
Met Pro Leu Ser	Ala Val Thr Gly Arg Ala	Glu Ile Met Asp Ala Pro	
	295	300	305
ggc ccc ggc gcg	ctc ggc gga acc tac ggc	gga aac ccc gtt gct tgc	1075
Gly Pro Gly Ala	Leu Gly Gly Thr Tyr Gly	Gly Asn Pro Val Ala Cys	
	310	315	320
gcc gcg gca ctt	gca gcc att gaa gtg atg	gaa caa gcc gac ctt aag	1123
Ala Ala Ala Leu	Ala Ala Ile Glu Val Met	Glu Gln Ala Asp Leu Lys	
	330	335	340
acc cgc gcg			1132
Thr Arg Ala			

&lt;210&gt; 516

&lt;211&gt; 344

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 516

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Gln Val Pro Gly Pro Lys Ser Lys Ala Leu Asp Glu Arg Arg Gln Ala
20 25 30

Ala Val Ala Arg Ala Leu Ala Pro Gly Leu Pro Gly Tyr Val Val Asp
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35					40					45						
Ala	Asp	Gly	Gly	Ile	Leu	Ala	Asp	Ala	Asp	Gly	Asn	Arg	Phe	Ile	Asp	
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Leu	Ala	Ser	Gly	Ile	Ala	Val	Thr	Thr	Val	Gly	Gly	Ser	Asn	Ala	Ala	
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Val	Ala	Lys	Ala	Val	Gly	Ala	Ala	Ala	Ala	Arg	Phe	Thr	His	Thr	Cys	
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Phe	Met	Val	Ser	Pro	Tyr	Glu	Thr	Tyr	Val	Ala	Met	Ala	Glu	Arg	Leu	
100					105					110						
Asn	Ala	Leu	Thr	Pro	Gly	Asp	His	Asp	Lys	Lys	Ser	Ala	Leu	Phe	Asn	
115					120					125						
Ser	Gly	Ala	Glu	Ala	Val	Glu	Asn	Ala	Val	Lys	Val	Ala	Arg	Ala	Tyr	
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Thr	Gly	Lys	Gly	Ala	Val	Val	Val	Phe	Asp	Asn	Ala	Tyr	His	Gly	Arg	
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Thr	Asn	Leu	Thr	Met	Ala	Met	Thr	Ala	Lys	Asn	Arg	Pro	Tyr	Lys	Ser	
165					170					175						
Gly	Phe	Gly	Pro	Leu	Ala	Ala	Asp	Val	Tyr	Arg	Ala	Pro	Met	Ser	Tyr	
180					185					190						
Pro	Leu	Arg	Asp	Gly	Leu	Ser	Gly	Pro	Glu	Ala	Ala	Glu	Arg	Ala	Ile	
195					200					205						
Ser	Val	Ile	Glu	Ser	Gln	Val	Gly	Ala	Glu	Asn	Leu	Ala	Cys	Val	Val	
210					215					220						
Ile	Glu	Pro	Ile	Gln	Gly	Glu	Gly	Gly	Phe	Ile	Val	Pro	Ala	Pro	Gly	
225					230					235					240	
Phe	Leu	Ala	Ala	Ile	Ser	Thr	Trp	Cys	Arg	Glu	Asn	Asp	Val	Val	Phe	
245					250					255						
Ile	Ala	Asp	Glu	Ile	Gln	Ser	Gly	Phe	Leu	Arg	Thr	Gly	Asp	Trp	Phe	
260					265					270						
Ala	Ser	Asp	Ala	Glu	Gly	Val	Ile	Pro	Asp	Val	Ile	Thr	Thr	Ala	Lys	
275					280					285						
Gly	Ile	Ala	Gly	Gly	Met	Pro	Leu	Ser	Ala	Val	Thr	Gly	Arg	Ala	Glu	
290					295					300						
Ile	Met	Asp	Ala	Pro	Gly	Pro	Gly	Ala	Leu	Gly	Gly	Thr	Tyr	Gly	Gly	
305					310					315					320	
Asn	Pro	Val	Ala	Cys	Ala	Ala	Ala	Leu	Ala	Ala	Ile	Glu	Val	Met	Glu	
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Gln	Ala	Asp	Leu	Lys	Thr	Arg	Ala									
340																

&lt;210&gt; 517

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 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1468)  
 <223> RXN02970

<400> 517

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ttatttaaag acttcataat attttgggga gtgaactggg 115
                                     Leu Ala Leu Lys Gly
                                     1 5

tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
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aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
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cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
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gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp
                55                60                65

atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga 355
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg
                70                75                80                85

tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn
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ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val
                105                110                115

tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly
                120                125                130

gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly
                135                140                145

cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga 595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly
                150                155                160                165

tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc 643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr
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acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc 691

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Ser	Phe	Phe	Ala	Thr	Thr	Gln	Glu	Glu	Glu	Cys	Glu	Arg	Ala	Leu	Lys	
		200					205					210				
cac	ttg	gaa	gat	gtc	atc	gcg	ttt	gaa	ggg	gct	ggc	atg	atc	gca	gcg	787
His	Leu	Glu	Asp	Val	Ile	Ala	Phe	Glu	Gly	Ala	Gly	Met	Ile	Ala	Ala	
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Ile	Val	Leu	Glu	Pro	Val	Val	Gly	Ser	Ser	Gly	Ile	Ile	Leu	Pro	Pro	
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Ala	Gly	Tyr	Leu	Asn	Gly	Val	Arg	Glu	Leu	Cys	Asn	Lys	His	Gly	Ile	
				250					255					260		
ctc	ttc	atc	gcc	gac	gaa	gtc	atg	gtc	gga	ttc	gga	cgc	acc	gga	aaa	931
Leu	Phe	Ile	Ala	Asp	Glu	Val	Met	Val	Gly	Phe	Gly	Arg	Thr	Gly	Lys	
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Leu	Phe	Ala	Tyr	Glu	His	Ala	Gly	Asp	Asp	Phe	Gln	Pro	Asp	Met	Ile	
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Thr	Phe	Ala	Lys	Gly	Val	Asn	Ala	Gly	Tyr	Ala	Pro	Leu	Gly	Gly	Ile	
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Val	Met	Thr	Gln	Ser	Ile	Arg	Asp	Thr	Phe	Gly	Ser	Glu	Ala	Tyr	Ser	
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Gly	Gly	Leu	Thr	Tyr	Ser	Gly	His	Pro	Leu	Ala	Val	Ala	Pro	Ala	Lys	
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gca	gcg	ctg	gag	att	tac	gcg	gaa	gga	gag	atc	att	cca	cgc	gta	gct	1171
Ala	Ala	Leu	Glu	Ile	Tyr	Ala	Glu	Gly	Glu	Ile	Ile	Pro	Arg	Val	Ala	
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cga	ctt	ggc	gct	gaa	ctg	atc	gaa	cct	cgc	ctt	cgt	gaa	cta	gcg	gaa	1219
Arg	Leu	Gly	Ala	Glu	Leu	Ile	Glu	Pro	Arg	Leu	Arg	Glu	Leu	Ala	Glu	
		360					365					370				
gaa	aac	gta	gcg	atc	gct	gac	gtg	cgg	ggc	atc	gga	ttc	ttc	tgg	gca	1267
Glu	Asn	Val	Ala	Ile	Ala	Asp	Val	Arg	Gly	Ile	Gly	Phe	Phe	Trp	Ala	
	375					380					385					
gtg	gag	ttc	aat	gca	gac	gcc	act	gcc	atg	gct	gcc	ggg	gct	gca	gaa	1315
Val	Glu	Phe	Asn	Ala	Asp	Ala	Thr	Ala	Met	Ala	Ala	Gly	Ala	Ala	Glu	
390					395				400						405	
ttc	aag	gaa	cgc	ggc	gtg	tgg	ccg	atg	atc	tcc	ggc	aac	cga	ttc	cac	1363
Phe	Lys	Glu	Arg	Gly	Val	Trp	Pro	Met	Ile	Ser	Gly	Asn	Arg	Phe	His	
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atc	gcg	ccg	ccg	ctg	acc	acc	act	gat	gac	gaa	ttg	gta	gca	ctg	ctg	1411
Ile	Ala	Pro	Pro	Leu	Thr	Thr	Thr	Asp	Asp	Glu	Leu	Val	Ala	Leu	Leu	

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gac gcg gtg gaa gct gca gcc caa gct gtc gag ctg acc ttc gct ggg 1459  
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Ala Leu Phe  
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<210> 518

<211> 456

<212> PRT

<213> Corynebacterium glutamicum

<400> 518

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Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro  
35 40 45

Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly  
50 55 60

Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly  
65 70 75 80

His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg  
85 90 95

Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val  
100 105 110

Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe  
115 120 125

Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala  
130 135 140

Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr  
145 150 155 160

His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg  
165 170 175

Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro  
180 185 190

Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys  
195 200 205

Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala  
210 215 220

Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly  
225 230 235 240

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Leu Ala Leu Lys Gly  
1 5

tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca	163
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala	
10 15 20	
aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc	211
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe	
25 30 35	
cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct	259
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala	
40 45 50	
gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac	307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp	
55 60 65	
atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga	355
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg	
70 75 80 85	
tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac	403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn	
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ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg	451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val	
105 110 115	
tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc	499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly	
120 125 130	
gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga	547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly	
135 140 145	
cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga	595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly	
150 155 160 165	
tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc	643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr	
170 175 180	
acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc	691
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser	
185 190 195	
tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag	739
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys	
200 205 210	
cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg	787
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala	
215 220 225	
atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca	835
Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro	
230 235 240 245	
gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc	883

Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile  
 250 255 260

ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa 931  
 Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys  
 265 270 275

ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc 979  
 Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile  
 280 285 290

acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc 1027  
 Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile  
 295 300 305

gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc 1075  
 Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser  
 310 315 320 325

ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag 1123  
 Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys  
 330 335 340

gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct 1171  
 Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala  
 345 350 355

cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa 1219  
 Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu  
 360 365 370

gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca 1267  
 Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala  
 375 380 385

gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa 1315  
 Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu  
 390 395 400 405

ttc aag gaa cgc ggc 1330  
 Phe Lys Glu Arg Gly  
 410

&lt;210&gt; 520

&lt;211&gt; 410

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 520

Leu Ala Leu Lys Gly Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe  
 1 5 10 15

Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp  
 20 25 30

Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro  
 35 40 45

Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly  
 50 55 60



Asn	Ala	Phe	Ile	Asp	Met	Gly	Ser	Gln	Leu	Val	Ser	Ala	Asn	Leu	Gly	65	70	75	80
His	Asn	Asn	Pro	Arg	Leu	Val	Glu	Ala	Ile	Gln	Arg	Gln	Ala	Ala	Arg	85	90	95	
Leu	Thr	Asn	Ile	Asn	Pro	Ala	Phe	Gly	Asn	Asp	Val	Arg	Ser	Asp	Val	100	105	110	
Ala	Ala	Lys	Ile	Val	Ser	Met	Ala	Arg	Gly	Glu	Phe	Ser	His	Val	Phe	115	120	125	
Phe	Thr	Asn	Gly	Gly	Ala	Asp	Ala	Ile	Glu	His	Ser	Ile	Arg	Met	Ala	130	135	140	
Arg	Leu	His	Thr	Gly	Arg	Asn	Lys	Ile	Leu	Ser	Ala	Tyr	Arg	Ser	Tyr	145	150	155	160
His	Gly	Ala	Thr	Gly	Ser	Ala	Met	Met	Leu	Thr	Gly	Glu	His	Arg	Arg	165	170	175	
Leu	Gly	Asn	Pro	Thr	Thr	Asp	Pro	Asp	Ile	Tyr	His	Phe	Trp	Ala	Pro	180	185	190	
Phe	Leu	His	His	Ser	Ser	Phe	Phe	Ala	Thr	Thr	Gln	Glu	Glu	Glu	Cys	195	200	205	
Glu	Arg	Ala	Leu	Lys	His	Leu	Glu	Asp	Val	Ile	Ala	Phe	Glu	Gly	Ala	210	215	220	
Gly	Met	Ile	Ala	Ala	Ile	Val	Leu	Glu	Pro	Val	Val	Gly	Ser	Ser	Gly	225	230	235	240
Ile	Ile	Leu	Pro	Pro	Ala	Gly	Tyr	Leu	Asn	Gly	Val	Arg	Glu	Leu	Cys	245	250	255	
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Gly	Arg	Thr	Gly	Lys	Leu	Phe	Ala	Tyr	Glu	His	Ala	Gly	Asp	Asp	Phe	275	280	285	
Gln	Pro	Asp	Met	Ile	Thr	Phe	Ala	Lys	Gly	Val	Asn	Ala	Gly	Tyr	Ala	290	295	300	
Pro	Leu	Gly	Gly	Ile	Val	Met	Thr	Gln	Ser	Ile	Arg	Asp	Thr	Phe	Gly	305	310	315	320
Ser	Glu	Ala	Tyr	Ser	Gly	Gly	Leu	Thr	Tyr	Ser	Gly	His	Pro	Leu	Ala	325	330	335	
Val	Ala	Pro	Ala	Lys	Ala	Ala	Leu	Glu	Ile	Tyr	Ala	Glu	Gly	Glu	Ile	340	345	350	
Ile	Pro	Arg	Val	Ala	Arg	Leu	Gly	Ala	Glu	Leu	Ile	Glu	Pro	Arg	Leu	355	360	365	
Arg	Glu	Leu	Ala	Glu	Glu	Asn	Val	Ala	Ile	Ala	Asp	Val	Arg	Gly	Ile	370	375	380	

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<210> 521

<211> 1998

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1975)

<223> RXA01551

<400> 521

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 Leu Lys Ala Val Pro  
 1 5  
 acg ggc gcc cga gca cgg gct gag atc gcg ctg att gct gcg cga gca 163  
 Thr Gly Ala Arg Ala Arg Ala Glu Ile Ala Leu Ile Ala Ala Arg Ala  
 10 15 20  
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 Pro Phe Glu Pro Val Arg Leu Ala Pro Ala Lys Glu Glu Arg Asn Gly  
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 Ala Met Thr Pro Thr Gln Asn Glu Ile His Pro Lys His Ser Tyr Ser  
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 Pro Ile Arg Lys Asp Gly Leu Glu Val Pro Glu Thr Glu Ile Arg Leu  
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 gat gac tcg cca agc ggc ccc aac gaa ccc ttc cgc atc tac cgc acc 355  
 Asp Asp Ser Pro Ser Gly Pro Asn Glu Pro Phe Arg Ile Tyr Arg Thr  
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 Ser Trp Ile Thr Ala Arg Gly Asp Val Ala Thr Tyr Gln Gly Arg Glu  
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 Arg Leu Leu Ile Asp Asp Gly Arg Ser Ala Met Arg Arg Gly Gln Ala  
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 Ser Ala Glu Trp Lys Gly Gln Lys Pro Ala Pro Leu Lys Ala Leu Pro  
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Gly 150	Lys	Arg	Val	Thr	Gln 155	Met	Ala	Tyr	Ala	Arg 160	Ala	Gly	Val	Ile	Thr 165	
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Val	Arg	Ser	Glu 185	Val	Ala	Arg	Gly	Arg 190	Ala	Ile	Ile	Pro	Asn	Asn	Val 195	
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Asn	His	Pro	Glu 200	Ser	Glu	Pro	Met 205	Ile	Ile	Gly	Arg	Lys 210	Phe	Leu	Thr	
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Lys	Ile 215	Asn	Ala	Asn	Ile	Gly 220	Asn	Ser	Ala	Val 225	Thr	Ser	Ser	Ile	Glu	
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Glu	Glu	Val	Ser	Lys	Leu 235	Gln	Trp	Ala	Thr	Arg 240	Trp	Gly	Ala	Asp	Thr 245	
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Val	Met	Asp	Leu	Ser 250	Thr	Gly	Asp	Asp	Ile 255	His	Thr	Thr	Arg	Glu	Trp 260	
att	atc	cgc	aac	tcc	ccc	gtt	cct	atc	ggc	acc	gtc	ccg	atc	tac	caa	931
Ile	Ile	Arg	Asn 265	Ser	Pro	Val	Pro	Ile	Gly 270	Thr	Val	Pro	Ile	Tyr	Gln 275	
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Ala	Leu	Glu	Lys 280	Val	Asn	Gly	Val 285	Ala	Ala	Asp	Leu	Asn 290	Trp	Glu	Val	
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Phe	Arg	Asp	Thr	Ile	Ile	Glu 300	Gln	Cys	Glu	Gln	Gly 305	Val	Asp	Tyr	Met	
acc	atc	cac	gcc	ggc	gtc	ctg	ctg	gct	tat	atc	cca	ctg	act	acc	cgt	1075
Thr	Ile	His	Ala	Gly	Val 315	Leu	Leu	Ala	Tyr 320	Ile	Pro	Leu	Thr	Thr	Arg 325	
cgt	gtc	acc	ggc	att	gtc	tcc	cgc	ggc	gga	tcc	att	atg	gcc	ggc	tgg	1123
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390	395	400	405	
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Asp Val Gln Val Met Val Glu Gly Pro Gly His Val Pro Leu Asn Met				
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atc cag gaa aac aac gag ctg gaa caa aag tgg gca gcg gac gca cct				1411
Ile Gln Glu Asn Asn Glu Leu Glu Gln Lys Trp Ala Ala Asp Ala Pro				
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ttt tac act ctt gga cca cta gtt acc gac atc gct cca ggt tat gac				1459
Phe Tyr Thr Leu Gly Pro Leu Val Thr Asp Ile Ala Pro Gly Tyr Asp				
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455	460	465		
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Ala Met Leu Cys Tyr Val Thr Pro Lys Glu His Leu Gly Leu Pro Asn				
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cgt gac gac gtc aaa acc ggc gta atc acc tac aag ctc gct gcc cac				1603
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Ala Ala Asp Val Ala Lys Gly His Pro Gly Ala Arg Ala Trp Asp Asp				
505	510	515		
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Ala Met Ser Lys Ala Arg Phe Glu Phe Arg Trp Asn Asp Gln Phe Ala				
520	525	530		
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Lys Phe Cys Ser Met Arg Ile Ser Gln Asp Ile Arg Asp Met Phe Gly				
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Asp Gln Ile Ala Glu Leu Gly Met Pro Gly Val Gly Asp Ser Ser Ser				
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gct gtt gct tct agt ggg gca cgg gag ggg atg gct gag aaa tcc cgg				1939
Ala Val Ala Ser Ser Gly Ala Arg Glu Gly Met Ala Glu Lys Ser Arg				
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<400> 522

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1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

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Pro	Leu	Thr	Thr	Arg	Arg	Val	Thr	Gly	Ile	Val	Ser	Arg	Gly	Gly	Ser
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Ile	Met	Ala	Gly	Trp	Cys	Leu	Ala	His	His	Arg	Glu	Ser	Phe	Leu	Tyr
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Glu	His	Phe	Asp	Glu	Leu	Cys	Glu	Ile	Phe	Ala	Gln	Tyr	Asp	Val	Ala
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Phe	Ser	Leu	Gly	Asp	Gly	Leu	Arg	Pro	Gly	Ser	Leu	Ala	Asp	Ala	Asn
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Asp	Ala	Ala	Gln	Phe	Ala	Glu	Leu	Lys	Thr	Ile	Gly	Glu	Leu	Thr	Gln
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Arg	Ala	Trp	Glu	Tyr	Asp	Val	Gln	Val	Met	Val	Glu	Gly	Pro	Gly	His
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Val	Pro	Leu	Asn	Met	Ile	Gln	Glu	Asn	Asn	Glu	Leu	Glu	Gln	Lys	Trp
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Lys	Leu	Ala	Ala	His	Ala	Ala	Asp	Val	Ala	Lys	Gly	His	Pro	Gly	Ala
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Ser	Met	Cys	Gly	Pro	Lys	Phe	Cys	Ser	Met	Arg	Ile	Ser	Gln	Asp	Ile
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<223> RXA01019

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Thr Val Gly Asp Leu Gly Glu Phe Glu Val Ile Arg Val Ile Thr Glu  
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caa gct gga tca tct ctc aac ggc gat gac gca gct gtg ctt cgg cat 144  
Gln Ala Gly Ser Ser Leu Asn Gly Asp Asp Ala Ala Val Leu Arg His  
35 40 45  
gca tca ccc aat tcc agg gct gtt gtc acc acc gac atg ttg gtt gcg 192  
Ala Ser Pro Asn Ser Arg Ala Val Val Thr Thr Asp Met Leu Val Ala  
50 55 60  
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Gly Arg His Phe Gln Leu Asp Trp Ser Thr Pro Glu Gln Ile Gly Gln  
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cca gta gcc gca ttg ttg gcg att tcc gcc ccc aca cac acc ccc gtg 336  
Pro Val Ala Ala Leu Leu Ala Ile Ser Ala Pro Thr His Thr Pro Val  
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Tyr Ser Ala Glu Leu Val Gly Gly Asp Ile Thr Ser Gly Asp Ser Leu  
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Val Ile Ala Val Thr Ala Ile Gly Gln Leu Gly Gly Ser Leu Pro Glu  
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Leu Thr Leu Gly Arg Ala Arg Pro Gly Gln Thr Leu Val Ala His Gly  
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Lys Ile Gly Tyr Ser Ala Ala Gly Leu Ala Leu Leu Gln His Phe Gly  
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 Pro Asp Asn Val Pro Glu His Leu Arg Pro Leu Val Asp Ala His Cys  
 195 200 205  
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 305 310 315 320  
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&lt;211&gt; 330

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 524

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Gly Arg His Phe Gln Leu Asp Trp Ser Thr Pro Glu Gln Ile Gly Gln



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Pro Val Ala Ala Leu Leu Ala Ile Ser Ala Pro Thr His Thr Pro Val	100	105	110
Glu Phe Val Arg Gly Leu Ala Arg Gly Met Asn Gln Arg Leu Glu Glu	115	120	125
Tyr Ser Ala Glu Leu Val Gly Gly Asp Ile Thr Ser Gly Asp Ser Leu	130	135	140
Val Ile Ala Val Thr Ala Ile Gly Gln Leu Gly Gly Ser Leu Pro Glu	145	150	155
Leu Thr Leu Gly Arg Ala Arg Pro Gly Gln Thr Leu Val Ala His Gly	165	170	175
Lys Ile Gly Tyr Ser Ala Ala Gly Leu Ala Leu Leu Gln His Phe Gly	180	185	190
Pro Asp Asn Val Pro Glu His Leu Arg Pro Leu Val Asp Ala His Cys	195	200	205
Ala Pro Val Leu Thr Pro Gly Arg Gly Met Val Ala Arg Ala Ala Gly	210	215	220
Ala Thr Ala Met Thr Asp Asn Ser Asp Gly Leu Ile Val Asp Leu Asn	225	230	235
Gln Met Ala Met Lys Ser Gly Val Arg Ile Asp Val Asp Ser Cys Ser	245	250	255
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Asp Ala Trp Arg Trp Ile Leu Ser Gly Gly Glu Asp His Thr Leu Leu	275	280	285
Ser Thr Thr Phe Gly Asp Ala Pro Ser Gly Phe Arg Thr Ile Gly Gln	290	295	300
Val Thr Lys Thr Arg His Glu Asp Leu Val Thr Val Asp Lys Lys Thr	305	310	315
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&lt;211&gt; 706

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(706)

&lt;223&gt; RXA01352

&lt;400&gt; 525

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Phe Asp Leu Arg Cys Tyr Val Val Thr Gly Ala Gly Ser Val Asp Glu
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Val Val His Thr Ala Ser Ala Ala Ala Arg Gly Gly Ala Gly Val Val
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Gln Val Arg Ser Lys Pro Ile Ser Pro Glu Ala Met Arg Glu Leu Ala
                               40                               45                               50

tca aag gtt gcg ctt gag gtt gcg cgg tgc agc cca aca acg agg gtg 307
Ser Lys Val Ala Leu Glu Val Ala Arg Cys Ser Pro Thr Thr Arg Val
                               55                               60                               65

ctt atc gac gac cac ctc cac gtt gct tct tcc tta atg cgc gaa gga 355
Leu Ile Asp Asp His Leu His Val Ala Ser Ser Leu Met Arg Glu Gly
                               70                               75                               80                               85

ctc ccg att cac ggt gtg cat ctt ggg cag gat gat atg tcg gtg ctt 403
Leu Pro Ile His Gly Val His Leu Gly Gln Asp Asp Met Ser Val Leu
                               90                               95                               100

gag gct cgt gag ttg ttg ggg cct gag gcg atc att ggg ttg act act 451
Glu Ala Arg Glu Leu Leu Gly Pro Glu Ala Ile Ile Gly Leu Thr Thr
                               105                               110                               115

gga acc cta gaa ctt gtg gcg gcg gcg aat gag ctg tcc gat gtg ttg 499
Gly Thr Leu Glu Leu Val Ala Ala Ala Asn Glu Leu Ser Asp Val Leu
                               120                               125                               130

gat tac atc ggt gct ggg ccg ttt cgg aag act ccc acc aag gat tca 547
Asp Tyr Ile Gly Ala Gly Pro Phe Arg Lys Thr Pro Thr Lys Asp Ser
                               135                               140                               145

ggt cgg cca ccg att ggc ctt gcg ggt tat ccc cct ttg gtg gaa ttg 595
Gly Arg Pro Pro Ile Gly Leu Ala Gly Tyr Pro Pro Leu Val Glu Leu
                               150                               155                               160                               165

tcc aag gtg ccg atc gtt gcg att ggt gat gtc acc cct gcc gat gtg 643
Ser Lys Val Pro Ile Val Ala Ile Gly Asp Val Thr Pro Ala Asp Val
                               170                               175                               180

cgc gct ctc agc gca acc ggt gtg gct ggc gtt gcc atg gtg cgg gct 691
Arg Ala Leu Ser Ala Thr Gly Val Ala Gly Val Ala Met Val Arg Ala
                               185                               190                               195

ttt tct gaa tct gat 706
Phe Ser Glu Ser Asp
                               200

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&lt;210&gt; 526

&lt;211&gt; 202

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 526

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Val Phe Glu Asn Arg Phe Asp Leu Arg Cys Tyr Val Val Thr Gly Ala
  1              5              10              15
Gly Ser Val Asp Glu Val Val His Thr Ala Ser Ala Ala Ala Arg Gly
              20              25              30
Gly Ala Gly Val Val Gln Val Arg Ser Lys Pro Ile Ser Pro Glu Ala
              35              40              45
Met Arg Glu Leu Ala Ser Lys Val Ala Leu Glu Val Ala Arg Cys Ser
              50              55              60
Pro Thr Thr Arg Val Leu Ile Asp Asp His Leu His Val Ala Ser Ser
              65              70              75              80
Leu Met Arg Glu Gly Leu Pro Ile His Gly Val His Leu Gly Gln Asp
              85              90              95
Asp Met Ser Val Leu Glu Ala Arg Glu Leu Leu Gly Pro Glu Ala Ile
              100              105              110
Ile Gly Leu Thr Thr Gly Thr Leu Glu Leu Val Ala Ala Ala Asn Glu
              115              120              125
Leu Ser Asp Val Leu Asp Tyr Ile Gly Ala Gly Pro Phe Arg Lys Thr
              130              135              140
Pro Thr Lys Asp Ser Gly Arg Pro Pro Ile Gly Leu Ala Gly Tyr Pro
              145              150              155              160
Pro Leu Val Glu Leu Ser Lys Val Pro Ile Val Ala Ile Gly Asp Val
              165              170              175
Thr Pro Ala Asp Val Arg Ala Leu Ser Ala Thr Gly Val Ala Gly Val
              180              185              190
Ala Met Val Arg Ala Phe Ser Glu Ser Asp
              195              200

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&lt;210&gt; 527

&lt;211&gt; 944

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(921)

&lt;223&gt; RXA01381

&lt;400&gt; 527

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tcc gca ggc gtt gga acc atc acg gtc atc gat gac gac acc gtc gac      48
Ser Ala Gly Val Gly Thr Ile Thr Val Ile Asp Asp Asp Thr Val Asp
  1              5              10              15
att tcc aac att cac cgc caa atc ctc ttc ggc gca agc gat gtc ggt      96

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Ile	Ser	Asn	Ile	His	Arg	Gln	Ile	Leu	Phe	Gly	Ala	Ser	Asp	Val	Gly	
			20					25					30			
cga	ccc	aag	gtc	gag	gtt	gcc	gcc	gag	cgc	ctc	aaa	gaa	ctc	caa	cca	144
Arg	Pro	Lys	Val	Glu	Val	Ala	Ala	Glu	Arg	Leu	Lys	Glu	Leu	Gln	Pro	
		35				40					45					
gac	atc	acc	gtc	aac	gcg	ttg	cac	gaa	cgg	atc	act	cca	gaa	aac	gcc	192
Asp	Ile	Thr	Val	Asn	Ala	Leu	His	Glu	Arg	Ile	Thr	Pro	Glu	Asn	Ala	
	50					55					60					
tgc	gag	ctg	ctc	aat	tcc	gtg	gac	ctc	gtc	tta	gac	ggc	tcc	gat	tct	240
Cys	Glu	Leu	Leu	Asn	Ser	Val	Asp	Leu	Val	Leu	Asp	Gly	Ser	Asp	Ser	
	65				70					75					80	
ttc	tcc	aca	aaa	tac	tta	gtg	tct	gat	gcc	gcc	gaa	atc	acc	gga	act	288
Phe	Ser	Thr	Lys	Tyr	Leu	Val	Ser	Asp	Ala	Ala	Glu	Ile	Thr	Gly	Thr	
				85					90					95		
ccc	ctc	atc	tgg	gca	acg	gta	ctg	cgc	ttt	cac	ggc	gaa	ctg	gca	ctc	336
Pro	Leu	Ile	Trp	Ala	Thr	Val	Leu	Arg	Phe	His	Gly	Glu	Leu	Ala	Leu	
			100					105					110			
ttc	aac	tct	ggc	ccc	gac	cac	cgc	gga	gtc	ggc	ctg	cgc	gac	gtc	ttc	384
Phe	Asn	Ser	Gly	Pro	Asp	His	Arg	Gly	Val	Gly	Leu	Arg	Asp	Val	Phe	
		115					120				125					
ccc	gaa	caa	ccc	tcc	gcc	gat	ttc	gtc	cct	gac	tgc	gcc	acc	gct	ggt	432
Pro	Glu	Gln	Pro	Ser	Ala	Asp	Phe	Val	Pro	Asp	Cys	Ala	Thr	Ala	Gly	
	130					135					140					
gtt	ctt	ggc	gcc	acc	aca	gcc	acc	atc	ggc	gca	ctc	atg	gcc	act	cac	480
Val	Leu	Gly	Ala	Thr	Thr	Ala	Thr	Ile	Gly	Ala	Leu	Met	Ala	Thr	His	
	145				150					155					160	
gcc	atc	gga	ttt	ctc	aca	gaa	atc	ggc	gac	gtc	caa	cca	ggc	aca	atc	528
Ala	Ile	Gly	Phe	Leu	Thr	Glu	Ile	Gly	Asp	Val	Gln	Pro	Gly	Thr	Ile	
				165					170					175		
ctc	tcc	tac	gac	gca	ttc	ccc	gcc	gcc	acg	cgc	agc	ttc	cgc	gtc	tcc	576
Leu	Ser	Tyr	Asp	Ala	Phe	Pro	Ala	Ala	Thr	Arg	Ser	Phe	Arg	Val	Ser	
			180					185						190		
gcc	gac	cgc	gcg	cgc	cca	ctg	gtc	acc	cgc	ctc	cgc	gcc	tcc	tac	gag	624
Ala	Asp	Pro	Ala	Arg	Pro	Leu	Val	Thr	Arg	Leu	Arg	Ala	Ser	Tyr	Glu	
		195				200						205				
gca	gcg	cgc	acc	gat	aca	act	tcg	ctt	atc	gac	gcc	acc	ctc	aac	ggc	672
Ala	Ala	Arg	Thr	Asp	Thr	Thr	Ser	Leu	Ile	Asp	Ala	Thr	Leu	Asn	Gly	
	210					215					220					
tcc	ctc	acc	gcc	ctc	gat	atc	cga	gag	cca	cat	gaa	gtt	ctg	ctc	aaa	720
Ser	Leu	Thr	Ala	Leu	Asp	Ile	Arg	Glu	Pro	His	Glu	Val	Leu	Leu	Lys	
	225				230					235					240	
gac	ctc	ccc	gag	ggc	gca	acg	tca	ctg	aag	ctc	ccc	tta	agc	cag	atc	768
Asp	Leu	Pro	Glu	Gly	Ala	Thr	Ser	Leu	Lys	Leu	Pro	Leu	Ser	Gln	Ile	
				245					250					255		
acc	tcg	gac	agc	gac	att	tta	gag	gca	ctg	tct	gga	atc	gac	ggc	gac	816
Thr	Ser	Asp	Ser	Asp	Ile	Leu	Glu	Ala	Leu	Ser	Gly	Ile	Asp	Gly	Asp	

260										265										270										
att	ttg	gtc	tac	tgc	gct	tcg	gga	atc	cgc	agt	tcc	gac	ttc	atc	gac		864													
Ile	Leu	Val	Tyr	Cys	Ala	Ser	Gly	Ile	Arg	Ser	Ser	Asp	Phe	Ile	Asp															
275					280					285																				
aac	tac	tcc	cac	ctc	ggc	cac	aaa	ttt	gtg	aat	ctt	ccc	ggg	ggg	gtc		912													
Asn	Tyr	Ser	His	Leu	Gly	His	Lys	Phe	Val	Asn	Leu	Pro	Gly	Gly	Val															
290					295					300																				
aac	gcg	ctg	tagctgtcaa	tttaagaggc	cag												944													
Asn	Ala	Leu																												
305																														

&lt;210&gt; 528

&lt;211&gt; 307

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 528

Ser	Ala	Gly	Val	Gly	Thr	Ile	Thr	Val	Ile	Asp	Asp	Asp	Thr	Val	Asp
1				5					10					15	

Ile	Ser	Asn	Ile	His	Arg	Gln	Ile	Leu	Phe	Gly	Ala	Ser	Asp	Val	Gly
		20						25					30		

Arg	Pro	Lys	Val	Glu	Val	Ala	Ala	Glu	Arg	Leu	Lys	Glu	Leu	Gln	Pro
		35					40					45			

Asp	Ile	Thr	Val	Asn	Ala	Leu	His	Glu	Arg	Ile	Thr	Pro	Glu	Asn	Ala
	50					55					60				

Cys	Glu	Leu	Leu	Asn	Ser	Val	Asp	Leu	Val	Leu	Asp	Gly	Ser	Asp	Ser
65					70					75					80

Phe	Ser	Thr	Lys	Tyr	Leu	Val	Ser	Asp	Ala	Ala	Glu	Ile	Thr	Gly	Thr
			85						90					95	

Pro	Leu	Ile	Trp	Ala	Thr	Val	Leu	Arg	Phe	His	Gly	Glu	Leu	Ala	Leu
		100						105					110		

Phe	Asn	Ser	Gly	Pro	Asp	His	Arg	Gly	Val	Gly	Leu	Arg	Asp	Val	Phe
	115						120					125			

Pro	Glu	Gln	Pro	Ser	Ala	Asp	Phe	Val	Pro	Asp	Cys	Ala	Thr	Ala	Gly
	130					135					140				

Val	Leu	Gly	Ala	Thr	Thr	Ala	Thr	Ile	Gly	Ala	Leu	Met	Ala	Thr	His
145					150					155					160

Ala	Ile	Gly	Phe	Leu	Thr	Glu	Ile	Gly	Asp	Val	Gln	Pro	Gly	Thr	Ile
			165						170					175	

Leu	Ser	Tyr	Asp	Ala	Phe	Pro	Ala	Ala	Thr	Arg	Ser	Phe	Arg	Val	Ser
		180						185					190		

Ala	Asp	Pro	Ala	Arg	Pro	Leu	Val	Thr	Arg	Leu	Arg	Ala	Ser	Tyr	Glu
		195					200						205		

Ala	Ala	Arg	Thr	Asp	Thr	Thr	Ser	Leu	Ile	Asp	Ala	Thr	Leu	Asn	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Thr Gly Gly Ala Thr Ser Gln Ala Leu Leu Glu Glu Ser Leu Val Ala

	20		25		30	
Ser Gly Thr Gln Leu Thr Thr Val Ala Met Arg Arg His Gln Ala Thr						
	35		40		45	
Thr Ser Ser Gly Glu						
	50					
<210> 531						
<211> 629						
<212> DNA						
<213> Corynebacterium glutamicum						
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<222> (1)..(606)						
<223> RXA01361						
<400> 531						
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Ala Asp Ala Val Ile Ser Ile Asp Gly His Asp Pro Cys Leu Thr Val						
1		5		10		15
acg atg aat tcg ggg gtg agg gtt gcg tcg aaa agc gtt gtt gtt ttg						96
Thr Met Asn Ser Gly Val Arg Val Ala Ser Lys Ser Val Val Val Leu						
	20		25		30	
gcg gcg ggc ctg ggc gcc gca agc att ccc ggc tgg ttt gag ggc gcg						144
Ala Ala Gly Leu Gly Ala Ala Ser Ile Pro Gly Trp Phe Glu Gly Ala						
	35		40		45	
aac cca ttg cag ttg agg ccg gtg tac ggc gat att gtg cgc gtg cgc						192
Asn Pro Leu Gln Leu Arg Pro Val Tyr Gly Asp Ile Val Arg Val Arg						
	50		55		60	
gtg ccg gag cga ctg cag ccg atg gtc acc aag gtg gtg cgc ggg ttt						240
Val Pro Glu Arg Leu Gln Pro Met Val Thr Lys Val Val Arg Gly Phe						
65		70		75		80
gtg gaa gat cgt cag att tat atc att ccg cgt acc gat ggc acc ctc						288
Val Glu Asp Arg Gln Ile Tyr Ile Ile Pro Arg Thr Asp Gly Thr Leu						
	85		90		95	
gcg atc ggc gcg aca agc cgt gag gat cac ccg caa cct cga acg ggc						336
Ala Ile Gly Ala Thr Ser Arg Glu Asp His Pro Gln Pro Arg Thr Gly						
	100		105		110	
gca gtg cat gat ttg cta cgc gat gct atc cgt ttg att ccg ggc att						384
Ala Val His Asp Leu Leu Arg Asp Ala Ile Arg Leu Ile Pro Gly Ile						
	115		120		125	
gaa gaa acc gaa ttt atc gaa gtc acc tgc ggc gcc cgc ccc ggc acc						432
Glu Glu Thr Glu Phe Ile Glu Val Thr Cys Gly Ala Arg Pro Gly Thr						
	130		135		140	
ccg gat gac ctg ccg tac ctg gga tgg gtt gga tcc aat gtg att gcg						480
Pro Asp Asp Leu Pro Tyr Leu Gly Trp Val Gly Ser Asn Val Ile Ala						
145		150		155		160
tcc aca gga tat ttc cgc cat gga att ttg ctg tca gcc ctt ggt gca						528

Ser Thr Gly Tyr Phe Arg His Gly Ile Leu Leu Ser Ala Leu Gly Ala  
 165 170 175

cgc gct gcc gtt gat atg gca acc aac cag cca ctg ttc ccc act ctt 576  
 Arg Ala Ala Val Asp Met Ala Thr Asn Gln Pro Leu Phe Pro Thr Leu  
 180 185 190

gat gtg tgc gat ccg ttt cgc cac caa att taaggatttt tcacaagtga 626  
 Asp Val Cys Asp Pro Phe Arg His Gln Ile  
 195 200

tta 629

&lt;210&gt; 532

&lt;211&gt; 202

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 532

Ala Asp Ala Val Ile Ser Ile Asp Gly His Asp Pro Cys Leu Thr Val  
 1 5 10 15

Thr Met Asn Ser Gly Val Arg Val Ala Ser Lys Ser Val Val Val Leu  
 20 25 30

Ala Ala Gly Leu Gly Ala Ala Ser Ile Pro Gly Trp Phe Glu Gly Ala  
 35 40 45

Asn Pro Leu Gln Leu Arg Pro Val Tyr Gly Asp Ile Val Arg Val Arg  
 50 55 60

Val Pro Glu Arg Leu Gln Pro Met Val Thr Lys Val Val Arg Gly Phe  
 65 70 75 80

Val Glu Asp Arg Gln Ile Tyr Ile Ile Pro Arg Thr Asp Gly Thr Leu  
 85 90 95

Ala Ile Gly Ala Thr Ser Arg Glu Asp His Pro Gln Pro Arg Thr Gly  
 100 105 110

Ala Val His Asp Leu Leu Arg Asp Ala Ile Arg Leu Ile Pro Gly Ile  
 115 120 125

Glu Glu Thr Glu Phe Ile Glu Val Thr Cys Gly Ala Arg Pro Gly Thr  
 130 135 140

Pro Asp Asp Leu Pro Tyr Leu Gly Trp Val Gly Ser Asn Val Ile Ala  
 145 150 155 160

Ser Thr Gly Tyr Phe Arg His Gly Ile Leu Leu Ser Ala Leu Gly Ala  
 165 170 175

Arg Ala Ala Val Asp Met Ala Thr Asn Gln Pro Leu Phe Pro Thr Leu  
 180 185 190

Asp Val Cys Asp Pro Phe Arg His Gln Ile  
 195 200

&lt;210&gt; 533



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<220>  
<221> CDS  
<222> (101) .. (904)  
<223> RXA01208
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aacctgctct	agctcgctact	agcgaaggga	tggccttaac	gtg Val	gct Ala	aac Asn	tcg Ser	ttt Phe	115							
				1				5								
ttg	gat	tct	tta	act	ctt	gtt	cga	caa	aac	act	ccc	ctt	gtt	cag	tgt	163
Leu	Asp	Ser	Leu	Thr	Leu	Val	Arg	Gln	Asn	Thr	Pro	Leu	Val	Gln	Cys	
				10					15					20		
ttg	acc	aac	tct	gtg	gtc	atg	caa	ttc	acg	gcc	aat	gtg	ttg	ctt	gcc	211
Leu	Thr	Asn	Ser	Val	Val	Met	Gln	Phe	Thr	Ala	Asn	Val	Leu	Leu	Ala	
				25				30					35			
gcg	ggt	gcg	acc	cct	gcg	atg	gtg	gat	act	cca	gct	gaa	tcg	gca	gaa	259
Ala	Gly	Ala	Thr	Pro	Ala	Met	Val	Asp	Thr	Pro	Ala	Glu	Ser	Ala	Glu	
			40				45					50				
ttc	gcc	gct	gtg	gcc	aat	gga	gtg	ctc	atc	aat	gcg	gga	act	cct	tct	307
Phe	Ala	Ala	Val	Ala	Asn	Gly	Val	Leu	Ile	Asn	Ala	Gly	Thr	Pro	Ser	
			55			60					65					
gcg	gag	caa	tac	caa	ggc	atg	acc	aag	gcc	att	gag	ggt	gca	cga	aaa	355
Ala	Glu	Gln	Tyr	Gln	Gly	Met	Thr	Lys	Ala	Ile	Glu	Gly	Ala	Arg	Lys	
	70				75				80						85	
gct	ggc	aca	cca	tgg	gtg	tta	gac	cca	gtt	gct	gtg	ggt	ggg	ttg	tcg	403
Ala	Gly	Thr	Pro	Trp	Val	Leu	Asp	Pro	Val	Ala	Val	Gly	Gly	Leu	Ser	
				90				95						100		
gag	agg	acc	aag	tat	gcg	gag	gga	atc	gtc	gat	aag	cag	cct	gcc	gca	451
Glu	Arg	Thr	Lys	Tyr	Ala	Glu	Gly	Ile	Val	Asp	Lys	Gln	Pro	Ala	Ala	
			105					110					115			
att	cgt	gga	aac	gcc	tca	gag	gtc	gtg	gcg	ctt	gcg	ggg	ctc	ggt	gcc	499
Ile	Arg	Gly	Asn	Ala	Ser	Glu	Val	Val	Ala	Leu	Ala	Gly	Leu	Gly	Ala	
			120				125					130				
ggt	ggg	cgc	ggc	gta	gac	gcg	acc	gat	tcc	gtg	gaa	gtg	gcg	ttg	gag	547
Gly	Gly	Arg	Gly	Val	Asp	Ala	Thr	Asp	Ser	Val	Glu	Val	Ala	Leu	Glu	
			135			140					145					
gcg	gcg	caa	ttg	ttg	gcc	aag	cgc	act	ggt	ggc	gtc	gtg	gct	gtc	tct	595
Ala	Ala	Gln	Leu	Leu	Ala	Lys	Arg	Thr	Gly	Gly	Val	Val	Ala	Val	Ser	
	150				155				160						165	
ggt	gcg	gag	gac	ttg	att	gtg	tct	gcg	gat	cgg	gtg	acg	tgg	ttg	cgt	643
Gly	Ala	Glu	Asp	Leu	Ile	Val	Ser	Ala	Asp	Arg	Val	Thr	Trp	Leu	Arg	
				170				175						180		
tcg	ggg	gat	ccg	atg	ttg	cag	ctg	gtg	att	ggc	act	gga	tgc	tct	ttg	691

Ser Gly Asp Pro Met Leu Gln Leu Val Ile Gly Thr Gly Cys Ser Leu  
 185 190 195

ggc gcg ctg aca gct gca tat cta ggc gcc acg gtt gac tca gat att 739  
 Gly Ala Leu Thr Ala Ala Tyr Leu Gly Ala Thr Val Asp Ser Asp Ile  
 200 205 210

tcc gcg cac gat gct gtg ttg gct gcg cat gcc cat gtg ggt gct gct 787  
 Ser Ala His Asp Ala Val Leu Ala Ala His Ala Val Gly Ala Ala  
 215 220 225

ggc cag att gca gca cag aag gca tcg gcg cca ggc agc ttt gcg gtg 835  
 Gly Gln Ile Ala Ala Gln Lys Ala Ser Ala Pro Gly Ser Phe Ala Val  
 230 235 240 245

gcg ttt att gat gcg ctt tat gac gtg gat gcc cag gct gtg gcc tcg 883  
 Ala Phe Ile Asp Ala Leu Tyr Asp Val Asp Ala Gln Ala Val Ala Ser  
 250 255 260

ttg gtt gat gtg cga gag gcc tgaaaagtac gtgactgatt ttt 927  
 Leu Val Asp Val Arg Glu Ala  
 265

<210> 534  
 <211> 268  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 534  
 Val Ala Asn Ser Phe Leu Asp Ser Leu Thr Leu Val Arg Gln Asn Thr  
 1 5 10 15

Pro Leu Val Gln Cys Leu Thr Asn Ser Val Val Met Gln Phe Thr Ala  
 20 25 30

Asn Val Leu Leu Ala Ala Gly Ala Thr Pro Ala Met Val Asp Thr Pro  
 35 40 45

Ala Glu Ser Ala Glu Phe Ala Ala Val Ala Asn Gly Val Leu Ile Asn  
 50 55 60

Ala Gly Thr Pro Ser Ala Glu Gln Tyr Gln Gly Met Thr Lys Ala Ile  
 65 70 75 80

Glu Gly Ala Arg Lys Ala Gly Thr Pro Trp Val Leu Asp Pro Val Ala  
 85 90 95

Val Gly Gly Leu Ser Glu Arg Thr Lys Tyr Ala Glu Gly Ile Val Asp  
 100 105 110

Lys Gln Pro Ala Ala Ile Arg Gly Asn Ala Ser Glu Val Val Ala Leu  
 115 120 125

Ala Gly Leu Gly Ala Gly Gly Arg Gly Val Asp Ala Thr Asp Ser Val  
 130 135 140

Glu Val Ala Leu Glu Ala Ala Gln Leu Leu Ala Lys Arg Thr Gly Gly  
 145 150 155 160

Val Val Ala Val Ser Gly Ala Glu Asp Leu Ile Val Ser Ala Asp Arg

165					170					175					
Val	Thr	Trp	Leu	Arg	Ser	Gly	Asp	Pro	Met	Leu	Gln	Leu	Val	Ile	Gly
			180					185					190		
Thr	Gly	Cys	Ser	Leu	Gly	Ala	Leu	Thr	Ala	Ala	Tyr	Leu	Gly	Ala	Thr
		195					200					205			
Val	Asp	Ser	Asp	Ile	Ser	Ala	His	Asp	Ala	Val	Leu	Ala	Ala	His	Ala
	210					215					220				
His	Val	Gly	Ala	Ala	Gly	Gln	Ile	Ala	Ala	Gln	Lys	Ala	Ser	Ala	Pro
225					230					235					240
Gly	Ser	Phe	Ala	Val	Ala	Phe	Ile	Asp	Ala	Leu	Tyr	Asp	Val	Asp	Ala
			245					250					255		
Gln	Ala	Val	Ala	Ser	Leu	Val	Asp	Val	Arg	Glu	Ala				
			260					265							

&lt;210&gt; 535

&lt;211&gt; 1023

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1000)

&lt;223&gt; RXA00838

&lt;400&gt; 535

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				Met	Lys	Ile	Ala	Ile	
				1				5	

gtt	ggc	gct	ggt	gca	gtt	ggt	gga	tat	ttc	gga	gcg	ttg	tta	caa	gaa	163
Val	Gly	Ala	Gly	Ala	Val	Gly	Gly	Tyr	Phe	Gly	Ala	Leu	Leu	Gln	Glu	
			10					15						20		

tct	ggt	gca	gat	atc	acg	atg	gtt	gca	cgt	gga	cga	aca	tta	gaa	gcc	211
Ser	Gly	Ala	Asp	Ile	Thr	Met	Val	Ala	Arg	Gly	Arg	Thr	Leu	Glu	Ala	
			25					30					35			

ttg	aag	tct	aaa	gga	ctc	cac	atc	aac	gat	gca	aga	ggc	gaa	cgc	tac	259
Leu	Lys	Ser	Lys	Gly	Leu	His	Ile	Asn	Asp	Ala	Arg	Gly	Glu	Arg	Tyr	
		40					45					50				

gta	cca	att	cct	gca	gtt	gcg	agc	gtg	caa	gaa	cta	aaa	gat	gca	gat	307
Val	Pro	Ile	Pro	Ala	Val	Ala	Ser	Val	Gln	Glu	Leu	Lys	Asp	Ala	Asp	
		55				60					65					

gta	gtg	atg	att	gct	act	aaa	gca	tta	tcg	cgg	tct	tta	gat	ctc	gct	355
Val	Val	Met	Ile	Ala	Thr	Lys	Ala	Leu	Ser	Arg	Ser	Leu	Asp	Leu	Ala	
	70				75				80						85	

gaa	ctt	ttg	ggt	ggg	ata	cct	gcg	aat	tcg	gtg	gtc	gcg	att	act	cag	403
Glu	Leu	Leu	Gly	Gly	Ile	Pro	Ala	Asn	Ser	Val	Val	Ala	Ile	Thr	Gln	
			90					95						100		

aat tcg att gaa tct gct gat cta gca gcg aag agt atc ggt gct gat 451  
Asn Ser Ile Glu Ser Ala Asp Leu Ala Ala Lys Ser Ile Gly Ala Asp  
105 110 115  
  
cgt gtg tgg cct ggt gtg gtt cgt ggg ttc ttt gtt cat gag ggg cca 499  
Arg Val Trp Pro Gly Val Val Arg Gly Phe Phe Val His Glu Gly Pro  
120 125 130  
  
gcc tca gtg tca tac aag gga ggc cca ctg tcc tac acg ttt ggt gat 547  
Ala Ser Val Ser Tyr Lys Gly Gly Pro Leu Ser Tyr Thr Phe Gly Asp  
135 140 145  
  
tct ggt gaa ctt tct agg caa ttc gca agc act ctt gaa cag gcc ggt 595  
Ser Gly Glu Leu Ser Arg Gln Phe Ala Ser Thr Leu Glu Gln Ala Gly  
150 155 160 165  
  
att gac gga gtt ctg cat ccc gat att ttg gtg gat gtg tgg gag aaa 643  
Ile Asp Gly Val Leu His Pro Asp Ile Leu Val Asp Val Trp Glu Lys  
170 175 180  
  
gcc atg ttc gta gag gtt ttc ggc ggg ttg ggg gct ttc gtc gaa aag 691  
Ala Met Phe Val Glu Val Phe Gly Gly Leu Gly Ala Phe Val Glu Lys  
185 190 195  
  
caa tta ggt acc ttg cgt acg cat ttt agg gct tcc ctg gaa gcc ttg 739  
Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala Ser Leu Glu Ala Leu  
200 205 210  
  
atg gaa gag gtg gct gag gtg gct cgc gcg gca ggt gtt gcg ttg ccg 787  
Met Glu Glu Val Ala Glu Val Ala Arg Ala Ala Gly Val Ala Leu Pro  
215 220 225  
  
agc gat gcg gtg gag cgc acc atg aat ttt gcg gat cgg atg cct gag 835  
Ser Asp Ala Val Glu Arg Thr Met Asn Phe Ala Asp Arg Met Pro Glu  
230 235 240 245  
  
aat tcg acg agt tcg atg cag cgt gat ttg gcc gcg gga gtg gct agt 883  
Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala Ala Gly Val Ala Ser  
250 255 260  
  
gag ctt gag gct cag aca ggt gca att gtg cgg gca gcg cac aaa gtg 931  
Glu Leu Glu Ala Gln Thr Gly Ala Ile Val Arg Ala Ala His Lys Val  
265 270 275  
  
ggt gtg aaa act ccg ctt cat gac ctt att tat gct ggt ctt aag ctg 979  
Gly Val Lys Thr Pro Leu His Asp Leu Ile Tyr Ala Gly Leu Lys Leu  
280 285 290  
  
aaa gaa gag gaa aat tca ctt tagggataga atcaagatcc atg 1023  
Lys Glu Glu Glu Asn Ser Leu  
295 300

&lt;210&gt; 536

&lt;211&gt; 300

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 536

Met Lys Ile Ala Ile Val Gly Ala Gly Ala Val Gly Gly Tyr Phe Gly

1	5	10	15
Ala Leu Leu Gln Glu Ser Gly Ala Asp Ile Thr Met Val Ala Arg Gly	20	25	30
Arg Thr Leu Glu Ala Leu Lys Ser Lys Gly Leu His Ile Asn Asp Ala	35	40	45
Arg Gly Glu Arg Tyr Val Pro Ile Pro Ala Val Ala Ser Val Gln Glu	50	55	60
Leu Lys Asp Ala Asp Val Val Met Ile Ala Thr Lys Ala Leu Ser Arg	65	70	75
Ser Leu Asp Leu Ala Glu Leu Leu Gly Gly Ile Pro Ala Asn Ser Val	85	90	95
Val Ala Ile Thr Gln Asn Ser Ile Glu Ser Ala Asp Leu Ala Ala Lys	100	105	110
Ser Ile Gly Ala Asp Arg Val Trp Pro Gly Val Val Arg Gly Phe Phe	115	120	125
Val His Glu Gly Pro Ala Ser Val Ser Tyr Lys Gly Gly Pro Leu Ser	130	135	140
Tyr Thr Phe Gly Asp Ser Gly Glu Leu Ser Arg Gln Phe Ala Ser Thr	145	150	155
Leu Glu Gln Ala Gly Ile Asp Gly Val Leu His Pro Asp Ile Leu Val	165	170	175
Asp Val Trp Glu Lys Ala Met Phe Val Glu Val Phe Gly Gly Leu Gly	180	185	190
Ala Phe Val Glu Lys Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala	195	200	205
Ser Leu Glu Ala Leu Met Glu Glu Val Ala Glu Val Ala Arg Ala Ala	210	215	220
Gly Val Ala Leu Pro Ser Asp Ala Val Glu Arg Thr Met Asn Phe Ala	225	230	235
Asp Arg Met Pro Glu Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala	245	250	255
Ala Gly Val Ala Ser Glu Leu Glu Ala Gln Thr Gly Ala Ile Val Arg	260	265	270
Ala Ala His Lys Val Gly Val Lys Thr Pro Leu His Asp Leu Ile Tyr	275	280	285
Ala Gly Leu Lys Leu Lys Glu Glu Glu Asn Ser Leu	290	295	300

&lt;210&gt; 537

&lt;211&gt; 693

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(670)

&lt;223&gt; RXA02400

&lt;400&gt; 537

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aggtgcccc aacgttgctt gttgactgca aattttccga aagaatccat aaactacttc 60

tttaagtcgc cagattaaag tcgtcaatga aaggacatac atg tct att tcc cgc 115
Met Ser Ile Ser Arg
1 5

acc gtc ttc ggc atc gca gcc acc gca gcc ctg tct gca gct ctc gtt 163
Thr Val Phe Gly Ile Ala Ala Thr Ala Ala Leu Ser Ala Ala Leu Val
10 15 20

gcg tgt tct cca cct cac cag cag gat tcc cca gtc cag cgc acc aat 211
Ala Cys Ser Pro Pro His Gln Gln Asp Ser Pro Val Gln Arg Thr Asn
25 30 35

gag atc ttg act act tct cag aac cca act tct gcg agc agc acc tca 259
Glu Ile Leu Thr Thr Ser Gln Asn Pro Thr Ser Ala Ser Ser Thr Ser
40 45 50

acc tct tcc gca acg act act tcc tca gct cct gtg gaa gag gac gta 307
Thr Ser Ser Ala Thr Thr Ser Ser Ala Pro Val Glu Glu Asp Val
55 60 65

gag atc gtt gtt tca cca gca gcg ttg gtg gac ggt gag cag gtt acc 355
Glu Ile Val Val Ser Pro Ala Ala Leu Val Asp Gly Glu Gln Val Thr
70 75 80 85

ttc gaa atc tct gga ctt gat cca gag ggc ggc tac tac gca gcg atc 403
Phe Glu Ile Ser Gly Leu Asp Pro Glu Gly Gly Tyr Tyr Ala Ala Ile
90 95 100

tgc gat tcc gta gcg aac cct ggt aac cca gtt cct tct tgc acc ggc 451
Cys Asp Ser Val Ala Asn Pro Gly Asn Pro Val Pro Ser Cys Thr Gly
105 110 115

gaa atg gct gat ttc acg tcc cag gca tgg ttg agc aac tcc cag ccc 499
Glu Met Ala Asp Phe Thr Ser Gln Ala Trp Leu Ser Asn Ser Gln Pro
120 125 130

ggc gcg act gta gag atc gca gaa gac ggc acc gca act gtg gag ctt 547
Gly Ala Thr Val Glu Ile Ala Glu Asp Gly Thr Ala Thr Val Glu Leu
135 140 145

gaa gct acc gca acc ggc act ggc ttg gac tgc acc act cag gct tgt 595
Glu Ala Thr Ala Thr Gly Thr Gly Leu Asp Cys Thr Thr Gln Ala Cys
150 155 160 165

gta gcg aag gtc ttc ggc gat cat acc gaa ggt ttc cgc gat gtt gct 643
Val Ala Lys Val Phe Gly Asp His Thr Glu Gly Phe Arg Asp Val Ala
170 175 180

gaa gtc cca gtt act ttc gca gcc gct taagttttct taaaacgcac 690
Glu Val Pro Val Thr Phe Ala Ala Ala
185 190

```

tca

693

&lt;210&gt; 538

&lt;211&gt; 190

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 538

Met Ser Ile Ser Arg Thr Val Phe Gly Ile Ala Ala Thr Ala Ala Leu  
 1 5 10 15

Ser Ala Ala Leu Val Ala Cys Ser Pro Pro His Gln Gln Asp Ser Pro  
 20 25 30

Val Gln Arg Thr Asn Glu Ile Leu Thr Thr Ser Gln Asn Pro Thr Ser  
 35 40 45

Ala Ser Ser Thr Ser Thr Ser Ser Ala Thr Thr Thr Ser Ser Ala Pro  
 50 55 60

Val Glu Glu Asp Val Glu Ile Val Val Ser Pro Ala Ala Leu Val Asp  
 65 70 75 80

Gly Glu Gln Val Thr Phe Glu Ile Ser Gly Leu Asp Pro Glu Gly Gly  
 85 90 95

Tyr Tyr Ala Ala Ile Cys Asp Ser Val Ala Asn Pro Gly Asn Pro Val  
 100 105 110

Pro Ser Cys Thr Gly Glu Met Ala Asp Phe Thr Ser Gln Ala Trp Leu  
 115 120 125

Ser Asn Ser Gln Pro Gly Ala Thr Val Glu Ile Ala Glu Asp Gly Thr  
 130 135 140

Ala Thr Val Glu Leu Glu Ala Thr Ala Thr Gly Thr Gly Leu Asp Cys  
 145 150 155 160

Thr Thr Gln Ala Cys Val Ala Lys Val Phe Gly Asp His Thr Glu Gly  
 165 170 175

Phe Arg Asp Val Ala Glu Val Pro Val Thr Phe Ala Ala Ala  
 180 185 190

&lt;210&gt; 539

&lt;211&gt; 1528

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1528)

&lt;223&gt; RXN01209

&lt;400&gt; 539

cagattgcag cacagaaggc atcggcgcca ggcagctttg cgggtggcggtt tattgatgcg 60

ctttatgacg tggatgccca ggctgtggcc tcgttggttg atg tgc gag agg cct 115  
 Met Cys Glu Arg Pro

																1	5	
gaa	aag	tac	gtg	act	gat	ttt	tct	ttg	tat	ctg	gtc	acc	gat	ccc	gtt			163
Glu	Lys	Tyr	Val	Thr	Asp	Phe	Ser	Leu	Tyr	Leu	Val	Thr	Asp	Pro	Val			
				10					15					20				
ttg	ggt	ggc	ggg	cca	aaa	aaa	gta	gct	gga	att	gtt	gac	agc	gca	att			211
Leu	Gly	Gly	Gly	Pro	Lys	Lys	Val	Ala	Gly	Ile	Val	Asp	Ser	Ala	Ile			
			25					30					35					
tcc	ggc	gga	gtt	tct	gtg	gtg	cag	ctg	cgc	gat	aag	aac	tca	ggc	gtg			259
Ser	Gly	Gly	Val	Ser	Val	Val	Gln	Leu	Arg	Asp	Lys	Asn	Ser	Gly	Val			
		40					45					50						
gaa	gat	gtt	cgt	gcg	gca	gca	aag	gag	ctg	aaa	gaa	ctc	tgc	gat	gct			307
Glu	Asp	Val	Arg	Ala	Ala	Ala	Lys	Glu	Leu	Lys	Glu	Leu	Cys	Asp	Ala			
	55					60					65							
cgc	ggg	gtg	gcg	ctt	gtt	gtc	aac	gat	tac	tta	gat	atc	gcc	gtt	gag			355
Arg	Gly	Val	Ala	Leu	Val	Val	Asn	Asp	Tyr	Leu	Asp	Ile	Ala	Val	Glu			
	70				75					80					85			
ctg	ggt	ctt	cac	ctg	cac	att	ggt	caa	ggc	gat	aca	cct	tat	acg	caa			403
Leu	Gly	Leu	His	Leu	His	Ile	Gly	Gln	Gly	Asp	Thr	Pro	Tyr	Thr	Gln			
			90					95					100					
gca	cgg	gag	ctg	ctt	cca	gct	cat	ctt	gaa	ttg	ggt	ttg	agc	att	gaa			451
Ala	Arg	Glu	Leu	Leu	Pro	Ala	His	Leu	Glu	Leu	Gly	Leu	Ser	Ile	Glu			
		105						110					115					
aac	ctg	gat	caa	ttg	cat	gct	gtg	atc	gcg	cag	tgc	gcc	gag	act	ggt			499
Asn	Leu	Asp	Gln	Leu	His	Ala	Val	Ile	Ala	Gln	Cys	Ala	Glu	Thr	Gly			
		120					125					130						
gtg	gca	ttg	ccc	gat	gtg	att	ggc	att	ggt	ccg	gtg	gcc	tct	act	gcg			547
Val	Ala	Leu	Pro	Asp	Val	Ile	Gly	Ile	Gly	Pro	Val	Ala	Ser	Thr	Ala			
	135					140					145							
acc	aaa	cca	gat	gcg	gca	ccc	gca	ttg	ggt	gtg	gag	ggc	atc	gct	gag			595
Thr	Lys	Pro	Asp	Ala	Ala	Pro	Ala	Leu	Gly	Val	Glu	Gly	Ile	Ala	Glu			
	150				155					160					165			
atc	gcc	gct	gta	gct	caa	gac	cac	ggc	atc	gca	tca	gta	gct	att	gga			643
Ile	Ala	Ala	Val	Ala	Gln	Asp	His	Gly	Ile	Ala	Ser	Val	Ala	Ile	Gly			
			170					175						180				
ggc	gtt	ggt	cta	cgc	aac	gcg	gcc	gaa	ctc	gct	gct	acg	ccc	atc	gac			691
Gly	Val	Gly	Leu	Arg	Asn	Ala	Ala	Glu	Leu	Ala	Ala	Thr	Pro	Ile	Asp			
			185					190					195					
ggt	ctg	tgc	gtg	gtc	tct	gaa	atc	atg	acc	gcc	gcc	aat	cca	gca	gct			739
Gly	Leu	Cys	Val	Val	Ser	Glu	Ile	Met	Thr	Ala	Ala	Asn	Pro	Ala	Ala			
		200					205					210						
gcg	gca	act	cgc	ctg	cgg	act	gct	ttt	caa	cct	act	ttc	tcg	cct	gaa			787
Ala	Ala	Thr	Arg	Leu	Arg	Thr	Ala	Phe	Gln	Pro	Thr	Phe	Ser	Pro	Glu			
	215					220					225							
act	caa	act	gaa	ctc	tct	caa	aca	gaa	ctc	caa	gga	gcc	ttc	gtg	aat			835
Thr	Gln	Thr	Glu	Leu	Ser	Gln	Thr	Glu	Leu	Gln	Gly	Ala	Phe	Val	Asn			
	230				235					240					245			



tcg cct tct gcc cca cgt gtg ttg tct att gca ggc act gat ccc aca	883
Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala Gly Thr Asp Pro Thr	
250 255 260	
ggg ggt gca ggt att cag gct gat ctg aag tcc att gca gca ggt ggc	931
Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser Ile Ala Ala Gly Gly	
265 270 275	
ggc tac ggc atg tgc gtt gtg acc tcg ctg gtc gcg caa aac acc cac	979
Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val Ala Gln Asn Thr His	
280 285 290	
ggc gtc aac acg atc cac acc cca ccc ttg acc ttt ttg gaa gaa cag	1027
Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr Phe Leu Glu Glu Gln	
295 300 305	
ctg gaa gcg gtc ttt tcc gat gtc acc gtc gat gcc atc aag ctc ggc	1075
Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp Ala Ile Lys Leu Gly	
310 315 320 325	
atg ttg ggc tct gcc gac acc gtc gat ctg gtg gct tca tgg ctt ggt	1123
Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val Ala Ser Trp Leu Gly	
330 335 340	
tcc cac gag cac ggt ccc gtg gtg ctt gat ccc gtc atg atc gcc acc	1171
Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr	
345 350 355	
agc ggt gat cgc cta ctg gat gcg agc gct gaa gaa tcg ctg cgc cgc	1219
Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg	
360 365 370	
ctg gcc gtg cac gtc gat gtg gtc acc ccg aat atc ccc gaa ctt gcc	1267
Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala	
375 380 385	
gtg ttg tgc gac agt gct cct gcc atc acc atg gat gag gcc att gct	1315
Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala	
390 395 400 405	
cag gct cag gga ttt gcg cgg act cat gac acc atc gtc att gtc aag	1363
Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys	
410 415 420	
ggg gga cat ctg act ggc gcg ctt gct gat aac gct gtc gtg cgc ccc	1411
Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro	
425 430 435	
gac ggc tcg gtg ttc cag gtg gaa aac ctg cgt gtc aac acc acc aac	1459
Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn	
440 445 450	
tcc cat ggc aca ggc tgt tcg ctc tct gcg tca ctt gcc acc aag atc	1507
Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser Leu Ala Thr Lys Ile	
455 460 465	
gcc gcc ggc gaa agc gtg gaa	1528
Ala Ala Gly Glu Ser Val Glu	
470 475	

&lt;210&gt; 540

&lt;211&gt; 476

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 540

Met Cys Glu Arg Pro Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu  
 1 5 10 15

Val Thr Asp Pro Val Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile  
 20 25 30

Val Asp Ser Ala Ile Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp  
 35 40 45

Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Lys Glu Leu Lys  
 50 55 60

Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu  
 65 70 75 80

Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp  
 85 90 95

Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu  
 100 105 110

Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln  
 115 120 125

Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro  
 130 135 140

Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val  
 145 150 155 160

Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala  
 165 170 175

Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala  
 180 185 190

Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala  
 195 200 205

Ala Asn Pro Ala Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro  
 210 215 220

Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln  
 225 230 235 240

Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala  
 245 250 255

Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser  
 260 265 270

Ile Ala Ala Gly Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val  
 275 280 285



259	tcc ggc gga gtt tct gtg gtg cag ctc ggc gat aag aac tca ggc gtg	Ser Gly Val	40	gaa gat gtt cgt gcg gca gca aag gag ctc aaa gaa ctc tgc gat gct	Glu Asp Val Arg Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	55	50
307	gaa gat gtt cgt gcg gca gca aag gag ctc aaa gaa ctc tgc gat gct	Glu Asp Val Arg Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	55	gaa gat gtt cgt gcg gca gca aag gag ctc aaa gaa ctc tgc gat gct	Glu Asp Val Arg Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	65	307
355	cgc ggc ggt ggc ggt ggc ggt ggc ggt ggc ggt ggc ggt ggc ggt	Arg Gly Val Ala Leu Val Val Val Val Val Val Val Val Val	70	gaa gat gtt cgt gcg gca gca aag gag ctc aaa gaa ctc tgc gat gct	Glu Asp Val Arg Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	80	355
403	ctg ggt ctt cac ctg ctt cac ctg ctt cac ctg ctt cac ctg ctt	Leu Gly Leu His Leu His Leu His Leu His Leu His Leu His Leu	90	gaa gat gtt cgt gcg gca gca aag gag ctc aaa gaa ctc tgc gat gct	Glu Asp Val Arg Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	95	403
451	gca cgg gag ggt ggt ggt ggt ggt ggt ggt ggt ggt ggt ggt ggt	Ala Arg Glu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu	105	gaa gat gtt cgt gcg gca gca aag gag ctc aaa gaa ctc tgc gat gct	Glu Asp Val Arg Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	110	451
499	aac ctg gat caa ttg cat gct gtc gtc gtc gtc gtc gtc gtc gtc	Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln Cys Ala Glu Thr Gly	120	gaa gat gtt cgt gcg gca gca aag gag ctc aaa gaa ctc tgc gat gct	Glu Asp Val Arg Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	130	499
547	gtg gca ttg ccc gat gtg att ggc att ggc att ggc att ggc att	Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro Val Ala Ser Thr Ala	140	gaa gat gtt cgt gcg gca gca aag gag ctc aaa gaa ctc tgc gat gct	Glu Asp Val Arg Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	145	547
595	acc aaa cca gat ggc gca ccc gca ttg ggt ggt ggt ggt ggt ggt	Thr Lys Pro Asp Ala Pro Ala Leu Gly Val Glu Gly Ile Ala Glu	155	gaa gat gtt cgt gcg gca gca aag gag ctc aaa gaa ctc tgc gat gct	Glu Asp Val Arg Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	160	595
643	atc gcc gct gta gct caa gac cac gac gac gac gac gac gac gac	Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala Ser Val Ala Ile Gly	170	gaa gat gtt cgt gcg gca gca aag gag ctc aaa gaa ctc tgc gat gct	Glu Asp Val Arg Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	175	643
691	ggc gtt ggt cta cgc aac ggc ggc gaa ctc gct gct gct gct gct	Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala Thr Pro Ile Asp	185	gaa gat gtt cgt gcg gca gca aag gag ctc aaa gaa ctc tgc gat gct	Glu Asp Val Arg Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	190	691
739	ggt ctg tgc gtc gtc tct gaa atc atg acc gcc gcc gcc gcc gcc	Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala Ala Asn Pro Ala Ala	200	gaa gat gtt cgt gcg gca gca aag gag ctc aaa gaa ctc tgc gat gct	Glu Asp Val Arg Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	210	739
787	ggc gca act cgc ctg cgg act gct ttt caa cct act ttc tgc cct gaa	Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro Thr Phe Ser Pro Glu	220	gaa gat gtt cgt gcg gca gca aag gag ctc aaa gaa ctc tgc gat gct	Glu Asp Val Arg Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	225	787
835	act caa act gaa ctc tct caa acc gaa ctc gaa ggc ttc gtg aat	Thr Gln Thr Glu Leu Ser Gln Thr Gln Leu Glu Gly Ala Phe Val Asn	235	gaa gat gtt cgt gcg gca gca aag gag ctc aaa gaa ctc tgc gat gct	Glu Asp Val Arg Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	240	835
883	tgc cct tct gcc cca cgt gtg ttg tct att gca ggc act gat ccc aca	Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala Gly Thr Asp Pro Thr	250	gaa gat gtt cgt gcg gca gca aag gag ctc aaa gaa ctc tgc gat gct	Glu Asp Val Arg Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	255	883
931	ggt ggt gca ggt att cag gct gat ctg aag tcc att gca gca ggt ggc	Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser Ile Ala Gly Gly	265	gaa gat gtt cgt gcg gca gca aag gag ctc aaa gaa ctc tgc gat gct	Glu Asp Val Arg Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	270	931

[illegible]

Val Thr Asp Pro Val Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile	20	25	30
Val Asp Ser Ala Ile Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp	35	40	45
Lys Asn Ser Gly Val Gln Asp Val Arg Ala Ala Lys Gln Leu Lys	50	55	60
Gln Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu	65	70	75
Asp Ile Ala Val Gln Leu Gly Leu His Ile Gly Gln Gly Asp	85	90	95
Thr Pro Tyr Thr Gln Ala Arg Gln Leu Pro Ala His Leu Gln Leu	100	105	110
Gly Leu Ser Ile Gln Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln	115	120	125
Cys Ala Gln Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro	130	135	140
Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val	145	150	155
Gln Gly Ile Ala Gln Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala	165	170	175
Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Gln Leu Ala	180	185	190
Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Gln Ile Met Thr Ala	195	200	205
Ala Asn Pro Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro	210	215	220
Thr Phe Ser Pro Gln Thr Gln Thr Gln Leu Ser Gln Thr Gln Leu Gln	225	230	235
Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala	245	250	255
Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser	260	265	270
Ile Ala Ala Gly Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val	275	280	285
Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr	290	295	300
Phe Leu Gln Gln Gln Leu Gln Ala Val Phe Ser Asp Val Thr Val Asp	305	310	315
Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val	325	330	335

Ala Ser Trp Leu Gly Ser His Gln His Gly Pro Val Val Leu Asp Pro  
340 345 350  
Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Gln  
355 360 365  
Gln Ser Leu Arg Arg Leu Ala Val His Val Asp Val Val Thr Pro Asn  
370 375 380  
Ile Pro Gln Leu Ala Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met  
385 390 395 400  
Asp Gln Ala Ile Ala Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr  
405 410 415  
Ile Val Ile Val Lys Gly His Leu Thr Gly Ala Leu Ala Asp Asn  
420 425 430  
Ala Val Val Arg Pro Asp Gly Ser Val Phe Gln Val Gln Asn Leu Arg  
435 440 445  
Val Asn Thr Thr Asn Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser  
450 455 460  
Leu Ala Thr Lys Ile Ala Ala Gly Gln Ser Val Gln  
465 470 475  
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115 Leu Thr His Leu Phe  
1 5  
tca gaa ctc gat gag cgt tta gta ctg ggt ggt gtt cag caa gat ggt tac  
163 Leu Gln Leu Asp Gln Arg Leu Val Leu Gly Val Gln Gln Asp Gly Tyr  
20 15  
caa tgg act gag cat tlg ttc cgg ctg cca ctg caa cat ctc cgt aac  
211 Gln Trp Thr Gln His Leu Phe Arg Leu Pro Leu Gln His Leu Arg Asn  
25 30 35  
tcg ccc aat gac ctg cag gga tlg aag ata cga tgg tgt gaa ctt tat  
259 Ser Pro Asn Asp Leu Gln Gly Leu Lys Ile Arg Trp Cys Gln Leu Tyr  
40 45 50  
tcc aca acg ggg aaa gat caa ggg gta gaa ctt ctg cct caa gca acc  
307 Ser Thr Thr Gly Lys Asp Gln Gly Val Gln Leu Leu Pro Gln Ala Thr  
55 60 65

gac gtc acc cca aat aac ttc gag gct tcc acc ctc tcc ggc ctc gag  
Val Val Thr Pro Asn Asn Phe Gln Ala Ser Thr Leu Ser Gly Leu Gln  
70 75 80 85  
403 aag ctc gag acc gtc gag gac ctc aag gag gct gcc cgc ctc att tat  
Lys Leu Gln Thr Val Gln Asp Leu Lys Gln Ala Ala Arg Leu Ile Tyr  
100  
451 gag caa ggc ccc cag tac gta gtc aag ggt ggc atg gag ttc ccc  
Gln Gln Gly Pro Gln Tyr Val Val Val Lys Gly Gly Met Asp Phe Pro  
105 110 115  
499 ggc gag aac gcc gtg gat gtg ctc ttc gac gga tcc tcc tac cac gtc  
Gly Gln Asn Ala Val Asp Val Leu Phe Asp Gly Ser Ser Tyr His Val  
120 125 130  
547 ttc tct gag cca aag att ggt gaa gag cgc gct tcc ggc gca gtc tgc  
Phe Ser Gln Pro Lys Ile Gly Gln Gln Arg Val Ser Gly Ala Val Cys  
135 140 145  
595 acc ttc gca gct gtc atc acc gca gag cta gca aag ggt gct gag gtc  
Thr Phe Ala Ala Val Ile Thr Ala Gln Leu Ala Lys Gly Ala Gln Val  
150 155 160 165  
643 gta gag cca gtc gca acc gca aag cgt gtg gtc acc cgt ggc gtc caa  
Val Asp Pro Val Ala Thr Ala Lys Arg Val Val Thr Arg Ala Val Gln  
170 175 180  
691 gat gct gtc gca tcc aac gca cct ttc acc tcc gta tgg ctc gct gag  
Asp Ala Val Ala Ser Asn Ala Pro Phe Thr Ser Val Trp Leu Ala Gln  
185 190 195  
723 gac aac aag tagagttta aaataccgat, caa  
Asp Asn Lys 200

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<213> Corynebacterium glutamicum  
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Gln Gln Asp Gly Tyr Gln Trp Thr Gln His Leu Phe Arg Leu Pro Leu  
20 25 30  
Gln His Leu Arg Asn Ser Pro Asn Asp Leu Gln Gly Leu Lys Ile Arg  
35 40 45  
Trp Cys Gln Leu Tyr Ser Thr Thr Gly Lys Asp Gln Gly Val Gln Leu  
50 55 60  
Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn Phe Gln Ala Ser Thr  
65 70 75 80  
Leu Ser Gly Leu Gln Lys Leu Thr Val Gln Asp Leu Lys Gln Ala  
85 90 95



Ala Arg Leu Ile Tyr Gln Gln Gly Pro Gln Tyr Val Val Val Lys Gly	100	105	110
Gly Met Asp Phe Pro Gly Gln Asn Ala Val Asp Val Leu Phe Asp Gly	115	120	125
Ser Ser Tyr His Val Phe Ser Gln Pro Lys Ile Gly Gln Arg Val	130	135	140
Ser Gly Ala Val Cys Thr Phe Ala Ala Val Ile Thr Ala Gln Leu Ala	145	150	155
Lys Gly Ala Gln Val Val Asp Pro Val Ala Thr Ala Lys Arg Val Val	165	170	175
Thr Arg Ala Val Gln Asp Ala Val Ala Ser Asn Ala Pro Phe Thr Ser	180	185	190
Val Trp Leu Ala Gln Asp Asn Lys	195	200	
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115			
Leu Ile Leu Lys Thr			
1			
act gga atc acc gtt ttg tcc cgg ttg gat gcg cag gtt atc gct aat			
163			
Thr Gly Ile Thr Val Leu Ser Arg Phe Asp Ala Gln Val Ile Ala Asn			
20			
cag atc gag gcc gcc acc gca gca gcg cac gat ctt gat gtt gttg aag atc			
211			
Gln Ile Gln Ala Thr Ala His Asp Leu Asp Val Val Lys Ile			
35			
ggt atg ttg ggt act cct gca acg atc gat act gttg gca acc gct ttg			
259			
Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr Ala Leu			
50			
gag gaa aac agc ttg aag cac gtt gtc cta gac ccg gta ctg atc tgc			
307			
Gln Gln Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu Ile Cys			
65			
aag ggc cag gag ccc ggc gcg gca ctt gat act gac act gac act gac			
355			
Lys Gly Gln Gln Pro Gly Ala Ala Leu Asp Thr Ala Leu Arg			
85			
Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn Phe Gln			
403			

90	95	100
451	499	547
gac acc acc cta ggc cta gac aag ctg gag acc atc gac gac ctg	gag gaa gca gca ggc cgc ctc atc cat gag caa gga cct cag tac gtc gtt	glt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac gta ctt
Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Gln Thr Ile Asp Asp Leu	Lys Gln Ala Ala Arg Leu Ile His Gln Gln Gly Pro Gln Tyr Val Val	Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp Val Leu
105	120	135
110	125	140
115	130	145
595	643	691
tac gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc ggc gac	gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc acc gca	gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc gct aag
Phe Asp Gly Thr Asp Tyr His Val Phe Ser Gln Pro Lys Ile Gly Asp	Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Val Ile Thr Ala	Gln Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr Ala Lys
150	170	185
155	175	190
160	180	195
739	792	795
cgc gta gtc acc cgc gca gta aag gac gct gtc gca tcc aac gca ccg	ttt acc tct gtg tgg gcg gaa gac aac aag tagaatctt aaacaagctc	cct
Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn Ala Pro	Phe Thr Ser Val Trp Leu Ala Gln Asp Asn Lys	
200	205	210
215	220	
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<213> Corynebacterium glutamicum		
<400> 546		
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1	20	35
5	25	40
10	30	45
15		
Val Ala Thr Ala Leu Gln Asn Ser Phe Lys His Val Val Leu Asp	Val Ala Thr Ala Leu Gln Asn Ser Phe Lys His Val Val Leu Asp	Pro Val Leu Ile Cys Lys Gly Gln Gln Pro Gly Ala Ala Leu Asp Thr
65	70	75
80		
85		
90		
95		

Pro Asn Asn Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu  
100 105 110

Thr Ile Asp Asp Leu Lys Glu Ala Arg Leu Ile His Glu Gln Gly  
115 120 125

Pro Gln Tyr Val Val Val Lys Gly Ile Asp Phe Pro Gly Asp Asn  
130 135 140

Ala Val Asp Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu  
145 150 155

Pro Lys Ile Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala  
165 170 175

Ala Val Ile Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala  
180 185 190

Val Thr Thr Thr Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val  
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Ala Ser Asn Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys  
210 215 220

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<211> 638

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (1)..(615)

<223> FRXA01617

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aag atc ggt atg ttg ggt act cct gca acg atc gat act gtg gca acc  
96 Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr  
20 25 30

gct ttg gag gaa aac agc ttc aag cac gtt gtc cta gac ccg gta ctg  
144 Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu  
35 40 45

atc tgc aag ggc cag gag ccc ggc gcg gca ctt gat act gac act gcc  
192 Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala  
50 55 60

ctt cgc gcg aag gtg ctg cca cag gca acc gtg gtt act cca aac aac  
240 Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn  
65 70 75 80

ttc gag gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac  
288 Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp

85 90 95

336 gac ctg aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac  
 Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr  
 100 105 110

384 gtc gtt gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac  
 Val Val Val Lys Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp  
 115 120 125

432 gta ctt ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc  
 Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile  
 130 135 140

480 ggc gac gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc  
 Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile  
 145 150 155 160

528 acc gca gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc  
 Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr  
 165 170 175

576 gct aag cgc gta gtc acc cgc gca gtc aag gac gct gtc gca tcc aac  
 Ala Lys Arg Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn  
 180 185 190

625 gca ccg ttt acc tct gtg tgg tgg gcg gaa gac aac aag tagaatctt  
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638 aaacaagctc cct

<210> 548

<211> 205

<212> PRT

<213> Corynebacterium glutamicum

<400> 548

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Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr  
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Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu  
 35 40 45

Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala  
 50 55 60

Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn  
 65 70 75 80

Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp  
 85 90 95

Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr  
 100 105 110

Val Val Val Lys Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp

GenBank accession number: F01111.1  
Gene: *Corynebacterium glutamicum*

115 120 125  
Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Gln Pro Lys Ile  
130 135 140  
Gly Asp Gln Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Val Ile  
145 150 155  
Thr Ala Gln Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr  
165 170 175  
Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn  
180 185 190  
Ala Pro Phe Thr Ser Val Trp Leu Ala Gln Asp Asn Lys  
195 200 205  
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115 Met Pro Ser Ala Gly  
1 5  
gag gag att tta gag cag cgc gca cag ctg gag ttg gat cag cgc cgc  
163 Gln Gln Ile Leu Gln Arg Ala Gln Leu Gln Phe Asp Gln Arg Arg  
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gcc gat gtg gtg atg atc gcc agc cag gtg gtt tat ggt tcc gtc ggg  
211 Ala Asp Val Val Met Ile Gly Ser Gln Val Val Tyr Gly Ser Val Gly  
25 30 35  
ctc agt gct gcc att ccg gtg atg cac aac gaa ggc ctc cgc gtg gtc  
259 Leu Ser Ala Ala Ile Pro Val Met His Asn Gln Gly Leu Arg Val Val  
40 45 50  
gct gtc ccc acc gtg tta agt tcc atg ccg cgt tat gca agt tct  
307 Ala Val Pro Thr Val Leu Ser Ser Met Pro Arg Tyr Ala Ser Ser  
55 60 65  
cac cgc cag cag atg tcg gac caa tgg ctc gcc gac ggc cgc cag gca gac  
355 His Arg Gln Pro Met Ser Asp Gln Trp Leu Ala Asp Ala Leu Gln Asp  
70 75 80  
ctg gtg gat ctg ggg atc atc gat gag gtt tcc acc att tcc acc ggc  
403 Leu Val Asp Leu Gly Ile Ile Asp Gln Val Ser Thr Ile Ser Thr Gly  
90 95 100  
tat ttt acc tcc gct tct cag gtg cgt gtc gct gct gcg tgg ctg cag  
451 Tyr Phe Thr Ser Ala Ser Gln Val Arg Val Val Ala Trp Leu Gln

499 aaa atc cgc gaa acc cat ccg cat gtc cgc atc gtc gat ccc atc  
 Lys Ile Arg Glu Thr His Pro His Val Arg Ile Val Val Asp Pro Ile  
 547 atg ggg gac agt gac gtc gga atc tat gtc gcc gac gag atc gca acc  
 Met Gly Asp Ser Asp Val Gly Ile Tyr Val Ala Asp Glu Ile Ala Thr  
 595 gcc atc tgc cag gac tca tgc cct ctg gct acc gga atc atc ccc aat  
 Ala Ile Cys Gln Asp Leu Cys Pro Leu Ala Thr Gly Ile Ile Pro Asn  
 643 gct ttc gag ctc tcc cac atg gtc gcc tcc ggc gat ccg cgc tgc ctg  
 Ala Phe Glu Leu Ser His Met Val Gly Ser Gly Asp Pro Arg Ser Leu  
 691 ctc ggc ccg ttt ggc gag tgg atc atc atc atc atc atc atc atc atc  
 Leu Gly Pro Phe Gly Glu Trp Ile Ile Ile Thr Ser Ala Thr Glu Thr  
 739 gtc ggc acc acc gtc acc cgc atc gtc acc cgt gac agc gtc cag gaa  
 Val Gly Thr Thr Val Thr Arg Ile Val Thr Arg Asp Ser Val Gln Glu  
 787 atc gcc tcc gcc acc gtc gat acc acg gcc aaa ggc gca ggc gag gtc  
 Ile Ala Ser Ala Thr Val Asp Thr Thr Ala Lys Gly Ala Gly Asp Val  
 835 tac gcc gca gca tta atc gcc gtc cat aaa gat ttt tgc ctt atc  
 Tyr Ala Ala Ala Leu Ile Ala Ala Leu His Lys Asp Phe Ser Leu Ile  
 883 gac gcc gcc agc cac gca tcc aac acc gtc tgc gcc ggc ctg cag acc  
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 Lys Ala Leu  
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 Phe Asp Gln Arg Arg Ala Asp Val Val Met Ile Gly Ser Gln Val Val  
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 Tyr Gly Ser Val Gly Leu Ser Ala Ala Ile Pro Val Met His Asn Glu  
 35  
 Gly Leu Arg Val Val Ala Val Pro Thr Val Val Leu Ser Ser Met Pro  
 50  
 55  
 60

65	Arg Tyr Ala Ser Ser His Arg Gln Pro Met Ser Asp Gln Trp Leu Ala	70	75	80
85	Asp Ala Leu Gln Asp Leu Val Asp Leu Gly Ile Ile Asp Gln Val Ser	90	95	
100	Thr Ile Ser Thr Gly Tyr Phe Thr Ser Ala Ser Gln Val Arg Val Val	105	110	
115	Ala Ala Trp Leu Gln Lys Ile Arg Gln Thr His Pro His Val Arg Ile	120	125	
130	Val Val Asp Pro Ile Met Gly Asp Ser Asp Val Gly Ile Tyr Val Ala	135	140	
145	Asp Gln Ile Ala Thr Ala Ile Cys Gln Asp Leu Cys Pro Leu Ala Thr	150	155	
165	Gly Ile Ile Pro Asn Ala Phe Gln Leu Ser His Met Val Gly Ser Gly	170	175	
180	Asp Pro Arg Ser Leu Leu Gly Pro Phe Gly Gln Trp Ile Ile Thr	185	190	
195	Ser Ala Thr Gln Thr Val Gly Thr Thr Val Thr Arg Ile Val Thr Arg	200	205	
210	Asp Ser Val Gln Gln Ile Ala Ser Ala Thr Val Asp Thr Thr Ala Lys	215	220	
225	Gly Ala Gly Asp Val Tyr Ala Ala Leu Ile Ala Ala Leu His Lys	230	235	
245	Asp Phe Ser Leu Ile Asp Ala Ala Ser His Ala Ser Asn Thr Val Cys	250	255	
260	Ala Gly Leu Gln Thr Lys Ala Leu			

211	cgc cgt gct gat tca acg ggg gct cct cgc gca gct tcc aag gaa gct	Arg Arg Ala Asp Ser Thr Gly Ala Pro Ala Ala Ser Lys Gln Ala	25	30	35
259	tcc caa caa atg gac gct gcc gga gtt ctt gag tgg gcc agg acc gct	Ser Gln Gln Met Asp Ala Ala Gly Val Leu Gln Trp Ala Arg Thr Ala	40	45	50
307	gtc gag cag ctt tct gaa cgt cgt gca gag atc aat gca ctg aat gtc	Val Gln Gln Leu Ser Gln Arg Arg Ala Gln Ile Asn Ala Leu Asn Val	55	60	65
355	ttt cct gtt cca gat gca gac act gga tca aac atg acc tac acc atg	Phe Pro Val Pro Asp Ala Asp Thr Gly Ser Asn Met Thr Tyr Thr Met	70	75	80
403	aca gct gcg ttg gat gaa gcg ctg aaa ctg ggg gag ttg gat gtc	Thr Ala Ala Leu Asp Gln Ala Leu Lys Leu Gly Gln Leu Gly Asp Val	90	95	100
451	gca agg att act gag gct ttg gct gtt ggt tct gtc gct gga gcc cga	Ala Arg Ile Thr Gln Ala Leu Ala Val Gly Ser Val Arg Gly Ala Arg	105	110	115
499	gga aat tct gga gta gta gtc ctt agt cag gtc ctt gcg gct att gct cag	Gly Asn Ser Ser Gly Val Val Leu Ser Gln Val Leu Arg Ala Ile Ala Gln	120	125	130
547	gca gct gct gac ggg gtt att gat ggc cac aca atc caa gaa gcg cta	Ala Ala Ala Asp Gly Val Ile Asp Gly His Thr Ile Gln Gln Ala Leu	135	140	145
595	tcc att gct cgc tcc cta gtt gat cgc gca att aca gat cct gtc gag	Ser Ile Ala Arg Ser Leu Val Asp Arg Ala Ile Thr Asp Pro Val Gln	150	155	160
622	ggc act gtt gtc act gtt gtt gtt gtt gtt gtt gtt gtt gtt gtt gtt	Gly Thr Val Val Thr Val Leu Arg Ser	170		
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<213> Corynebacterium glutamicum					
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20	Ser Val Gln Pro Gln Arg Arg Ala Asp Ser Thr Gly Ala Pro Ala Ala	Ser Val Gln Pro Gln Arg Arg Ala Asp Ser Thr Gly Ala Pro Ala Ala	20	25	30
35	Ala Ser Lys Gln Ala Ser Gln Gln Met Asp Ala Ala Gly Val Leu Gln	Ala Ser Lys Gln Ala Ser Gln Gln Met Asp Ala Ala Gly Val Leu Gln	35	40	45
50	Trp Ala Arg Thr Ala Val Gln Gln Leu Ser Gln Arg Arg Ala Gln Ile	Trp Ala Arg Thr Ala Val Gln Gln Leu Ser Gln Arg Arg Ala Gln Ile	50	55	60
65	Asn Ala Leu Asn Val Phe Pro Val Pro Asp Ala Asp Thr Gly Ser Asn	Asn Ala Leu Asn Val Phe Pro Val Pro Asp Ala Asp Thr Gly Ser Asn	65	70	75
80					

1000  
 900  
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 700  
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 100  
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[illegible]

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 Ile Gln Met Met Arg Lys Gln His  
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 115 Met Asp Val Ala His  
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ggc tta gat ctg gcc cac cac gtc tca gat caa gtc cga ggc acc acc  
 163 Ala Leu Asp Leu Ala His His Val Ser Asp Gln Val Arg Gly Thr Thr  
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agc cct aat ccg cca gtc ggc gtc gtc gtc atc ttg gac gcc gac ggc gag  
 211 Ser Pro Asn Pro Pro Val Ile Leu Asp Ala Asp Gly Gln  
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gtc gtc ggc gtc ggc ggc ggc gca cct cct ggt ggc ccg cac gcc gaa  
 259 Val Val Gly Val Gly Ala Thr Ala Pro Pro Gly Pro His Ala Gln  
 50

gtg gtg ggc gtc gca gct gcc gga gtc gtc gtc aac gcc aac ggc ggc acc  
 307 Val Val Ala Leu Ala Ala Gly Val Arg Ala Asn Gly Gly Thr Ala  
 65

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 355 Val Val Thr Leu Gln Pro Cys Asn His Tyr Gly Arg Thr Gly Pro Cys  
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 403 Ser Lys Ala Leu Leu Asp Ala Gly Ile Ala His Val Phe Tyr Ala Asn  
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ggc gat ccc ttc ccg tca gcc gct ggc ggc ggc ggt gcc ttg ggc gag  
 451 Ala Asp Pro Phe Pro Ser Ala Ala Gly Gly Gly Ala Phe Leu Ala Gln  
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ggc ggc gtc gat acc cat ttt tta gat gag cgg atc agg gca ctg gag  
 499 Ala Gly Val Asp Thr His Phe Leu Asp Gln Arg Ile Arg Ala Leu Gln  
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ccc tgg ctg gtc gtc ggc acc gct ctg ggc agg ccc cat gtc acc tgg aag  
 547 Pro Trp Leu Val Ala Thr Arg Leu Gly Arg Pro His Val Thr Leu Lys  
 145

595	ttt gcg tcc acc gtt gac ggt ttt gct ggt gcc acc gat ggc acc agc	150	Phe Ala Ser Thr Val Asp Gly Phe Ala Gly Ala Thr Asp Gly Thr Ser	155	160	165
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691	agt aaa aga gat gcg atc atc gtt ggt acc ggt act gcg ttg act gat	185	Ser Lys Arg Asp Ala Ile Ile Val Gly Thr Ala Leu Thr Asp	190	195	
739	aat ccc tcc ttg acg gcg acc gat acc ggt ggt ctt tat gaa aat caa	200	Asn Pro Ser Leu Thr Ala Arg Thr Asp Thr Gly Leu Tyr Gln Asn Gln	205	210	
787	ccc agg cgc gtt gtt att ggc tcc cgc gag gtt cca gca gat tcc aac	215	Pro Arg Arg Val Val Ile Gly Ser Arg Gln Val Pro Ala Asp Ser Asn	220	225	
835	ttg gct cgc ttg gga tat gag cag tac gcg gga ata cca gag gct tta	230	Leu Ala Arg Leu Gly Tyr Gln Gln Tyr Ala Gly Ile Pro Gln Ala Leu	235	240	245
883	tca gcg ctg ttg gat aaa ggg tgc cga gac att tta atc gaa ggt ggc	250	Ser Ala Leu Trp Asp Lys Gly Cys Arg Asp Ile Leu Ile Gln Gly Gly	255	260	
931	cca acg tta gct ggg gca gcg ctg cgc tta ggc att gtt gat cag gttg	265	Pro Thr Leu Ala Gly Ala Leu Arg Leu Gly Ile Val Asp Gln Val	270	275	
979	cag gcc tat gtt gcc ccc gct ttg ttg ggc gct gga cga tca gtt att	280	Gln Ala Tyr Val Ala Pro Ala Leu Leu Gly Ala Gly Arg Ser Val Ile	285	290	
1027	aac tgg cca caa gaa acc acg atg gat cag att atg cgt ttt gac acc	295	Asn Trp Pro Gln Gln Thr Thr Met Asp Gln Ile Met Arg Phe Asp Thr	300	305	
1075	acg tcc gtt aga cag ttg ggt tca gat gta ttg ata gaa atg atg aga	310	Thr Ser Val Arg Gln Leu Gly Ser Asp Val Leu Ile Gln Met Met Arg	315	320	325
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Gly	Pro	His	Ala	Glu	Val	Val	Ala	Leu	Ala	Ala	Gly	Val	Arg	Ala	50
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Arg	Thr	Gly	Pro	Cys	Ser	Lys	Ala	Leu	Leu	Asp	Ala	Gly	Ile	Ala	85
Val	Phe	Tyr	Ala	Asn	Ala	Asp	Pro	Phe	Pro	Ser	Ala	Ala	Gly	Gly	100
Ala	Phe	Leu	Ala	Glu	Ala	Gly	Val	Asp	Thr	His	Phe	Leu	Asp	Glu	115
Ile	Arg	Ala	Leu	Glu	Pro	Trp	Leu	Val	Ala	Thr	Arg	Leu	Gly	Arg	130
His	Val	Thr	Leu	Lys	Phe	Ala	Ser	Thr	Val	Asp	Gly	Phe	Ala	Gly	145
Thr	Asp	Gly	Thr	Ser	Gln	Trp	Ile	Thr	Gly	Pro	Asp	Ala	Arg	Ala	165
Val	His	Glu	Asp	Arg	Ser	Lys	Arg	Asp	Ala	Ile	Ile	Val	Gly	Thr	180
Thr	Ala	Leu	Thr	Asp	Asn	Pro	Ser	Leu	Thr	Ala	Arg	Thr	Asp	Thr	195
Leu	Tyr	Glu	Asn	Gln	Pro	Arg	Arg	Val	Val	Ile	Gly	Ser	Arg	Glu	210
Pro	Ala	Asp	Ser	Asn	Leu	Ala	Arg	Leu	Gly	Tyr	Gln	Gln	Tyr	Ala	225
Ile	Pro	Glu	Ala	Leu	Ser	Ala	Leu	Trp	Asp	Lys	Gly	Cys	Arg	Asp	245
Leu	Ile	Glu	Gly	Gly	Pro	Thr	Leu	Ala	Gly	Ala	Ala	Leu	Arg	Leu	260
Ile	Val	Asp	Gln	Val	Gln	Ala	Tyr	Val	Ala	Pro	Ala	Leu	Leu	Gly	275
Gly	Arg	Ser	Val	Ile	Asn	Trp	Pro	Gln	Gln	Thr	Thr	Met	Asp	Gln	290
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Met Phe Thr Gly Ile  
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Val Glu Glu Leu Gly Ser Val Ala Gly Val Glu His Leu  
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atc cgg atg cag att tcc gcg tcc acc gtt tta gag ggt gtc cat ttg  
Ile Arg Met Gln Ile Ser Ala Ser Thr Val Leu Glu Gly Val His Leu  
25 30 35

ggg gat tcc att tct gtc aat ggt gtc tgc tgc tgc tgc tgc tgc ttc  
Gly Asp Ser Ile Ser Val Asn Gly Val Cys Leu Thr Val Ala Ser Phe  
40 45 50

ggc gag gga cat ttc act gca gac ctc atg cag gaa acc tta gat cgc  
Gly Glu Gly His Phe Thr Ala Asp Leu Met Gln Glu Thr Leu Asp Arg  
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agc tcc ctg ggc gca tta tcc acc ggt agc aaa gtc aac ctt gag cgc  
Ser Ser Leu Gly Ala Leu Ser Thr Gly Ser Lys Val Asn Leu Glu Arg  
70 75 80 85

ggc atg gca gcc gat ggc cgt ctg ggt gga cac atc atg caa ggc cat  
Ala Met Ala Ala Asp Gly Arg Leu Gly Gly His Ile Met Gln Gly His  
90 95 100

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Asp Val Leu Arg Phe Glu Leu Pro Ala Asp Leu Ala Arg Tyr Val Val  
120 125 130

gaa aaa ggc tcc atc gca ctc aat ggc aca tcc ttg act gta tgc tct  
Glu Lys Gly Ser Ile Ala Leu Asn Gly Thr Ser Leu Thr Val Ser Ser  
135 140 145

ttg ggt gat gat tgg ttt gag gtt tcc ctg atc tcc acc acc ttg cgc  
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150 155 160 165

gac acc acc ccc ggc gaa ctg gcg gta ggg gat atc gta aac att gag  
Asp Thr Thr His Gly Glu Leu Ala Val Gly Asp Ile Val Asn Ile Glu  
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gtt gat gtc atc gct aag tac gtc gaa cgc atg atg acg cgc ggc gtc  
Val Asp Val Ile Ala Lys Tyr Val Glu Arg Met Met Thr Arg Gly Val  
185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995

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Glu Gly Val His Leu Gly Asp Ser Ile Ser Val Asn Gly Val Cys Leu  
 35 40 45

Thr Val Ala Ser phe Gly Glu Gly His phe Thr Ala Asp Leu Met Gln  
 50 55 60

Glu Thr Leu Asp Arg Ser Ser Leu Gly Ala Leu Ser Thr Gly Ser Lys  
 65 70 75 80

Val Asn Leu Glu Arg Ala Met Ala Ala Asp Gly Arg Leu Gly Gly His  
 85 90 95

Ile Met Gln Gly His Val Asp Ala Thr Thr Ser Leu Ile Lys Arg Thr  
 100 105 110

Ser Ser Glu Asn Trp Asp Val Leu Arg phe Glu Leu Pro Ala Asp Leu  
 115 120 125

Ala Arg Tyr Val Val Glu Lys Gly Ser Ile Ala Leu Asn Gly Thr Ser  
 130 135 140

Leu Thr Val Ser Ser Leu Gly Asp Asp Trp phe Glu Val Ser Leu Ile  
 145 150 155 160

Pro Thr Thr Leu Arg Asp Thr Thr His Gly Glu Leu Ala Val Gly Asp  
 165 170 175

Ile Val Asn Ile Glu Val Asp Val Ile Ala Lys Tyr Val Glu Arg Met  
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Thr Arg Asp  
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<210> 559  
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GenBank accession number: F01001.1  
Gene: *Corynebacterium glutamicum*

<213> *Corynebacterium glutamicum*

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Val Ser Gln His Gln  
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163 cag gca cac agc caa tta gat tct gtt gaa gag gcc atc gct gag atc  
Gln Ala His Ser Gln Leu Asp Ser Val Gln Ala Ile Ala Asp Ile  
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211 gct gcg ggt aaa gcc gtc gtc gtc gta gat gat gaa gat cgt gaa aat  
Ala Ala Gln Lys Ala Val Val Val Val Val Val Val Val Val Val Val  
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259 gaa ggc gac atc atc ttc gcc gcc gaa tta gcc act cca gaa tta gtc  
Glu Gln Gly Asp Ile Ile Phe Ala Ala Gln Leu Ala Thr Pro Gln Leu Val  
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307 gct ttc atg gtg cgt tat tcc tcc gga tac atc tgt gcg cca tta acc  
Ala Phe Met Val Arg Tyr Ser Ser Ser Gly Tyr Ile Cys Ala Pro Leu Thr  
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355 gca aag gat gca gat cgt ctt gat ctg cct ccg atg acc gcg cac aat  
Ala Lys Asp Ala Asp Arg Leu Asp Leu Pro Pro Met Thr Ala His Asn  
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403 cag gat gcc gcc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc  
Gln Asp Ala Arg Gly Thr Ala Tyr Thr Val Thr Val Thr Val Thr Val Thr  
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Gly Thr Thr Thr Gly Ile Ser Ala Thr Asp Arg Ala His Thr Leu Arg Leu  
115

499 ctt gct gat cca gaa gcc gac gcg acg gat ttc acc cgt ccc gga cac  
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547 gtt gtg cca cta cgt gct gct gaa ggt ggc ggc ggc ggc ggc ggc ggc  
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145

595 cac acc gaa gca gct gtc gat ttg gct gcg gct gca ggc cta gcg cca  
His Thr Gln Ala Val Asp Leu Ala Arg Ala Ala Gly Leu Arg Pro  
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643 gca ggt gtt atc tgc gaa gtc agt gaa gag gac gcc acc ggc atg  
Ala Gly Val Ile Cys Gln Val Val Ser Gln Gln Asp Pro Thr Gly Met  
180

691 gct cgg gtt cct gag cgc cgc ttc tgc gat gag cac gat ctg aag  
Ala Arg Val Pro Gln Leu Arg Arg Phe Cys Asp Gln His Asp Leu Lys  
195

[illegible]

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35 40 45  
Thr Pro Gln Leu Val Ala Phe Met Val Arg Tyr Ser Ser Gly Tyr Ile  
50 55 60  
Cys Ala Pro Leu Thr Ala Lys Asp Ala Asp Arg Leu Asp Leu Pro Pro  
65 70 75 80  
Met Thr Ala His Asn Gln Asp Ala Arg Gly Thr Ala Tyr Thr Val Thr  
85 90 95  
Val Asp Ala Asn Thr Gly Thr Thr Gly Ile Ser Ala Thr Asp Arg Ala  
100 105 110  
His Thr Leu Arg Leu Leu Ala Asp Pro Gln Ala Asp Arg Thr Asp Phe  
115 120 125  
Thr Arg Pro Gly His Val Val Pro Leu Arg Ala Arg Gln Gly Val  
130 135 140  
Leu Val Arg Ala Gly His Thr Gln Ala Ala Val Asp Leu Ala Arg Ala  
145 150 155 160  
Ala Gly Leu Arg Pro Ala Gly Val Ile Cys Gln Val Val Ser Gln Gln  
165 170 175  
Asp Pro Thr Gly Met Ala Arg Val Pro Gln Leu Arg Arg Phe Cys Asp  
180 185 190  
Gln His Asp Leu Lys Leu Ile Ser Ile Gln Gln Leu Ile Gln Trp Arg  
195 200 205  
Arg Lys Asn Gln Ile Leu Val Gln Arg Gln Val Gln Thr Val Leu Pro  
210 215 220  
Thr Asp Phe Gly Thr Phe Lys Ala Val Gly Tyr Arg Ser Ile Ile Asp  
225 230 235 240  
Gly Thr Gln Leu Val Ala Ile Val Ala Gly Asp Val Ala Ser Asp Gly  
245 250 255  
Gly Gln Asn Val Leu Val Arg Val His Ser Gln Cys Leu Thr Gly Asp  
260 265 270  
Val Phe Gly Ser Arg Arg Cys Asp Cys Gly Gln Gln Leu His Gln Ser  
275 280 285

Leu Arg Leu Ile Gln Ala Gly Arg Gly Val Val Tyr Met Arg 290  
 Gly His Gln Gly Arg Gly Ile Gly Leu Leu Ala Lys Leu Arg Ala Tyr 305  
 Gln Leu Gln Asp Gln Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu 320  
 Gly Leu Pro Ala Asp Ala Arg Gln Phe Gly Thr Ser Ala Gln Ile Leu 335  
 Tyr Asp Leu Gly Val Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala 350  
 Lys Lys Val Gly Leu Gln Gly His Gly Ile Ser Ile Ala Ser Arg Thr 365  
 Pro Ile Pro Val Ala Val His Gln Asp Asn Val Arg Tyr Leu Lys Thr 380  
 Lys Arg Asp Arg Met Gly His Asp Leu Pro Asp Val Ala Leu Trp Gln 400  
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 Gln Ala His Ser Gln Leu Asp Ser Val Gln Gln Ala Ile Ala Asp Ile 20  
 gct gcg ggt aaa gcc gtc gtg gta gat gat gaa gat cgt gaa aat 211  
 Ala Ala Gly Lys Ala Val Val Val Val Val Val Val Val Val Val 30  
 gaa gcc gac atc atc ttt gcc gcc gaa tta gcc act cca gaa tta gtc 259  
 Gln Gly Asp Ile Ile Phe Ala Ala Gln Leu Ala Thr Pro Gln Leu Val 50  
 gct ttc atg gtg cgt tat tcc tcg gga tac atc tgt gcg cca tta acc 307  
 Ala Phe Met Val Arg Tyr Ser Ser Gly Tyr Ile Cys Ala Pro Leu Thr 65

355	Ala	Lys	Asp	Ala	Asn	85
403	Cys	Gln	Gat	Gcc	Aac	acc
451	Ggc	acc	aca	ggc	atc	tgc
499	Leu	Ala	Asp	Pro	Gln	His
547	Glt	Gtg	cca	ctg	cgc	gga
595	Cac	acc	gaa	gca	gct	cga
643	Gca	ggt	ggt	atc	tgc	gca
691	Gct	cgg	ggt	cct	gag	ctg
739	Ctg	atc	tct	atc	gag	cat
787	Ttg	gtg	gag	cgc	cag	gga
835	Ttc	aag	gct	ggt	tac	ctc
883	Gcc	atc	gtt	gcc	gac	gtg
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979	Cgc	tgc	gac	tgt	gga	cag
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1389 1363 1315 1267 1219 1171 1123 310 315 320 325 340 355 370 385 395 400 405 410 415 420

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1123 330 335 340  
Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu Gly Leu Pro Ala Asp  
1171 345 350 355  
Ala Arg Gln Phe Gly Thr Ser Ala Gln Ile Leu Tyr Asp Leu Gly Val  
1219 360 365 370  
Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala Lys Lys Val Gly Leu  
1267 375 380 385  
Gln Gly His Gly Ile Ser Ile Ala Ser Arg Thr Pro Ile Pro Val Ala  
1315 390 395 400 405  
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Val His Gln Asp Asn Val Arg Tyr Leu Lys Thr Lys Arg Asp Arg Met  
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Gly His Asp Leu Pro Asp Val Ala Leu Trp Gln Gln His Pro Gln  
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Asn  
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Thr Pro Gln Leu Val Ala Phe Met Val Arg Tyr Ser Ser Gly Tyr Ile  
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Cys Ala Pro Leu Thr Ala Lys Asp Ala Asp Arg Leu Asp Leu Pro Pro  
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Met Thr Ala His Asn Gln Asp Ala Arg Gly Thr Ala Tyr Thr Val Thr  
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Val Asp Ala Asn Thr Gly Thr Thr Gly Ile Ser Ala Thr Asp Arg Ala  
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His Thr Leu Arg Leu Leu Ala Asp Pro Gln Ala Asp Arg Thr Asp Phe  
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1000 900 800 700 600 500 400 300 200 100 0

Thr Arg Pro Gly His Val Val Pro Leu Arg Ala Arg Gly Gly Val	130	135	140
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Ala Gly Leu Arg Pro Ala Gly Val Ile Cys Gln Val Val Ser Gln Gln	165	170	175
Asp Pro Thr Thr Gly Met Ala Arg Val Pro Gln Leu Arg Arg Phe Cys Asp	180	185	190
Gln His Asp Leu Lys Leu Ile Ser Ile Gln Gln Leu Ile Gln Trp Arg	195	200	205
Arg Lys Asn Gln Ile Leu Val Gln Arg Gln Val Thr Val Leu Pro	210	215	220
Thr Asp Phe Gly Thr Phe Lys Ala Val Gly Tyr Arg Ser Ile Ile Asp	225	230	235
Gly Thr Gln Leu Val Ala Ile Val Ala Gly Asp Val Ala Ser Asp Gly	245	250	255
Gly Gln Asn Val Leu Val Arg Val His Ser Gln Cys Leu Thr Gly Asp	260	265	270
Val Phe Gly Ser Arg Arg Cys Asp Cys Gly Gln Gln Leu His Gln Ser	275	280	285
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Gly Leu Pro Ala Asp Ala Arg Gln Phe Gly Thr Ser Ala Gln Ile Leu	340	345	350
Tyr Asp Leu Gly Val Arg Ser Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala	355	360	365
Lys Lys Val Gly Leu Gln Gly His Gly Ile Ser Ile Ala Ser Arg Thr	370	375	380
Pro Ile Pro Val Ala Val His Gln Asp Asn Val Arg Tyr Leu Lys Thr	385	390	395
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Leu Pro Ala Val Gln Leu Pro Asp Ala Ser Gly Leu Lys Val Ala Val  
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Val Thr Ala Arg Trp Asn Ala Gln Ile Cys Asp Arg Leu His Lys His  
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Ala Val Asp Ala Gly Arg Ala Gly Ala Thr Val Ser Gln Tyr Arg  
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gtc atc ggc gcc ctg gaa ctc cca gtc gta gtc caa gaa ctg gca cgc 307  
Val Ile Gly Ala Leu Gln Leu Pro Val Val Val Gln Leu Ala Arg  
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Thr His Asp Ala Val Ala Leu Gly Cys Val Val Arg Gly Gly Thr  
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Asn Thr Gln Gln Ala Val Gln Arg Ser Gly Gly Gln Gly Ser Val  
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gag gac aaa ggc gca gag gca atg gtc gct gca ctc gat act gcc ctc 547  
Glu Asp Lys Gly Ala Gln Ala Met Val Ala Ala Leu Asp Thr Ala Leu  
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ctg

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Gln Glu Leu Ala Arg Thr His Asp Ala Val Val Ala Leu Gly Cys Val 65  
Val Arg Gly Gly Thr Pro His Phe Asp Tyr Val Cys Asp Ser Val Thr 85  
Glu Gly Leu Thr Arg Ile Ala Leu Asp Thr Ser Thr Pro Ile Gly Asn 100  
Gly Val Leu Thr Thr Asn Thr Glu Glu Gln Ala Val Glu Arg Ser Gly 115  
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Met Ala Lys Glu Gly 1  
Leu Pro Ala Val Thr Ala Arg Trp Asn Ala Glu Ile Cys Asp Arg Leu His Lys His 211  
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Val Thr Ala Arg Trp Asn Ala Glu Ile Cys Asp Arg Leu His Lys His 35  
gca gta gat gcg gga cgt gca gca gga gca acg gtg agc gaa tac cgc 259  
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8	8	36	224
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08 5/ 0/ 59

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 163 Pro Asp Gly Ala Thr Asn Ile Asn Asn Ala His Ser Gly Ala Val  
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 211 Gly Lys Pro Lys Val Gln Leu Ser Asp Ala Gln Ile Gln Gln Tyr Thr  
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 Gly Val Val Ala Thr Lys Gly Val Ser Ala Tyr Pro Ser Ser Val Ser Leu  
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 Ala Arg Thr Thr Gly Thr Ser Val Arg Leu Ile Asp Thr Ser Leu Asp  
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 His Gln Ala Trp Gly Asp Gln Arg Val Ser Arg Ser Cys Gly Ser Ile  
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 Leu Ile Pro Gly Asp Leu Gly Ile Gly Asn Thr Thr Thr Ala Ala Ala  
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ctc gtt gga acg ttc acc ctc gca gag cct gtt gtt gtc gta ggc cgc  
 Leu Val Gly Thr Phe Thr Leu Ala Gln Pro Val Val Val Gly Arg  
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ggc acc gga atc gac gat gaa gcc tgg aaa ctc aaa gtc tcc gcg atc 739



1197	gag taactttcta agcgatgtcc ggc	Gln
1171	gta gtc gat gga ccc cta aac ggc tct tcc gaa gcg ccc gag caa aac acg	Val Asp Gly Pro Leu Asn Ala Ser Ser Gln Ala Pro Gln Asn Thr
1123	att gcc gtt gac ctg aac gac atg tgc aca ttt tct tcc gcc ggc	Ile Ala Val Asp Leu Met Asn Asp Met Ser Thr Phe Ser Ser Ala Gly
1075	tcc ctt ggc gaa ggc tcc ggc gca gcc acc gca ctc ccc ctg gtc aag	Ser Leu Gly Gln Gly Ser Gly Ala Ala Thr Ala Leu Pro Leu Val Lys
1027	gta gct cta aac gca ctg gcc ctt gat ccc atc ctg gaa ctt gga atg	Val Ala Leu Asn Ala Leu Ala Leu Asp Pro Ile Leu Gln Leu Gly Met
979	agg cgt tgg ttc atc gca gga cac cgc tcc acc gaa cca gcg cat tcc	Arg Arg Trp Phe Ile Ala Gly His Arg Ser Thr Gln Pro Ala His Ser
931	gta gtc acc gcc gca gcc ctc cta gcc aac aaa ctg gcc cca ggt gcc	Val Val Thr Ala Ala Leu Leu Ala Asn Lys Leu Ala Pro Gly Ala
883	att gcc caa gca gca gtc cga acc ccc gtg ctt ctc gac ggc gtt	Ile Ala Gln Ala Ala Val Arg Arg Thr Pro Val Leu Leu Asp Gly Val
835	atc gcc cgg aaa atc tct tcc cca gac ctt gca gcc atg gca gca ttc	Ile Ala Arg Lys Ile Ser Ser Pro Asp Leu Ala Met Ala Ala Phe
787	cgc gac gcc atg ttc cgc gcc cgc gac ctg cgc caa gac ccc atc gcc	Arg Asp Ala Met Phe Arg Ala Arg Asp Leu Arg Gln Asp Pro Ile Ala
	Gly Thr Gly Ile Asp Asp Gln Ala Trp Lys Leu Lys Val Ser Ala Ile	200
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 Gly Ser Leu Gly Lys Leu Gln Ile Gly Cys Phe Ile Ser Ala Cys  
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 45  
 Gln Gly Gln Ile Pro Pro Arg Pro Leu Asn Asn Ser Lys Ile Val Val  
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Phe Ala Gly Asp His Gly Val Ala Thr Lys Gly Val Ser Ala Tyr Pro 65  
70 75

Ser Ser Val Ser Leu Gln Met Ala Gln Asn Ile Thr Asn Gly Gly Ala 85  
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Ala Ile Asn Val Ile Ala Arg Thr Thr Gly Thr Ser Val Arg Leu Ile 100  
105 110

Asp Thr Ser Ser Leu Asp His Gln Ala Trp Gly Asp Gln Arg Val Ser Arg 115  
120 125

Ser Cys Gly Ser Ile Asp Val Gln Asp Ala Met Thr Gln Gln Val 130  
135 140

Gln Arg Ala Leu Lys Ile Gly Lys Arg Ile Ala Asp Gln Gln Val Asp 145  
150 155

Ala Gly Ala Asp Ile Leu Ile Pro Gly Asp Leu Gly Ile Gly Asn Thr 160  
165 170 175

Thr Thr Ala Ala Leu Val Gly Thr Phe Thr Leu Ala Gln Pro Val 180  
185 190

Val Val Val Gly Arg Gly Thr Gly Ile Asp Asp Gln Ala Trp Lys Leu 195  
200 205

Lys Val Ser Ala Ile Arg Asp Ala Met Phe Arg Ala Arg Asp Leu Arg 210  
215 220

Gln Asp Pro Ile Ala Ile Ala Arg Lys Ile Ser Ser Pro Asp Leu Ala 225  
230 235

Ala Met Ala Ala Phe Ile Ala Gln Ala Ala Val Arg Arg Thr Pro Val 240  
245 250 255

Leu Leu Asp Gly Val Val Thr Ala Ala Leu Leu Ala Asn Lys 260  
265 270

Leu Ala Pro Gly Ala Arg Arg Trp Phe Ile Ala Gly His Arg Ser Thr 275  
280 285

Gln Pro Ala His Ser Val Ala Leu Asn Ala Leu Ala Leu Asp Pro Ile 290  
295 300

Leu Gln Leu Gly Met Ser Leu Gly Gln Gly Ser Gly Ala Ala Thr Ala 305  
310 315 320

Leu Pro Leu Val Lys Ile Ala Val Asp Leu Met Asn Asp Met Ser Thr 325  
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Phe Ser Ser Ala Gly Val Asp Gly Pro Leu Asn Ala Ser Ser Gln Ala 340  
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Pro Gln Gln Asn Thr Gln 355

<210> 573  
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>222> (101) .. (1123)
>223> RXA01489
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<223> RXA01489

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Val Asp Ile Trp Ser 1  
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163 gga cta gac agc gtt ccg gct gat ctt caa gga tca gta gtc acc att  
Gly Leu Asp Ser Val Pro Ala Asp Leu Gln Gly Ser Val Val Thr Ile  
10 15 20

211 ggt gtg ttt gat ggg ctc cac cgg ggg cat caa agt tta atc ggc gag  
Gly Val Phe Asp Gly Leu His Arg Gly His Gln Ser Leu Ile Gly Gln

*gcc* aag aag cag gcc gag gln ala gln glu leu gly ggt gat pro cys val met thr  
Ala Lys Lys Gln Ala Gln Gln Leu Gly Val Pro Cys Val Met Val Thr  
40  
45  
50  
259

307 ttt gac ccy cat ccy his pro ile ala val phe len pro gly lys glu pro thr 55  
55 phe asp pro his pro ile ala val phe len pro gly lys glu pro thr 60  
65 ttt gac ccy cat ccy his pro ile ala val phe len pro gly lys glu pro thr 65

355	cgt ttg gct cct ttg gat tat cgc ctt aat ttg gct gcg gaa tgt ggc	85
	Arg Leu Ala Pro Leu Asp Tyr Arg Leu Asn Leu Ala Ala Glu Cys Gly	70
		75
		80

	gtc gat gct gcg ttg	90	Val Ile Asp Phe Thr Lys Gln Leu Ala Gly Leu	100	403
	Val Asp Ala Ala Leu Val				
	ggt gaa gga ggc gac gca ggt ctt	95			

451 agc gct gaa gag tat ttc acc acc atg atc gtc gat acg ctg cat gcg Ser Ala Gln Gln Tyr Phe Thr Thr Met Ile Val Asp Thr Leu His Ala

499	cgt tca gct	120	Arg Ser Val
	gtc gtc gtc		Val Val Val
	ggg ggg ggg		Gly Gly Gly
	gag gag gag	125	Gln Asn Asn
	aac ttc acc		Phe Phe Phe
	acc ttc acc		Thr Thr Thr
	gtc ttc ggt	130	Gly Val Val
	gtc aat ggc		Asn Gly Ala

	ggc	act	gag	tcc	acc	atg	cgt	ctt	agg	gaa	atg	gga	gln	gla	lys	phe	gly	val	asn	
547		gly	thr	glu	ser	thr	met	arg	cgg	gaa	atg	gga	gln	gla	lys	phe	gly	val	asn	
									140						145					

	Val Thr Ile Ala Pro Leu Leu His Asp Asp Asp Gln Arg Ile Cys Ser	150
gac acg att gct ccg ctg ctg ctg ctg ctg ctg ctg ctg ctg ctg		155
	Asp Asp Asp Asp Asp Asp Asp Asp Asp Asp Asp Asp Asp Asp	160
att tgc ttc cag cgt cag gac gac gac gac gac gac gac gac gac		165

	acc	ctg	ctg	cgc	gat	tac	ctg	gat	cag	ggc	gag	gtt	gag	cgc	gcg	aac	643
	Thr	Leu	Val	Arg	Asp	Tyr	Leu	Asp	Gln	Gly	Glu	Val	Glu	Arg	Ala	Asn	
										175					180		

Trg ggc ctt ggt cga cgc tat gcc gat gcc arg ggc gaa gtc gtc cgt ggt  
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691

185	190	195
gct ggc cgt ggc ggc aaa gaa ttg ggc tat ccc acc gcg aat ctc tac	Ala Gly Arg Gly Gly Lys Gln Leu Gly Tyr Pro Thr Ala Asn Leu Tyr	739
ctg ccg acc tct gtg gcg ctg ccc gcc gat ggc gtg tat gca ggc tgg	Leu Pro Thr Ser Val Ala Leu Pro Ala Asp Gly Val Tyr Ala Gly Trp	787
ttc acc atc acc gat gac cgc gaa atc gac aag gaa atc tcc cgc gat	Phe Thr Ile Thr Asp Asp Arg Gln Ile Asp Lys Gln Ile Ser Arg Asp	835
atc gac ggc acc atg gtc cca ggc gtc gtc cgt tac caa act gcc att tcc	Ile Asp Gly Thr Met Val Pro Gly Val Arg Tyr Gln Thr Ala Ile Ser	883
gtg ggc acc aat ccc acc ttc ggc gat gac ggc arg ggc agc gtc gag gca	Val Gly Thr Asn Pro Thr Phe Gly Asp Gln Arg Arg Ser Val Gln Ala	931
ttc atc ctc gac cag gaa gcc gac ctg tac ggt cac cat gtc atg gtg	Phe Ile Leu Asp Gln Gln Ala Asp Leu Tyr Gly His Val Met Val	979
gaa ttc gtg gga cac ttg cgc gac atg gtc aaa ttc aac ggc gtc gac	Gln Phe Val Gly His Leu Arg Asp Met Val Lys Phe Asn Gly Val Asp	1027
gag cta cta gac gcc atg gcc cga gat gtc acc aac gcc cgc gac atc	Gln Leu Leu Asp Ala Met Ala Arg Asp Val Thr Asn Ala Arg Asp Ile	1075
ctt gcc aaa gac aaa ttg ctc gac gcc gac acc cag ccc agc gct	Leu Ala Lys Asp Lys Leu Leu Asp Ala Asp Thr Gln Pro Ser Ala	1123
taagccggt caccggcat caa		
<210> 574	<211> 341	<212> PRT
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Ser Val Val Thr Ile Gly Val Phe Asp Gly Leu His Arg Gly His Gln	20	
Ser Leu Ile Gly Gln Ala Lys Lys Gln Ala Gln Gln Leu Gly Val Pro	35	
Cys Val Met Val Thr Phe Asp Pro His Pro Ile Ala Val Phe Leu Pro	50	
Gly Lys Gln Pro Thr Arg Leu Ala Pro Leu Asp Tyr Arg Leu Asn Leu	65	

100 200 300 400 500 600 700 800 900 1000 1100 1200 1300 1400 1500 1600 1700 1800 1900 2000 2100 2200 2300 2400 2500 2600 2700 2800 2900 3000 3100 3200 3300 3400 3500 3600 3700 3800 3900 4000 4100 4200 4300 4400 4500 4600 4700 4800 4900 5000 5100 5200 5300 5400 5500 5600 5700 5800 5900 6000 6100 6200 6300 6400 6500 6600 6700 6800 6900 7000 7100 7200 7300 7400 7500 7600 7700 7800 7900 8000 8100 8200 8300 8400 8500 8600 8700 8800 8900 9000 9100 9200 9300 9400 9500 9600 9700 9800 9900 10000

Ala Ala Glu Cys Gly Val Asp Ala Ala Leu Val Ile Asp Phe Thr Lys 85 90 95

Glu Leu Ala Gly Leu Ser Ala Glu Glu Tyr Phe Thr Met Ile Val 100 105 110

Asp Thr Leu His Ala Arg Ser Val Val Val Gly Glu Asn Phe Thr Phe 115 120 125

Gly Val Asn Gly Ala Gly Thr Glu Ser Thr Met Arg Glu Leu Gly Gln 130 135 140

Lys Phe Gly Val Asn Val Thr Ile Ala Pro Leu Leu His Asp Asp 145 150 155 160

Gln Arg Ile Cys Ser Thr Leu Val Arg Asp Tyr Leu Asp Gln Gly Gln 165 170 175

Val Glu Arg Ala Asn Trp Ala Leu Gly Arg Arg Tyr Ala Val Arg Gly 180 185 190

Glu Val Val Arg Gly Ala Gly Arg Gly Gly Lys Glu Leu Gly Tyr Pro 195 200 205

Thr Ala Asn Leu Tyr Leu Pro Thr Ser Val Ala Leu Pro Ala Asp Gly 210 215 220

Val Tyr Ala Gly Trp Phe Thr Ile Thr Asp Asp Arg Glu Ile Asp Lys 225 230 235 240

Glu Ile Ser Arg Asp Ile Asp Gly Thr Met Val Pro Gly Val Arg Tyr 245 250 255

Gln Thr Ala Ile Ser Val Gly Thr Asn Pro Thr Phe Gly Asp Glu Arg 260 265 270

Arg Ser Val Glu Ala Phe Ile Leu Asp Gln Glu Ala Asp Leu Tyr Gly 275 280 285

His His Val Met Val Glu Phe Val Gly His Leu Arg Asp Met Val Lys 290 295 300

Phe Asn Gly Val Asp Glu Leu Leu Asp Ala Met Ala Arg Asp Val Thr 305 310 315 320

Asn Ala Arg Asp Ile Leu Ala Lys Asp Lys Leu Leu Leu Asp Ala Asp 325 330 335

Thr Gln Pro Ser Ala 340

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<213> Corynebacterium glutamicum

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&lt;223&gt; RXN01712

&lt;400&gt; 575

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Met Val Asp Ile Leu Gln Ile Gly  
5ccc cta cct ttc ttg tct acc cca gag tta agg gca atc gtc ttg act 161  
Pro Leu Pro Phe Val Ser Thr Pro Gln Leu Arg Ala Ile Val Val Thr 25gcc att aat ggt tcc acc act att aat ggc acg tct ggt cag ctt gga 209  
Ala Ile Asn Gly Ser Thr Thr Ile Asn Gly Thr Ser Gly Gln Leu Gly 40aat tcc acc gat acc gaa ctt ctg ttg gcg ctt cgc agg ttg ttg gac 257  
Asn Ser Thr Asp Thr Gln Leu Leu Leu Ala Leu Arg Arg Trp Ser Asp 55gtg gtg ttg ttg gtt ggt tgg agc agc gtg aag gct gaa aat tat ggt ggc 305  
Val Val Leu Val Gly Ser Ser Thr Val Lys Ala Gln Asn Tyr Gly Gly 70gtg gag ggt ttg tgg cct gaa atc cag aag caa cgc cag gag ttg ggt cag 353  
Val Gln Val Ser Pro Gln Ile Gln Lys Gln Arg Gln Gln Leu Gly Gln 85gaa gcg att cgc cgc att gcg gtg atg tca ggg ttg ttg aat ttt gat 401  
Gln Ala Ile Pro Ile Ala Val Met Ser Gly Ser Leu Asn Phe Asp 105gtg gat act cgc ttt ttc ctt gag gcc gaa gtt cgc cgc atc atc atc 449  
Val Asp Thr Arg Phe Phe Leu Gln Ala Gln Val Pro Ile Ile Ile 120acg gat aat tcc gat caa gca aag cag cag cag cgt ctt gtt gat gct ggg 497  
Thr Asp Asn Ser Asp Gln Ala Lys Gln Arg Leu Val Asp Ala Gly 135gct cag gtt att gag gtg gag agt ttg acg gcg gag ggt ggc gtc gaa 545  
Ala Gln Val Ile Gln Val Gln Thr Leu Thr Ala Gln Val Gly Val Gln 150aag ctt agg tct ttg ggt tac gcc cgc att gat tgt gag ggc ggt gca 593  
Lys Leu Arg Ser Leu Gly Tyr Ala Arg Ile Asp Cys Gln Gly Gly Ala 165acg ttg tat ggg cag atg ttg gcc gcc gat ctt gtt gat gtt ttg cat 641  
Thr Leu Tyr Gln Met Leu Ala Ala Asp Leu Val Asp Val Trp His 185cac acc att gat cgc acc ttg ttg agc ttg gag cgc ccc acc gtt 689  
His Thr Ile Asp Pro Thr Leu Ser Gly Ser Val Gln Arg Pro Thr Val 200aag ggc ggc gat gat ggc ccg ccg ccg cga ttc gcg ttg gag cac gtc ttt 737  
Lys Gly Gly Asp Asp Ala Pro Arg Arg Phe Ala Leu Gln His Val Phe 215

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<212> PRT  
<213> Corynebacterium glutamicum

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Ile Asn Gly Thr Ser Gly Glu Leu Gly Asn Ser Thr Asp Thr Glu Leu  
35 40 45  
Leu Leu Ala Leu Arg Arg Trp Ser Asp Val Val Leu Val Gly Ser Ser  
50 55 60  
Thr Val Lys Ala Glu Asn Tyr Gly Gly Val Glu Val Ser Pro Glu Ile  
65 70 75 80  
Gln Lys Gln Arg Gln Glu Leu Gly Gln Glu Ala Ile Pro Pro Ile Ala  
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Glu Ala Glu Val Pro Pro Ile Ile Ile Thr Asp Asn Ser Asp Gln Ala  
115 120 125  
Lys Gln Gln Arg Leu Val Asp Ala Gly Ala Gln Val Ile Glu Val Glu  
130 135 140  
Thr Leu Thr Ala Glu Val Gly Val Glu Lys Leu Arg Ser Leu Gly Tyr  
145 150 155 160  
Ala Arg Ile Asp Cys Glu Gly Gly Ala Thr Leu Tyr Gly Gln Met Leu  
165 170 175  
Ala Ala Asp Leu Val Asp Val Trp His His Thr Ile Asp Pro Thr Leu  
180 185 190  
Ser Gly Ser Val Glu Arg Pro Thr Val Lys Gly Gly Asp Asp Ala Pro  
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Arg Arg Phe Ala Leu Glu His Val Phe Val Asp Asp Ser Thr Leu  
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Phe Leu Arg Tyr Lys Arg Ala Lys  
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<222> (55) ..(555)  
<223> FRXA01712

<400> 577

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105    Lys Ala Glu Asn Tyr Gly Gly Val Glu Val Ser Pro Glu Ile Gln Lys
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caa cgc cag gag ttg ggt cag gaa gcg atc cgc cgc att gcg gtg atg
153    Gln Arg Gln Glu Leu Gly Gln Glu Ala Ile Pro Pro Ile Ala Val Met
      20
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201    Ser Gly Ser Leu Asn Phe Asp Val Asp Thr Arg Phe Phe Leu Glu Ala
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249    Glu Val Pro Pro Ile Ile Ile Thr Asp Asn Ser Asp Gln Ala Lys Gln
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297    Gln Arg Leu Val Asp Ala Gly Ala Gln Val Ile Glu Val Glu Thr Leu
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345    Thr Ala Glu Val Gly Val Glu Lys Leu Arg Ser Leu Gly Tyr Ala Arg
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393    Ile Asp Cys Glu Gly Gly Ala Thr Leu Tyr Gly Gln Met Leu Ala Ala
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      85
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489    Ser Val Glu Arg Pro Thr Val Lys Gly Gly Asp Asp Ala Pro Arg Arg
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<213> Corynebacterium glutamicum  
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 35 40 45  
 Ala Glu Val Pro Ile Ile Thr Asp Asn Ser Asp Glu Ala Lys  
 50 55 60  
 Glu Glu Arg Leu Val Asp Ala Gly Ala Glu Val Ile Glu Val Glu Thr  
 65 70 75 80  
 Leu Thr Ala Glu Val Gly Val Glu Lys Leu Arg Ser Leu Gly Tyr Ala  
 85 90 95  
 Arg Ile Asp Cys Glu Gly Gly Ala Thr Leu Tyr Gly Glu Met Leu Ala  
 100 105 110  
 Ala Asp Leu Val Asp Val Trp His His Thr Ile Asp Pro Thr Leu Ser  
 115 120 125  
 Gly Ser Val Glu Arg Pro Thr Val Lys Gly Gly Asp Asp Ala Pro Arg  
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 Val Thr Arg Arg Leu  
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 Ile Leu Leu Arg His Gly Glu Thr Glu Tyr Asn Ala Thr Ser Arg Met  
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 Glu Gly Glu Leu Asp Thr Glu Leu Ser Asp Leu Gly Phe Glu Ala  
 25 30 35

gac agc gca gcc tca gtc ctg gtc caa aaa aac atc acc cat gtc ttc  
 Ala Ser Ala Ala Ser Val Leu Val Gln Lys Asn Ile Thr His Val Phe  
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 agc tcg gat ctt tcc cgc gcc ttc aac acc gca agc gca gtc gtc ggc  
 Ser Ser Asp Leu Ser Arg Ala Phe Asn Thr Ala Ser Ala Val Ala Ala  
 55 60 65  
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 ctg att gac gcg gag gtc cgc gat aag cgt ctt cgg gaa acg cat  
 Leu Ile Asp Ala Gln Val Arg Val Asp Lys Arg Leu Arg Gln Thr His  
 70 75 80 85  
 403  
 ttg ggt gag tgg cag gcc aaa acc cac act gag gtc gat tcc gaa tat  
 Leu Gln Trp Gln Ala Lys Thr His Thr Gln Val Asp Ser Gln Tyr  
 90 95 100  
 451  
 cca ggt gcg cgc gct caa tgg cgc cac gat cgg cag tgg gca cca ccc  
 Pro Gln Trp Arg His Asp Pro Gln Trp Ala Pro Pro  
 105 110 115  
 499  
 ggc ggc gaa tgc cgc gtc gat gtc ggc cgc cgg gca cgc caa gtc gtc  
 Gly Gly Gln Ser Arg Val Asp Val Ala Arg Arg Arg Gln Val Val  
 120 125 130  
 547  
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 Asp Gln Leu Met Val Ser Leu Asp Asp Trp Asp Gln Gly Thr Val Leu  
 135 140 145  
 595  
 atc gtc gct cac ggt ggc acg att aat ggc ctg acc tcg aat ctt ttg  
 Ile Val Ala His Gly Gly Thr Ile Asn Ala Leu Thr Ser Asn Leu Leu  
 150 155 160 165  
 643  
 gac ctg gcg tat gat cag tac ccc atg ttc tct gga ctt gga aat acc  
 Asp Leu Ala Tyr Asp Gln Tyr Pro Met Phe Ser Gly Leu Gly Asn Thr  
 170 175 180  
 691  
 tgt tgg gca caa ttg acc gcc cga cct cgc tat tat gca ggt agt gag  
 Cys Trp Ala Gln Leu Thr Ala Arg Pro Arg Tyr Tyr Ala Gly Ser Gln  
 185 190 195  
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Ile Thr His Val Phe Ser Ser Asp Leu Ser Arg Ala Phe Asn Thr Ala 50 55 60

Ser Ala Val Ala Ala Leu Ile Asp Ala Gln Val Arg Val Asp Lys Arg 65 70 75 80

Leu Arg Gln Thr His Leu Gly Gln Trp Gln Ala Lys Thr His Thr Gln 85 90 95

Val Asp Ser Ser Gln Tyr Pro Gly Ala Arg Ala Gln Trp Arg His Asp Pro 100 105 110

Gln Trp Ala Pro Pro Gly Gly Gln Ser Arg Val Asp Val Ala Arg Arg 115 120 125

Ala Arg Gln Val Val Asp Gln Leu Met Val Ser Leu Asp Asp Trp Asp 130 135 140

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Tyr Ala Gly Ser Gln Asn Pro Gln Asp Asp Leu Lys Ile Ser Ser Ala 195 200 205

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Glu Pro Tyr Ala Pro Asp Thr Met Val Gln Pro Asp Asp Ile Trp 85 90 95

Phe Tyr Arg Met Pro Ala Ala Gln Arg Pro Ile Pro Tyr Lys Ile His 100 105 110

Val Ile His Gln Asp Asp Ile Leu Val Ile Asp Lys Pro Pro Tyr 115 120 125

Leu Ala Thr Met Pro Arg Gly Arg His Ile Thr Gln Thr Ala Leu Val 130 135 140

Lys Met Arg Val Leu Thr Gly Asn Asn Asp Leu Thr Pro Ala His Arg 145 150 155 160

Leu Asp Arg Leu Thr Ser Gly Val Leu Val Met Val Lys Lys Pro Gln 165 170 175

Leu Arg Gly Ala Tyr Gln Thr Leu Phe Ala Arg Arg Gln Ala Ser Lys 180 185 190

Thr Tyr Gln Ala Ile Ala Gln Phe Val Pro Gly Leu Leu Asp Asp Gly 195 200 205

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Val Thr Pro Val Gln Asp Ala Gln Gln Ser Ile Leu Gln Gln Met His 245 250 255

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Lys Thr His Gln Leu Arg Ile His Met Arg Asp Phe Ala Pro Ile 275 280 285

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Val Trp Pro Ile Ala Ile Ala Leu Ala Met Leu Thr Glu Thr Val Glu 115

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120 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995

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Pro Trp Glu Lys Ala Asn Lys Lys Val Ser Pro Ala Glu Asp Arg Tyr	50	55	60	
Leu Met Thr Val Ile Ala Thr Ala Ser Asn Pro Arg Phe Met Val Ser	65	70	75	80
Arg Val Asp Ile Asp Arg Gly Gly Asp Thr Tyr Thr Ile Asp Thr Leu	85	90	95	
Gln Asp Leu Ser Lys Gln Tyr Pro Asp Ala Gln Leu Tyr Phe Ile Thr	100	105	110	
Gly Ala Asp Ala Leu Ala Gln Ile Val Thr Trp Arg Asp Trp Glu Lys	115	120	125	
Thr Phe Glu Leu Ala His Phe Val Gly Val Thr Arg Pro Gly Tyr Glu	130	135	140	
Leu Asp Gly Asn Ile Ile Pro Glu Met His Gln Asp Arg Val Ser Leu	145	150	155	160
Val Asp Ile Pro Ala Met Ala Ile Ser Ser Thr Asp Cys Arg Glu Arg	165	170	175	
Ser Ser Glu Arg Pro Val Trp Tyr Leu Val				

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 Leu Asp Leu Val Tyr Val Pro Thr Gly Gln Pro Trp Gln Lys Ala 50  
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 Lys Arg Arg Ala Arg Ile Gly Ile Met Gly Gly Thr Phe Asp Pro Ile  
 tgcctcagcaa ggtggtgtgc gaacacata ctgtccactc atg act aca acg gtg  
 Met Thr Thr Val  
 5

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att ccg gaa atg cac caa gat cga gtc tca ttg gtg gat atc ccc gcc  
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Pro Val Trp Tyr Leu Val Pro Asp Gly Val Val Gln Tyr Ile Ala Lys  
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Pro Trp Gln Lys Ala Asn Lys Lys Val Ser Pro Ala Glu Asp Arg Tyr  
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Val Asp Ile Pro Ala Met Ala Ile Ser Ser Thr Asp Cys Arg Glu Arg  
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 307 ggc att gtt gag gag atc gaa gat gag atg acc aag gct ggt ttc gag  
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 Tyr Gly Leu Asp Arg Tyr Arg Asp Cys Pro Leu Ile Gln Ile Gln  
 499 gga ctt gaa acc ttc aag cgt gaa tcc tcc tgg tct gat gag gcg gat  
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 499 gga ctt gaa acc ttc aag cgt gaa tcc tcc tgg tct gat gag gcg gat  
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 Lys Ala Gly Phe Glu Pro Lys Arg Arg Glu Gly Asn Arg Glu Asn Arg  
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1747	gtt ccc ggc ggc cca gtc ggc gag ggt cgt ttc cgt ctg ctg ggc gat	535	Val Pro Gly Ala Pro Val Gly Asp Gly Arg Phe Arg Leu Ala Asp	545
1795	cac ggc ggc gtc caa ggc cgt ttc tgg cag ggc cgc gag atc ggc	550	His Gly Gly Val Gln Gly Ala Arg Gln Ala Arg Gln Ile Ala	560
1843	acc ggc aag gaa gtc ggc ctg atc ttt gtc gat att tcc ggc aac ggc	570	Thr Gly Lys Gln Val Ala Leu Ile Phe Val Asp Thr Ser Gly Asn Ala	580
1891	cca ttt ggc cca ctg tct tcc gca ggc gca ggc ggc ggc atc ggc tac gag	590	Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala Gly Ile Ala Tyr Gln	595
1939	gtg cag cgc cgc acc aag aag ctg ggc agc tgg ggc agc tgg ggc gta	605	Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu Gly Ser Leu Ala Val	610
1987	gcc ccc aac atc cac tcc gag ggc tac cgc aac ggt tgc ctg att gtc	620	Ala Pro Asn Ile His Ser Gln Ala Tyr Arg Asn Gly Cys Leu Ile Val	625
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2083	gcc gat ccc cgc ggc ggc ttc ggc ctg ggc ggc gaa cta act gaa acc	650	Ala Asp Pro Arg Ala Ala Phe Ala Leu Ala Gln Leu Thr Gln Thr	660
2131	atc ggc gag ggc cac gag atg ggt atc cgc ggc ggc ggc tgg gac aac aag	670	Ile Gly Gln Ala His Gln Met Gly Ile Pro Ala Gly Leu Asp Asn Lys	675
2179	tgc cga att cgt atc aac acc gac ggc cat ggc gtc gtc gtc gtc ctg ccg	685	Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala Val Leu Ala Leu Pro	690
2227	gcg att ttg ccc gat gcc tca gag ctg cgc gag ggc aag tcc ctg ggc	700	Ala Ile Leu Pro Asp Ala Ser Gln Leu Arg Asp Ala Lys Ser Leu Ala	705
2275	tcg gcc gcc gcc gag atg ctt atc gag ggc acc ctc gct ccc agc gag gtc	715	Ser Ala Ala Gln Met Leu Ile Asp Ala Thr Leu Ala Pro Ser Asp Val	725
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2419	gag gaa cca acc cac ctt gtg val gaa aag gaa aag aca cca aag cct	Glu Glu Pro Thr His Leu Val Lys Lys Glu Lys Thr Pro Lys Pro	760	765	770
2467	gcg aca cgt gat ggt ttc ggt ggc tcc gac tac acc gtc aag ggc atg	Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr Thr Val Lys Gly Met	775	780	785
2515	gca gcc atc gcc gct gtg atc atc atg gtt tcc ctg gtg gcc gcc	Ala Ala Ile Ala Val Ile Leu Val Ser Leu Val Ala Ala	790	795	800
2563	ggt acc gcg ttc ctc acc agc ttc ttc ggc agc agc acc aac gaa caa	Gly Thr Ala Phe Leu Thr Ser Phe Gly Ser Ser Thr Asn Glu Glu	810	815	820
2611	tcc ccg ttg gcc tct gtt gaa gcc acc acc tct gca aca cca gaa cct	Ser Pro Leu Ala Ser Val Glu Ala Thr Thr Ser Ala Thr Pro Glu Pro	825	830	835
2659	gtg ggg cca ccg gtc tac ctg gat ctg gat cca gcc ccg acg tgg gat	Val Gly Pro Pro Val Tyr Leu Asp Leu Asp Glu Ala Arg Thr Trp Asp	840	845	850
2707	gac ggt gca gga aca gat gtc acc gac gtc acc gac ggc aac acc tcc	Asp Gly Ala Gly Thr Asp Val Thr Asp Val Thr Asp Gly Asn Thr Ser	855	860	865
2755	acc gca tgg acc tcc acc gcc gcc gcc ggc gac ggc cta gtt gac ctg tcc	Thr Ala Trp Thr Ser Thr Gly Gly Asp Gly Leu Leu Val Asp Leu Ser	870	875	880
2803	acg cct gcc gcg ctc gcc gac cgc gac ggc gtc atc ttg acc acc gcc	Thr Pro Ala Arg Leu Asp Arg Val Ile Leu Thr Thr Gly Thr Gly Ser	890	895	900
2851	gac agc aac gac gtc acc tcc acc gtc aag atc tac gca ttc aac gac gcc	Asp Ser Asn Val Thr Ser Thr Val Lys Ile Tyr Ala Phe Asn Asp Ala	905	910	915
2899	tca cca cac tcc ctg tgg gaa ggc atc gag atc ggc acc gtc gat tat	Ser Pro His Ser Leu Ser Glu Gly Ile Glu Ile Gly Thr Val Asp Tyr	920	925	930
2947	tcc ggc cgc agt ctc agc cac agc atc cgc gat tcc tcc aag ctt ccg	Ser Gly Arg Ser Leu Ser His Ser Ile Arg Asp Ser Ser Lys Leu Pro	935	940	945
2995	ggt cag ctg gaa tcc gtg atc ctg gtc gat gag gtt cgt tcc tca	Gly Glu Val Glu Ser Val Ile Leu Val Asp Glu Val Arg Ser Ser	950	955	960
3043	caa acc tca gac acc aat cca cag atg cag atc gct gaa gta caa ctt	Gln Thr Ser Asp Thr Asn Pro Gln Met Gln Ile Ala Glu Val Gln Leu	970	975	980

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Arg Glu Val Phe Lys Pro Gly Ala Trp Ala Pro Val Val Asn Asn Val  
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Pro Tyr Leu Arg Arg Ala Gly Ile Asp Met Arg Pro Leu Trp Gly Ile  
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Asp Ala Arg Leu Lys Gln Phe Gly Gly Met Ala Met Ala Ile Ile Val  
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Tyr Val Ala Ile Ser Gln Phe Gly Tyr Ile Ile Thr Thr Arg Ile Ala  
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Val Val Ser Asp Leu Gln Leu Gly Ser Lys Leu Thr Phe Ile Ala Leu  
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 Gly Leu Phe Ala Tyr Gly Gln Phe Asp Ala Asn Ala Ala Asn Ile Leu 290  
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Gly Ser Leu Ala Val Ala Pro Asn Ile His Ser Gln Ala Tyr Arg Asn  
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Gly Leu Asp Asn Lys Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala  
675 680 685  
Val Leu Ala Leu Pro Ala Ile Leu Pro Asp Ala Ser Gln Leu Arg Asp  
690 695 700  
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Thr Gln Asp Asn Pro Asp Tyr Ala Ser Leu Ala Met Ala Met Arg Thr  
740 745 750  
Cys Gly Leu Phe Thr Gln Gln Pro Thr His Leu Val Val Lys Lys Gln  
755 760 765  
Lys Thr Pro Lys Pro Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr  
770 775 780  
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785 790 795 800  
Ser Leu Val Ala Ala Gly Thr Ala Phe Leu Thr Ser Phe Gly Ser  
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 Tyr Phe Thr Ser Ala Ser Gln Val Arg Val Val Ala Ala Trp Leu Gln 115  
 aaa atc cgc gaa acc cat ccg cat gtg cgc atc gtg gtg gat ccc atc 499



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643	gct ttc gag ctc tcc cac atg gtc gcc tcc gcc gat ccg cgc tcg ctg	Ala Phe Gln Leu Ser His Met Val Gly Ser Gly Asp Pro Arg Ser Leu	170	180
691	ctc ggc ccg ttt gcc gag tgg atc atc atc atc atc acc agc gcc act gaa act	Leu Gly Pro Phe Gly Gln Trp Ile Ile Ile Thr Ser Ala Thr Gln Thr	185	195
739	vtg ggc acc acc gtc acc cgc atc gtc acc cgt gac agc gtc cag gaa	Val Gly Thr Thr Val Thr Arg Ile Val Thr Arg Asp Ser Val Gln Gln	200	210
787	atc gcc tcc gcc acc gtc gat acc acc ggc aaa ggg gca ggc gag gac gtc	Ile Ala Ser Ala Thr Val Asp Thr Thr Ala Lys Gly Ala Gly Asp Val	215	225
835	tac gcc gca gca tta atc gcc gcc gtc cat gaa gat ttt tcg ctt atc	Tyr Ala Ala Ala Leu Ile Ala Leu Ile Ala Leu Ile Phe Ser Leu Ile	230	245
883	gac gcc gcc agc cac gca tcc aac acc gtc tgc gcc ggc ctg cag acc	Asp Ala Ala Ser His Ala Ser Asn Thr Val Cys Ala Gly Leu Thr	250	260
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	Tyr Gly Ser Val Gly Leu Ser Ala Ala Ile Pro Val Met His Asn Gln	35	40	45
	Gly Leu Arg Val Val Ala Val Pro Thr Val Val Leu Ser Ser Met Pro	50	55	60
	Arg Tyr Ala Ser Ser His Arg Gln Pro Met Ser Asp Gln Trp Leu Ala	65	70	80

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 Thr Ile Ser Thr Gly Tyr Phe Thr Ser Ala Ser Gln Val Arg Val Val  
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 Val Val Asp Pro Ile Met Gly Asp Ser Asp Val Gly Ile Tyr Val Ala  
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 Gly Ile Ile Pro Asn Ala Phe Gln Leu Ser His Met Val Gly Ser Gly  
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 180 185 190  
 Ser Ala Thr Gln Thr Val Gly Thr Thr Val Thr Arg Ile Val Thr Arg  
 195 200 205  
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	Pro Ser Thr	Phe Glu Val	Phe Ser	Arg Arg	Leu Pro	Asn Glu	Arg Arg		
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	Tyr Gly	Val Val	Ala Gly	Thr Ala	Arg Val	Leu Lys	Ala Ile	Arg Asp	
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	Arg Thr Leu	Glu Tyr	Leu Arg	Asn Tyr	Arg Phe	Thr Gly	Gln Val	Asp	
451	ggc tac cgc	gaa ggc	gaa atc	tac ttc	cgc cag	tcc cct	ctt cgt	act	115
	Gly Tyr Arg	Glu Glu	Ile Tyr	Phe Pro	Gln Ser	Pro Leu	Leu Thr		
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	Val Arg Gly	Thr Phe	Ala Glu	Cys Val	Ile Leu	Glu Thr	Val Ile	Leu	
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	Ser Ile Met	Asn Ala	Asp Ser	Ala Val	Ala Ser	Ala Ala	Ala Arg	Met	
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	Val Thr Ala	Ala Asp	Gly Arg	Pro Ile	Ile Glu	Met Gly	Ser Arg	Arg	
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	Thr His Glu	Tyr Ser	Ala Val	Thr Ala	Ser Arg	Ala Ala	Tyr Leu	Ala	
691	gga ttc tcc	acc tcc	aac ctc	gag ggc	gag gcc	tac cgc	tac gga	att	190
	Gly Phe Ser	Thr Thr	Ser Asn	Leu Glu	Ala Ala	Tyr Tyr	Arg Gly	Ile	
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	Pro Ala Ser	Gly Thr	Ser Ala	His Ala	Trp Thr	Leu Leu	His Ile	Asn	
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	Asp Asp Gly	Thr Pro	Asn Glu	Ala Ala	Ala Phe	Lys Ala	Gln Val	Glu	
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	Ser Leu Gly	Val Val	Asp Thr	Thr Leu	Val Thr	Tyr Tyr	Asp Ile	Thr	
883	caa ggt gtc	gcc acc	gcc atc	gaa gtt	gca ggt	cca gac	ctt ggt	ggc	255
	Gln Gly	Val Ala	Thr Ala	Ile Glu	Val Ala	Gly Pro	Asp Leu	Gly	
931	gta cgt atc	gac tcc	ggc gac	cta ggt	gtg ctt	gcc cga	aag gtc	cgc	275
	Val Arg Ile	Asp Ser	Gly Asp	Leu Gly	Val Leu	Ala Arg	Lys Val	Arg	

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 Val Pro Gly Leu Pro Thr Leu Glu Asp Ser Arg Ala Tyr Leu Ala Lys  
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 Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu Pro Asn Glu Arg Arg  
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 Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu Lys Ala Ile Arg Asp  
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 Phe Val Phe Thr Glu Gln Ala Asp Leu Asp Phe Leu Asp Asp  
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 Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe Thr Gly Gln Val Asp  
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 ggc tac cgc gaa ggc gaa atc tac ttc ccg cag tcc cct ctt ctg act  
 Gly Tyr Arg Glu Gly 105 110 115  
 Gly Tyr Arg Glu Thr

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547	tcc atc atg aat gca gat tct gcc gtc gct tcc gcc gct gcg cgc atg	Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser Ala Ala Arg Met	135
595	gtc acc gca gct gat ggt cgc ccc atc atc gaa atg gga tcc agg cgc	Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Gln Met Gly Ser Arg Arg	150
643	acc cac gaa tac tcg gca gtc acc gca tcc cgc gca gca tac ctc gct	Thr His Gln Tyr Ser Ala Val Thr Ala Ser Arg Ala Tyr Leu Ala	165
691	gga ttc tcc acc acc tcc aac ctc gag gcg gcc tac cgc tac gga att	Gly Phe Ser Thr Ser Asn Leu Gln Ala Ala Tyr Arg Tyr Gly Ile	180
739	cca gca tcc gga acc tcc gcc cac gca tgg act ttg ctc cac atc aac	Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr Leu His Ile Asn	195
787	gat gac ggc acc ccc aac gaa gca gca gct ttc aaa gca cag gtc gaa	Asp Asp Gly Thr Pro Asn Gln Ala Ala Phe Lys Ala Gln Val Gln	210
835	tcc ctc ggc gtc gac acc acc ttg ctg gta gat act tat gac atc acc	Ser Leu Gly Val Asp Thr Thr Leu Val Asp Thr Tyr Asp Ile Thr	225
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35	Gly Ser Ala Gln Arg Pro Ser Thr Phe Gln Val Phe Ser Arg Arg Leu		45
50	Pro Asn Gln Arg Arg Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu		60
65	Lys Ala Ile Arg Asp Phe Val Phe Thr Gln Gln Leu Ala Asp Leu		75
85	Asp Phe Leu Asp Asp Arg Thr Leu Gln Tyr Leu Arg Asn Tyr Arg Phe		95

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336	gat act gga aag ctc gac act ttc agc ctc acc atc cca ttc atg cgc	110	Asp Thr Gly Lys Leu Asp Thr Leu Ser Leu Thr Ile Pro Leu Met Arg	110
384	gac ggt gaa atc gtc cca ggt ttc cct act ttc gaa gat tcc cga gcg	125	Asp Gly Glu Ile Val Pro Gly Leu Pro Thr Leu Glu Asp Ser Arg Ala	125
432	tat ttc ggc aag caa ttc gtc tct tta cca tgg gaa ggc ctt gca ctg	140	Tyr Leu Ala Lys Glu Leu Val Ser Leu Pro Trp Glu Gly Leu Ala Leu	140
480	tct cgc gat gag cct gtc ttc cac act cgt ttc gtc ggt ttc ccg ccg	155	Ser Arg Asp Glu Pro Val Leu His Thr Arg Phe Val Gly Phe Pro Pro	160
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	Ala Ala			
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	Ile Gly Glu Val Ala Gly His Pro Val Ala Lys Arg Ser Arg Asn Lys	50		
	Glu Ser Tyr Gly Gly Gly Lys Lys Ala Val Arg Thr His Arg Lys Ser	65		
	Gly Thr Ala Ile Glu Ile Val Tyr Pro Phe Asn Ala Glu Ala Pro	85		
	Asp Thr Gly Lys Leu Asp Thr Leu Ser Leu Thr Ile Pro Leu Met Arg	100		
	Asp Gly Glu Ile Val Pro Gly Leu Pro Thr Leu Glu Asp Ser Arg Ala	115		
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	Tyr Leu Ala Lys Glu Leu Val Ser Leu Pro Trp Glu Gly Leu Ala Leu	135		
	Tyr Leu Ala Lys Glu Leu Val Ser Leu Pro Trp Glu Gly Leu Ala Leu	140		
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Val Val Ala Arg Glu Pro Gly Val Phe Ser Gly Gln Ala Leu Asp  
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Ala Ser Phe Arg Leu Val Asp Pro Arg Ile Asn Ala Ser Leu Lys Val  
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Pro Gly Leu Arg Ile Ile Glu Arg Gln Ala Val Arg Asp Gly Gly  
135 140 145





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403	gtg gtt	atc cta	gga cac	tac ttc	cag cgc	gat gaa	gtc atc	caa cac	Val Val Ile	90	Gly	Val Ile	Gln His
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547	gaa acc	gct gat	ctg tta	tcc acc	gat gaa	caa tca	gtg atc	ctc ccc	Val Ile Leu	135	Gln	Thr Ala	Pro
595	aac ctt	gcc gca	ggt tgc	tcc atg	gca gat	atg gac	gtc gat	ctt gat	ctc	155	Asn	Leu Ala	Ser
643	gtc gaa	gac tgc	tgg ggg	caa ctc	acc tca	att tta	tat ggc	gat gac	acc	170	Val	Gln Asp	Thr
691	ctg atc	cct gtt	acc tac	atg aat	tcc tct	gca ggc	ctc aaa	ggt ttc	ctc	185	Leu	Ile Pro	Phe
739	gtg ggt	gag cac	ggc gga	att gta	tgc acc	tcc tca	aat gca	cgt tcc	ctc	200	Val	Gly Gln	Arg Ser
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835	gat cag	cac ttg	ggt cga	aac acc	gca aaa	gcc atg	ggc att	ggg atc	atc	235	Asp	Gln His	Ile
883	gat caa	atg ccc	ctg tgg	aat ccc	aac aaa	cca ctg	ggc aac	acc acc	acc	250	Asp	Gln Met	Thr
931	gtt tcc	gag cta	gaa aac	gca aag	gta ctg	ctc tgg	cat ggt	tgc tgc	ctc	265	Val	Ser Gln	Cys

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 979 Ser Val His Lys Arg phe Thr Val Gln Ile Asn Lys Ala Arg Ala  
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 1123 Ala Ile Gln Ala Ala Pro Ala Gly Ser Thr phe Ala Ile Gly Thr Gln  
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 Arg Ala Ser Asp Asp Gln Leu His Arg Arg Ile Arg Gln Ala Lys Asp  
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Lys Gln Val Gln Phe Arg Val Gln Phe Leu Val Asp Tyr Leu Arg Ala 35

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Ser His Thr Lys Gly Phe Val Leu Gly Ile Ser Gly Gln Asp Ser 50

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Thr Leu Ala Gly Arg Leu Thr Gln Leu Ala Val Gln Arg Ile Arg Ala 65

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Ala Pro Asp Lys Ser Val Thr Val Asn Val Lys Asp Ala Thr Asp Ala 115

acc gaa gca act gtt gca gct gct ttg gaa ctt cct gag ctg acc gac 499  
Thr Gln Ala Thr Val Ala Ala Leu Gln Leu Pro Gln Leu Thr Asp 130

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Phe Asn Arg Gly Asn Ile Lys Ala Arg Gln Arg Met Val Ala Gln Tyr 145

gca atc gca ggc cag ttg ggc ttg ctg gtt att ggc act gat cac gcg 595



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 Ala Gln Asn Val Thr Gly Phe Phe Thr Lys Phe Gly Asp Gly Ala Ala 180  
 gac ctg ctt cct ttg gca ggt ttg agc aag cgt caa gga gct gcc att 691  
 Asp Leu Leu Pro Leu Ala Gly Leu Ser Lys Arg Gln Gly Ala Ala Ile 195  
 ctg gag cac ctg ggt gca cct tca agc acg tgg acc aag gtt cct acc 739  
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 Ala Asp Leu Gln Asp Arg Pro Ala Leu Pro Asp Gln Gln Ala Leu 225  
 ggt ttg tgg tat gcg gac atc gat aat tac ctg gaa aac aag ccc gat 835  
 Gly Val Ser Tyr Ala Asp Ile Asp Asn Tyr Leu Gln Asn Lys Pro Asp 245  
 gtc agt gaa aaa gcc cag cag cgc att gag cac ctg tgg aag ttg ggc 883  
 Val Ser Gln Lys Ala Gln Gln Arg Ile Gln His Leu Trp Lys Val Gly 260  
 cag cac aag cgc cac ctg cct gct acc cgg cag gaa aat tgg tgg cgt 931  
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 Gly Gly Gln Asp Ser Thr Leu Ala Gly Arg Leu Thr Gln Leu Ala Val 50  
 Gln Arg Ile Arg Ala Gln Gln Asn Ser Thr Asp Tyr Val Phe Tyr Ala 65  
 Val Arg Leu Pro Tyr Ala Ile Gln Ala Asp Asp Asp Ala Gln Val 85  
 Ala Leu Gln Phe Ile Ala Pro Asp Lys Ser Val Thr Val Asn Val Lys 100  
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1027 tcc gac ctg gat gaa tcc gcc atc gcc ggt ctt cgc ggc gaa cca gtt  
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 1123 acc gct ggc ctc gtg tac aag atc ggg gaa gtt gcc ggt cac cct gtg  
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 335  
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 1171 ggc aag cgt tcc cga aac aag gaa agc tac ggt ggt ggc aag aag gct  
 Ala Lys Arg Ser Arg Asn Lys Gln Ser Tyr Gly Gly Lys Lys Ala  
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 1219 gtg cgc acc ccc cac cgc aag tcc ggt acc gca atc gaa gaa atc gtc tac  
 Val Arg Thr His Arg Lys Ser Gly Thr Ala Ile Gln Ile Val Tyr  
 360  
 365  
 370  
 1267 cca ttc aat gcc gaa gca cca gat act gga aag ctc gac act ttg agc  
 Pro Phe Asn Ala Gln Ala Pro Asp Thr Gly Lys Leu Asp Thr Leu Ser  
 375  
 380  
 385  
 1315 ctg acc atc cca ttg atg cgc gac ggt gaa atc gtt cca ggt ttg cct  
 Leu Thr Ile Pro Leu Met Arg Asp Gly Gln Ile Val Pro Gly Leu Pro  
 390  
 395  
 400  
 405  
 1363 act ttg gaa gat tcc cga gcg tat ttg gcc aag caa ttg gtc tct tta  
 Thr Leu Gln Asp Ser Arg Ala Tyr Leu Ala Lys Gln Leu Val Ser Leu  
 410  
 415  
 420  
 1411 cca tgg gaa ggc ctt gca ctg tct cgc gat gag cct gtt ttg cac act  
 Pro Trp Gln Gly Leu Ala Leu Ser Arg Asp Gln Pro Val Leu His Thr  
 425  
 430  
 435  
 1458 cgt ttc gtg ggt ttc ccg ccg gcc gct tagacaattc ggtctcacca  
 Arg Phe Val Gly Phe Pro Ala Ala  
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 aac  
 1461

<210> 610  
 <211> 446  
 <212> PRT  
 <213> Corynebacterium glutamicum  
 <400> 610  
 Val Asn Thr Asn Pro Ser Gln Phe Ser Ser Asn Arg Ser Thr Ala Leu  
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 Leu Thr Asp Lys Tyr Gln Leu Thr Met Leu Gln Ala Leu Ala Asp  
 20  
 25  
 30  
 Gly Ser Ala Gln Arg Pro Ser Thr Phe Gln Val Phe Ser Arg Arg Leu  
 35  
 40  
 45  
 Pro Asn Gln Arg Arg Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu  
 50  
 55  
 60

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Lys Ala Ile Arg Asp Phe Val Phe Thr Gln Gln Leu Ala Asp Leu	65
Asp Phe Leu Asp Asp Arg Thr Leu Gln Tyr Leu Arg Asn Tyr Arg Phe	85
Thr Gly Gln Val Asp Gly Tyr Arg Gln Gly Gln Ile Tyr Phe Pro Gln	100
Ser Pro Leu Leu Thr Val Arg Gly Thr Phe Ala Gln Cys Val Ile Leu	115
Glu Thr Val Ile Leu Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser	130
Ala Ala Tyr Leu Ala Gly Phe Ser Thr Thr Ser Asn Leu Gln Ala Ala	180
Tyr Arg Tyr Gly Ile Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr	195
Leu Leu His Ile Asn Asp Asp Gly Thr Pro Asn Gln Ala Ala Phe	210
Lys Ala Gln Val Gln Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp	225
Thr Tyr Asp Ile Thr Gln Gly Val Ala Thr Ala Ile Gln Val Ala Gly	245
Pro Asp Leu Gly Gly Val Arg Ile Asp Ser Gly Asp Leu Gly Val Leu	260
Ala Arg Lys Val Arg Lys Gln Leu Asp Asp Leu Asn Ala His Asn Thr	275
Lys Ile Val Val Ser Ser Asp Leu Asp Gln Phe Ala Ile Ala Gly Leu	290
Arg Gly Gln Pro Val Asp Val Phe Gly Val Gly Thr Ser Val Val Thr	305
Gly Ser Gly Ala Pro Thr Ala Gly Leu Val Tyr Lys Ile Gly Gln Val	325
Ala Gly His Pro Val Ala Lys Arg Ser Arg Asn Lys Gln Ser Tyr Gly	340
Gly Gly Lys Lys Ala Val Arg Thr His Arg Lys Ser Gly Thr Ala Ile	355
Gln Gln Ile Val Tyr Pro Phe Asn Ala Gln Ala Pro Asp Thr Gly Lys	370
	380

Leu Asp Thr Leu Ser Leu Thr Ile Pro Leu Met Arg Asp Gly Glu Ile 385  
 Val Pro Gly Leu Pro Thr Leu Glu Asp Ser Arg Ala Tyr Leu Ala Lys 405  
 Gln Leu Val Ser Leu Pro Trp Glu Gly Leu Ala Leu Ser Arg Asp Glu 420  
 Pro Val Leu His Thr Arg Phe Val Gly Phe Pro Pro Ala Ala 435  
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 <213> Corynebacterium glutamicum

<220>  
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 <223> RXA02299

<400> 611  
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taaaacttgc aggaacaacc ccataagagc accacagagac atg ctg cgc acc atc 115  
 Met Leu Arg Thr Ile 1  
 5

ctc gga agt aag att cac cga gcc act gtc act caa gct gat cta gat 163  
 Leu Gly Ser Lys Ile His Arg Ala Thr Val Thr Gln Ala Asp Leu Asp 20

tat gtt ggc tct gta acc atc gac gcc gac ctg gtt cac gcc ggc gga 211  
 Tyr Val Gly Ser Val Thr Ile Asp Ala Asp Leu Val His Ala Gly 35

ttg atc gaa ggc gaa aaa gtt gcc atc gta gac atc acc aac ggc gct 259  
 Leu Ile Glu Gly Glu Lys Val Ala Ile Val Asp Ile Thr Asn Gly Ala 50

cgt ctg gaa act tat gtc atc gtc ggc gac gcc gga acg ggc aat atc 307  
 Arg Leu Glu Thr Tyr Val Ile Val Gly Asp Ala Gly Thr Gly Asn Ile 65

tgc atc aat ggt gcc gct gca cac ctg atc atc aat cct ggc gat ctg 355  
 Cys Ile Asn Gly Ala Ala His Leu Ile Asn Pro Gly Asp Leu Val 85

atc atc atg agc tac ctc cag gca act gat ggc gaa gcc aag ggc tat 403  
 Ile Ile Met Ser Tyr Leu Gln Ala Thr Asp Ala Glu Ala Lys Ala Tyr 100

gag cca aag att gtc cac gtc gac gcc gac aac cgc atc gtc ggc ctg 451  
 Glu Pro Lys Ile Val His Val Asp Ala Asp Asn Arg Ile Val Ala Leu 115

ggc aac gat ctc gcg gaa gca cta cct gga tcc ggg ctt ttg acg tgc 499  
 Gly Asn Asp Leu Ala Glu Ala Leu Pro Gly Ser Gly Leu Thr Ser 130

aga agc att tagcgttta gctcgccaat att  
Arg Ser Ile  
135

<210> 612  
<211> 136  
<212> PRT  
<213> Corynebacterium glutamicum  
<400> 612  
Met Leu Arg Thr Ile Leu Gly Ser Lys Ile His Arg Ala Thr Val Thr  
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Gln Ala Asp Leu Asp Tyr Val Gly Ser Val Thr Ile Asp Ala Asp Leu

Val His Ala Ala Gly Leu Ile Gln Gly Gln Lys Val Ala Ile Val Asp  
35  
40  
45  
Ile Thr Asn Gly Ala Arg Leu Gln Thr Tyr Val Ile Val Gly Asp Ala  
50  
55  
60  
Gly Thr Gly Asn Ile Cys Ile Asn Gly Ala Ala His Leu Ile Asn  
65  
70  
75  
80  
Pro Gly Asp Leu Val Ile Ile Met Ser Tyr Leu Gln Ala Thr Asp Ala  
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90  
95  
Gln Ala Lys Ala Tyr Gln Pro Lys Ile Val His Val Asp Ala Asp Asn  
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105  
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Arg Ile Val Ala Leu Gly Asn Asp Leu Ala Gln Ala Leu Pro Gly Ser  
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Gly Leu Leu Thr Ser Arg Ser Ile  
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<210> 613  
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<212> DNA  
<213> Corynebacterium glutamicum

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<222> (101) .. (937)  
<223> RXA01928

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tccacgcgagg taccttccca ggcgaagcgg agtcccttta atg cag gta gca acc 115  
Met Gln Val Ala Thr  
1  
5  
163  
aca aag cag gcg ctt atc gac gcc ctc ctc cac cac aaa tcc gtc ggg  
Thr Lys Gln Ala Leu Ile Asp Ala Leu Leu His His Lys Ser Val Gly  
10  
15  
20

211	ctc gtc ccc acc atg ggt gcg cta cac agc gga cac gcc tgc tgc gtc	Leu Val Pro Thr Met Gly Ala Leu His Ser Gly His Ala Ser Leu Val	25	30	35
259	aaa gca gca cgc gct gaa aac gac act gtt gta gcc agt att ttt gtc	Lys Ala Ala Arg Ala Gln Asn Asp Thr Val Val Ala Ser Ile Phe Val	40	45	50
307	aat ccc ctc cag ttg gaa gca ctc ggt gat tgc gat gaa asp tyr arg asn	Asn Pro Leu Gln Phe Gln Ala Leu Gly Asp Cys Asp Tyr Arg Asn	55	60	65
355	tat ccc cgc caa ctc gac gcc gat tta gca ctg ctt gaa gag gca ggt	Tyr Pro Arg Gln Leu Asp Ala Leu Ala Leu Gln Gln Ala Gly	70	75	80
403	gtg gat att gtc ttc gca ccc gat gtc gag gaa atg tac ccc ggt ggc	Val Asp Ile Val Phe Ala Pro Asp Val Gln Met Tyr Pro Gly Gly	90	95	100
451	ttg cca cta gtc tgg gcg cgc acc ggt tcc atc gga aca aaa tgc gag	Leu Pro Leu Val Trp Ala Arg Thr Gly Ser Ile Gly Thr Lys Leu Gln	105	110	115
499	ggt gcc agc agc agt cct ggc cat ttc gat ggt gtc gct acc gtc gtc	Gly Ala Ser Arg Pro Gly His Phe Asp Gly Val Ala Thr Val Val Ala	120	125	130
547	aag ctg ttc aat ttg gtc cgc cct gat cgt gca tat ttc gga caa aaa	Lys Leu Phe Asn Leu Val Arg Pro Asp Arg Ala Tyr Phe Gly Gln Lys	135	140	145
595	gat gct cag cag cag gtc gtc gtc gtc gtc gtc gtc gtc gtc gtc gtc	Asp Ala Gln Gln Val Ala Val Ile Arg Arg Leu Val Ala Asp Leu Asp	150	155	160
643	att ccc gtc gag att cgt ccc gtt ccg att att cgt ggc ggc gat ggc	Ile Pro Val Gln Ile Arg Pro Val Pro Ile Ile Arg Gly Ala Asp Gly	170	175	180
691	tta gcc gaa tcc agc cgc aat caa cgt ctt tct ggc gat cag cga ggc	Leu Ala Gln Ser Ser Arg Asn Gln Arg Leu Ser Ala Asp Gln Arg Ala	185	190	195
739	caa gct ctc gtc gtc ctc cag gtc gtc gtc gtc gtc gtc gtc gtc gtc	Gln Ala Leu Val Leu Pro Gln Val Leu Ser Gly Leu Gln Arg Arg Lys	200	205	210
787	gca gct ggt gaa gcg cta gat atc caa ggt gcg cgc gac acc tgc ggc	Ala Ala Gly Gln Ala Leu Asp Ile Gln Gly Ala Arg Asp Thr Leu Ala	215	220	225
835	agc gcc gac gac gtc gtc gtc gtc gtc gtc gtc gtc gtc gtc gtc gtc	Ser Ala Asp Gly Val Arg Leu Asp His Leu Gln Ile Val Asp Pro Ala	235	240	245
883	acc ctc gaa cca tta gaa atc gac ggc ctg ctc acc caa cca ggc tgc	Thr Leu Gln Pro Leu Gln Ile Asp Gly Leu Leu Thr Gln Pro Ala Leu	250	255	260
931	gtg gtc ggc ggc ggc att ttc gtc ggc cgc gtc gtc gtc gtc gtc gtc				



Val Val Gly Ala Ile Phe Val Gly Pro Val Arg Leu Ile Asp Asn Ile  
265 270 275

gag ctc tagtaccac cctgcgttc agc

Glu Leu

<210> 614

<211> 279

<212> PRT

<213> Corynebacterium glutamicum

<400> 614

Met Gln Val Ala Thr Thr Lys Gln Ala Leu Ile Asp Ala Leu His  
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His Lys Ser Val Gly Leu Val Pro Thr Met Gly Ala Leu His Ser Gly  
20 25 30

His Ala Ser Leu Val Lys Ala Ala Arg Ala Gln Asn Asp Thr Val Val  
35 40 45

Ala Ser Ile Phe Val Asn Pro Leu Gln Phe Gln Ala Leu Gly Asp Cys  
50 55 60

Asp Asp Tyr Arg Asn Tyr Pro Arg Gln Leu Asp Ala Asp Leu Ala Leu  
65 70 75 80

Leu Gln Gln Ala Gly Val Asp Ile Val Phe Ala Pro Asp Val Gln Gln  
85 90 95

Met Tyr Pro Gly Gly Leu Pro Leu Val Trp Ala Arg Thr Gly Ser Ile  
100 105 110

Gly Thr Lys Leu Gln Gly Ala Ser Arg Pro Gly His Phe Asp Gly Val  
115 120 125

Ala Thr Val Val Ala Lys Leu Phe Asn Leu Val Arg Pro Asp Arg Ala  
130 135 140

Tyr Phe Gly Gln Lys Asp Ala Gln Gln Val Ala Val Ile Arg Arg Leu  
145 150 155 160

Val Ala Asp Leu Asp Ile Pro Val Gln Ile Arg Pro Val Pro Ile Ile  
165 170 175

Arg Gly Ala Asp Gly Leu Ala Gln Ser Ser Arg Asn Gln Arg Leu Ser  
180 185 190

Ala Asp Gln Arg Ala Gln Ala Leu Val Leu Pro Gln Val Leu Ser Gly  
195 200 205

Leu Gln Arg Arg Lys Ala Ala Gly Gln Ala Leu Asp Ile Gln Gly Ala  
210 215 220

Arg Asp Thr Leu Ala Ser Ala Asp Gly Val Arg Leu Asp His Leu Gln  
225 230 235 240

Ile Val Asp Pro Ala Thr Leu Gln Pro Leu Gln Ile Asp Gly Leu Leu  
245 250 255

60 aaaaatttgac tccataacga gaacttaac gagcaacacc cctgaacagt gaatcaaatc  
 115 ggaaatttat tattctgagc tggcatcac atctatactc atg ccc atg tca ggc  
 Met Pro Met Ser Gly  
 1  
 163 att gat gca aag aaa atc cgc acc cgt cat ttc cgc gaa gct aaa gta  
 Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe Arg Gln Ala Lys Val  
 20  
 211 aac ggc cag aaa gtt tcg gtt ctc acc agc tat gat ggc ctt tcg ggc  
 Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala Leu Ser Ala  
 35  
 259 cgc att ttt gat gag gct ggc gtc gat atg ctc ctt gtt ggt gat tcc  
 Arg Ile Phe Asp Gln Ala Gly Val Asp Met Leu Leu Val Gly Asp Ser  
 50  
 307 gct gcc aac gtt gtt gtt gtt ggt ggc ggt gat acc acc acc ttt  
 Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser Ile Thr Leu  
 65  
 355 gat gag atg att gtt gtt gtc ggc aag ggc gtt gtt gtt gtt gtt gtt  
 Asp Gln Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala Thr Lys Arg  
 85  
 403 gcg ctt gtt gtt gtt gtt gtt gat ctt gtt gtt gtt gtt gtt gtt  
 Ala Leu Val Val Val Val Val Val Val Val Val Val Val Val Val  
 100  
 451 aat cag ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc  
 Asn Gln Ala Val Val Ser Ala Ile Arg Val Met Arg Gln Thr Gly Ala  
 115  
 499 gct ggc gtt aag atc gag ggt ggc gtt gag atc ggc ggc ggc ggc  
 Ala Ala Val Lys Ile Gln Gly Val Gln Ile Ala Gln Thr Ile Arg  
 130  
 547 cgc att gtt gat gct gga att cgc ggt gtc ggc cac atc ggc tac acc  
 Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly His Ile Gly Tyr Thr  
 145

<210> 615  
 <211> 936  
 <212> DNA  
 <213> Corynebacterium glutamicum  
 <220>  
 <221> CDS  
 <222> (101)..(913)  
 <223> RXN01929  
 <400> 615

Leu Ile Asp Asn Ile Gln Leu  
 275  
 Thr Gln Pro Ala Leu Val Val Gly Ala Ile Phe Val Gly Pro Val Arg  
 260  
 270



Arg Gln Thr Gly Ala Ala Val Lys Ile Gln Gly Val Gln Ile 115  
 120  
 125  
 Ala Gln Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly 130  
 135  
 His Ile Gly Tyr Thr Pro Gln Ser Gln His Ser Leu Gly Gly His Val 145  
 150  
 155  
 Val Gln Gly Arg Gly Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg 165  
 170  
 175  
 Ala Leu Gln Gln Ala Gly Ala Phe Ala Val Val Leu Gln Met Val Pro 180  
 185  
 Ala Gln Ala Ala Arg Gln Val Thr Gln Asp Leu Ser Ile Thr Ile 195  
 200  
 205  
 Gly Ile Gly Ala Gly Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln 210  
 215  
 Asp Ala Phe Gly Leu Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Gln 225  
 230  
 Tyr Ala Thr Leu Gly Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile 245  
 250  
 255  
 Ala Asp Ile His Ala Gly Thr Phe Pro Gly Gln Ala Gln Ser Phe 260  
 265  
 270

<210> 617  
 <211> 930  
 <212> DNA  
 <213> Corynebacterium glutamicum  
 <220>  
 <221> CDS  
 <222> (101)..(907)  
 <223> FRXA01929  
 <400> 617  
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 115 tattattct gactgtgtca tcacatctat actcatgccc atg tca ggc att gat  
 Met Ser Gly Ile Asp  
 1  
 5  
 gca aag aaa atc cgc acc cgt cat ttc cgc gaa gct aaa gta aac ggc  
 10  
 15  
 20  
 Ala Lys Lys Ile Arg Thr Arg His Phe Arg Gln Ala Lys Val Asn Gly  
 25  
 30  
 35  
 cag aaa gtc tcg gtc acc agc tat gat ggc ctt tcg ggc cgc att  
 Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala Leu Ser Ala Arg Ile  
 40  
 45  
 50  
 ttt gat gag gct ggc gtc gat atg ctc ctt gtt ggt gat tcc gct gcc  
 Phe Asp Gln Ala Gly Val Asp Met Leu Leu Val Gly Asp Ser Ala Ala

<210> 618  
<211> 269  
<212> PRT  
<213> Corynebacterium glutamicum

&lt;400&gt; 618

Met Ser Gly Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe Arg Gln

Ala Lys Val Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala

Leu Ser Ala Arg Ile Phe Asp Gln Ala Gly Val Asp Met Leu Val

Gly Asp Ser Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser

Ile Thr Leu Asp Asp Gln Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala

Thr Lys Arg Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr Tyr Gln

Val Ser Pro Asn Gln Ala Val Gln Ser Ala Ile Arg Val Met Arg Gln

Thr Gly Ala Ala Val Lys Ile Gln Gly Gly Val Gln Ile Ala Gln

Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly His Ile

Gly Tyr Thr Pro Gln Ser Gln His Ser Leu Gly Gly His Val Val Gln

Gly Arg Gly Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu

Gln Gln Ala Gly Ala Phe Ala Val Val Leu Gln Met Val Pro Ala Gln

Ala Ala Arg Gln Val Thr Gln Asp Leu Ser Ile Thr Thr Ile Gly Ile

Gly Ala Gly Asn Gly Thr Asp Gly Gln Val Val Leu Val Trp Gln Asp Ala

Phe Gly Leu Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Gln Tyr Ala

Thr Leu Gly Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp

Ile His Ala Gly Thr Phe Pro Gly Gln Ala Gln Ser Phe

&lt;210&gt; 619

&lt;211&gt; 921

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

BGI-121CP

<222> (101) . . (898)  
<223> RXA01521

<400> 619

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115	cgcagaatat	tgagctgtg	gcaatcaga	agagagacg	tgaagt	ctc acg cat
					1	5
						Leu Ser Phe Thr His

ggt cag ggc aga gtt ttt gat acc gtc gag cag atc cgc atg ttc ggc 163  
gln gln gly arg val phe asp thr val gln gln ile arg met phe gly 20

agc gcc ctg cgc aaa acc ggc aaa cca gtg gta ctc gta ccc ttg gga  
Ser Ala Leu Arg Lys Thr Gly Lys Pro Val Val Leu Val Pro Leu Gly

25 30 35

211

aat ggc ctc cac gca ggc cat atc ggc ctc atc cgc gca gca aaa cgc 259  
Asn Gly Leu His Ala Gly His Ile Ala Leu Ile Arg Ala Ala Lys Arg 50  
45

[illegible]

cac gca cgt tta agg gaa gag ctt atc gac gcg atc ttc ccg ttc aat 355  
 His Ala Arg Leu Arg Glu Glu Ile Asp Ala Ile Phe Pro Phe Asn 70  
 80 85

ccc gaa acg cta tgg cct cac ggc atc cgg gtg gaa gtc aca ggt ggc  
Pro Glu Thr Leu Trp Pro His Gly Ile Arg Val Glu Val Thr Gly Gly

90                      95                      100

403

451 cca aca ctt acc cca caa ggt gcg gaa gta acc aag gtc ctc ggc ggc ctc  
Pro Thr Leu Thr Pro Gln Gly Ala Gln Val Thr Lys Val Leu Gly Leu 115

499	ctg gga atc acc gga gca act gat gtc gtc gtc ggc gaa aag gac tat	120	Leu Gly Ile Thr Gly Ala Thr Asp Val Val Leu Gly Gln Lys Asp Tyr
		125	
		130	

54 / gag cgg ggc Val Leu Val Val Leu Val Gln Gln Arg Ala Leu Asn Asp Leu His Ile Pro  
135  
140  
145

gca aaa cgg cat ccc gcc cca acc ggc cgc acg cca gat gga cta gcc  
Val Lys Leu His Ser Val Pro Thr Val Arg Met Pro Asp Gly Leu Ala  
150 155 160 165

175 180

Year	1985	1990	1995
Leu Ser Leu Ala Ala Ala Leu Thr Ala Gly Ala His Ser Ala Glu His	185	190	195

210 205 200

gag gtc acc ccc gat tat gta gaa atc cgt ggc ctg gat ctt gga cca  
 Gly Val Thr Pro Asp Tyr Val Gln Ile Arg Gly Leu Asp Leu Gly Pro  
 215 220 225  
 ggc ccc gaa atc gga gac gcc cga ctc ttc gca gcc atc acg ctt ggc  
 Ala Pro Gln Ile Gly Asp Ala Arg Leu phe Ala Ile Thr Leu Gly  
 230 235 240 245  
 gat gtc caa ctc cac gac aac gtc ggc cta ccc ctt gga atc ggc ttc  
 Asp Val Gln Leu His Asp Asn Val Gly Leu Pro Leu Gly Ile Gly Phe  
 250 255 260  
 aaa aac atc gaa ggc tgcacccggt ttaccagtt cgc  
 Lys Asn Ile Gln Gly  
 265

<210> 620  
 <211> 266  
 <212> PRT  
 <213> Corynebacterium glutamicum  
 <400> 620

Leu Ser Phe Thr His Gly Gln Gly Arg Val Phe Asp Thr Val Gln Gln  
 1 5 10 15  
 Ile Arg Met Phe Gly Ser Ala Leu Arg Lys Thr Gly Lys Pro Val Val  
 20 25  
 Leu Val Pro Leu Gly Asn Gly Leu His Ala Gly His Ile Ala Leu Ile  
 35 40 45  
 Arg Ala Ala Lys Arg Ile Pro Gly Ala Val Val Val Ala Tyr Ala  
 50 55 60  
 Gly Pro Gln Ser Asp His Ala Arg Leu Arg Gln Gln Leu Ile Asp Ala  
 65 70 75 80  
 Ile Phe Pro Phe Asn Pro Gln Thr Leu Trp Pro His Gly Ile Arg Val  
 85 90 95  
 Gln Val Thr Gly Gly Pro Thr Leu Thr Pro Gln Gly Ala Gln Val Thr  
 100 105 110  
 Lys Val Leu Gly Leu Leu Gly Ile Thr Gly Ala Thr Asp Val Val Leu  
 115 120 125  
 Gly Gln Lys Asp Tyr Gln Leu Val Val Leu Val Gln Arg Ala Leu Asn  
 130 135 140  
 Asp Leu His Ile Pro Val Lys Leu His Ser Val Pro Thr Val Arg Met  
 145 150 155 160  
 Pro Asp Gly Leu Ala Ile Ser Leu Arg Asn Ile Ser Val Pro Gln Asp  
 165 170 175  
 Ser Arg Gln Thr Ala Leu Ser Leu Ala Ala Leu Thr Ala Gly Ala  
 180 185 190  
 His Ser Ala Gln His Gly Ala Val Val Lys Gln Thr Val Thr Gln



195 200 205

Val Leu Lys Ala Ala Gly Val Thr Pro Asp Tyr Val Gln Ile Arg Gly  
210 215 220

Leu Asp Leu Gly Pro Ala Pro Gln Ile Gly Asp Ala Arg Leu Phe Ala  
225 230 235 240

Ala Ile Thr Leu Gly Asp Val Gln Leu His Asp Asn Val Gly Leu Pro  
245 250 255

Leu Gly Ile Gly Phe Lys Asn Ile Gln Gly  
260 265

<210> 621  
<211> 1137  
<212> DNA  
<213> *Corynebacterium glutamicum*  
<220>  
<221> CDS  
<222> (101)..(1114)  
<223> RXS01145  
<400> 621

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ctttccacca aattttac gaaggcgag attttctccc atg gct att gaa ctg 115  
Met Ala Ile Gln Leu 5

ctt tat gat gct gac gct gac ctc tcc ttg atc cag ggc cgt aag gtt 163  
Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gly Arg Lys Val 20

gcc atc gtt ggc tac ggc tcc cag ggc cac gca cac tcc cag aac ctg 211  
Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala His Ser Gln Asn Leu 35

cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag 259  
Arg Asp Ser Gly Val Gln Val Ile Gly Leu Arg Gln Gly Ser Lys 50

tcc gca gag aag gca aag gaa gca ggc ttc gag gtc aag acc acc gct 307  
Ser Ala Gln Lys Ala Lys Gln Ala Gly Phe Gln Val Lys Thr Thr Ala 65

gag gct gca gct tgg gct gac gtc atc atg ctc ctg gct cca gac acc 355  
Gln Ala Ala Ala Trp Ala Asp Val Ile Met Leu Leu Ala Pro Asp Thr 85

tcc cag gca gaa atc ttc acc aac gac atc gag cca aac ctg aac gca 403  
Ser Gln Ala Gln Ile Phe Thr Asn Asp Ile Gln Pro Asn Leu Asn Ala 100

ggc gac gca ctg ttc ggc cac ggc ctg aac att cac ttc gac ctg 451  
Gly Asp Ala Leu Phe Gly His Gly Leu Asn Ile His Phe Asp Leu 115

atc aag cca gct gac gac atc atc gtc ggc atg gtt gcg cca aag ggc 499

[illegible]

<213> Corynebacterium glutamicum

<400> 622  
Met Ala Ile Glu Leu Tyr Asp Ala Asp Leu Ser Ile  
1  
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10  
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Thr Lys Arg Leu Ile Ala Asn Val Glu Asn Gly Asn Thr Glu Glu  
Lys Ser Arg Met Lys Asp Ile Leu Thr Asp Ile Glu Asp Gly Thr Phe  
Glu Phe Gly Gly Tyr Leu Ser Gly Pro Arg Val Ile Asp Ala Asp Thr  
Phe Glu Gly Ile Ser Asn Met Asn Tyr Ser Val Ser Asp Thr Ala  
Ala Tyr Phe Glu Val Leu His Glu Leu Lys Leu Ile Val Asp Leu Met  
Lys Val Gly Phe Glu Val Leu Thr Glu Ala Gly Tyr Glu Pro Glu Met  
Leu Phe Gly Glu Glu Ala Val Leu Cys Gly Gly Thr Glu Leu Val  
Arg Ala Gly Val Ile Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp  
Thr Ala Glu Ala Leu Thr Leu Ser Tyr Ala Ala Ile Gly Ala  
Gly Lys Gly Val Pro Cys Leu Ile Ala Val Asp Glu Asp Pro Thr Gly  
Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Glu Phe Val Asp  
Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met  
Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn  
Leu Ala Pro Asp Thr Ser Glu Ala Glu Ile Phe Thr Asn Asp Ile Glu  
Val Lys Thr Thr Ala Glu Ala Ala Trp Ala Asp Val Ile Met Leu  
Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu  
His Ser Glu Asn Leu Arg Asp Ser Gly Val Glu Val Ile Gly Leu  
Gln Gly Arg Lys Val Ala Ile Val Gly Tyr Gly Ser Glu His Ala  
Met Ala Ile Glu Leu Tyr Asp Ala Asp Leu Ser Ile

Position	Protein	Residue	Mass
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136	His	Leu	146
137	Val	Val	117
138	Arg	Arg	172
139	Arg	Arg	172
140	Gln	Gln	146
141	Phe	Phe	166
142	Val	Val	117
143	Asp	Asp	133
144	Gly	Gly	75
145	Gly	Gly	75
146	Asp	Asp	133
147	Gly	Gly	75
148	Gly	Gly	75
149	Val	Val	117
150	Met	Met	149
151	Val	Val	117
152	Ala	Ala	89
153	Pro	Pro	97
154	Lys	Lys	146
155	Gly	Gly	75
156	Ala	Ala	89
157	Leu	Leu	146
158	Leu	Leu	146
159	Phe	Phe	166
160	Asp	Asp	133
161	Gly	Gly	75
162	Gly	Gly	75
163	Ala	Ala	89
164	Leu	Leu	146
165	Leu	Leu	146
166	Phe	Phe	166
167	Asp	Asp	133
168	Gly	Gly	75
169	Gly	Gly	75
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171	Leu	Leu	146
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174	Asp	Asp	133
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178	Leu	Leu	146
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229	Phe	Phe	166
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Cys Leu Ile  
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Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu  
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Val Lys Thr Thr Ala Glu Ala Ala Trp Ala Asp Val Ile Met Leu  
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Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn  
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Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met  
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Val Pro Met Thr His  
1 5  
gtt tca agc ccc tcc gca ccc cgc aac gtg gtt gtt ggt gtc gcc ggc 163

Val Ser Ser Pro Ser Ala Pro Arg Asn Val Val Val Gly Val Ala Gly	10	15	20
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gly ile ala ala tyr lys ala cys his ile val arg ala phe lys glu	40	45	50
gca ggc gat aat gat cgc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc	55	60	65
gag ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc	70	75	80
gaa gct gat tgc atc gtc gtc gtc gtc gtc gtc gtc gtc gtc gtc gtc	85	90	95
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gat ttc atc gtc atg gcg gca gca gta gct gat ttc acc ggc gca tcg	Asp Phe Ile Val Met Ala Ala Val Ala Asp Phe Thr Pro Ala Ser	979	
cag gcg aca tcg aag ttg aag aag ggc tca gat tct gat gaa gac gca	Gln Ala Thr Ser Lys Leu Lys Lys Gly Ser Asp Ser Asp Gln Asp Ala	1027	
ttg agc acc atc tcg ttg ttg gaa aac ccg gat atc ttg gct acc acg	Leu Ser Thr Ile Ser Leu Val Gln Asn Pro Asp Ile Leu Ala Thr Thr	1075	
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ggt ttt gct gcg gaa act gga gac gag cac acc acc ggc ttg gag tat	Gly Phe Ala Ala Gln Thr Gly Asp Gln His Thr Thr Ala Leu Gln Tyr	1171	
gcg cgc aag aag aaa ctg cag aag aag ggc tgc gac ctg atg tgt aat	Ala Arg Lys Lys Leu Gln Lys Lys Gly Cys Asp Leu Leu Met Cys Asn	1219	
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 Val Val Met Ile Ala Thr Lys Ala Leu Ser Arg Ser Leu Asp Leu Ala  
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 Gln Leu Leu Gly Ile Pro Ala Asn Ser Val Val Ala Ile Thr Gln  
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 Asn Ser Ile Gln Ser Ala Asp Leu Ala Ala Lys Ser Ile Gly Ala Asp  
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 547 gcc tca gtt tca tca aag gga ggc cca ctg tcc tac acg ttt ggt gat  
 Ala Ser Val Ser Tyr Lys Gly Phe Thr Tyr Thr Phe Gly Asp  
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 175  
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691	gac atg ttc gta gag gtc ttc ggc ggg tgg ggg gct ttc gtc gaa aag	Ala Met Phe Val Gln Val Phe Gly Gly Leu Gly Ala Phe Val Gln Lys	185	190	195	739	caa tta ggt acc tgg cgt acg cat ttc agg gct tcc ctg gaa gcc tgg	Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala Ser Leu Gln Ala Leu	200	205	210	787	atg gaa gag ggt gct gag gtc gct cgc gca ggt gtc ggc tgg ccg	Met Gln Gln Val Ala Gln Val Ala Arg Ala Gly Val Ala Leu Pro	215	220	225	835	agc gat gcg gtc gag cgc acc atg aat ttt gcg gat cgg atg cct gag	Ser Asp Ala Val Gln Arg Thr Met Asn Phe Ala Asp Arg Met Pro Gln	230	235	240	245	883	aat tgg acg agt tgg atg cag cgt gat tgg gcc gcg gga gtc agt	Asn Ser Thr Ser Met Gln Arg Asp Leu Ala Gly Val Ala Ser	250	255	260	931	gag ctt gag gct cag aca ggt gca atg gtc cgg gca gca gca aag gtc	Gln Leu Gln Ala Gln Thr Gly Ala Ile Val Arg Ala Ala His Lys Val	265	270	275	979	ggt gtc aaa act cgg ctt cat gac ctt att tat gct gct aag ctg	Gly Val Lys Thr Pro Leu His Asp Leu Ile Tyr Ala Gly Leu Lys Leu	280	285	290	1023	aaa gaa gag gaa aat tca ctt taggagataga atcaagatcc atg	Lys Gln Gln Gln Asn Ser Leu	295	<210> 630	<211> 300	<212> PRT	<213> Corynebacterium glutamicum	<400> 630	Met Lys Ile Ala Ile Val Gly Ala Gly Ala Val Gly Tyr Phe Gly	1	5	10	15	Ala Leu Leu Gln Gln Ser Gly Ala Asp Ile Thr Met Val Ala Arg Gly	20	25	30	Arg Thr Leu Gln Ala Leu Lys Ser Lys Gly Leu His Ile Asn Asp Ala	35	40	45	Arg Gly Gln Arg Tyr Val Pro Ile Pro Ala Val Ala Ser Val Gln Gln	50	55	60	Leu Lys Asp Ala Asp Val Val Met Ile Ala Thr Lys Ala Leu Ser Arg	65	70	75	Ser Leu Asp Leu Ala Gln Leu Leu Gly Ile Pro Ala Asn Ser Val	85	90	95	Val Ala Ile Thr Gln Asn Ser Ile Gln Ser Ala Asp Leu Ala Lys	100	105	110	Ser Ile Gly Ala Asp Arg Val Trp Pro Gly Val Val Arg Gly Phe Phe
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115 120 125

Val His Gln Gly Pro Ala Ser Val Ser Tyr Lys Gly Gly Pro Leu Ser 130 135 140

Tyr Thr Phe Gly Asp Ser Gly Gln Leu Ser Arg Gln Phe Ala Ser Thr 145 150 155 160

Leu Gln Gln Ala Gly Ile Asp Gly Val Leu His Pro Asp Ile Leu Val 165 170 175

Asp Val Trp Gln Lys Ala Met Phe Val Gln Val Phe Gly Gly Leu Gly 180 185 190

Ala Phe Val Gln Lys Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala 195 200 205

Ser Leu Gln Ala Leu Met Gln Val Val Ala Gln Val Ala Arg Ala Ala 210 215 220

Gly Val Ala Leu Pro Ser Asp Ala Val Gln Arg Thr Met Asn Phe Ala 225 230 235 240

Asp Arg Met Pro Gln Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala 245 250 255

Ala Gly Val Ala Ser Gln Leu Gln Ala Gln Thr Gly Ala Ile Val Arg 260 265 270

Ala Ala His Lys Val Gly Val Lys Thr Pro Leu His Asp Leu Ile Tyr 275 280 285

Ala Gly Leu Lys Leu Lys Gln Gln Asn Ser Leu 290 295 300

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Val Thr Asn Val Ser 1

aac gag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att 163

Asn Gln Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile 20

acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac 211

Thr Ala Pro Pro Ile Asp Gln Leu Leu Asp Lys Val Thr Ser Lys Tyr 35

25 30

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gcc ctc gtg atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc
259 Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe
40 Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe
307 TAC CAT CAG GCA GAT GAG GGA GTA TTC GAG TTC ATC GGA CCA TGG GTT
Tyr His Gln Ala Asp Gln Gly Val Phe Gln Phe Ile Gly Pro Leu Val
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act ccg cag cca ggc gaa aag cca ctt tct att gct ctg cgt gag atc
355 Thr Pro Gln Pro Gly Gln Lys Pro Leu Ser Ile Ala Leu Arg Gln Ile
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cac
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35
Gln Ile Asn Ser Phe Tyr His Gln Ala Asp Gln Gly Val Phe Gln Phe
50
Ile Gly Pro Leu Val Thr Pro Gln Pro Gly Gln Lys Pro Leu Ser Ile
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Corynebacterium glutamicum
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115 Val Ser Lys Leu Lys
1
5

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163 ggc tca aga tgc ctt ctc gac gtc ggc tcc ggc gat cac tcc ggc  
 10 Gly Ser Arg Ser Leu Leu Asp Val Gly Ser Gly Asp His Ser Phe Ala  
 15  
 211 gac ctg gcc ggc cgc cag gtc ggc cat gtc gat gtc gtc gat cct ctt  
 35 Asp Leu Ala Gly Arg Gln Val Ala His Val Asp Val Val Asp Pro Leu  
 30  
 259 att aat aca acc ttt gaa gaa ttc cag cgc acc caa agc tac gat gcc  
 40 Ile Asn Thr Thr Phe Gln Phe Gln Pro Thr Gln Ser Tyr Asp Ala  
 45  
 307 atc acg ttc atc atc gcg tcc ctc cat cac atg aac gcg gaa gaa gga ctt  
 55 Ile Thr Phe Ile Ala Ser Leu His His Met Asn Ala Gln Gly Leu  
 60  
 355 aac aaa gca gtc cga atc ctc aat cct ggc ggc aag ctc atc gta  
 70 Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly Lys Leu Leu Ile Val  
 75  
 403 ggc ctc gcc aaa aac aaa acc gcc tcc gac tgg atc atc tcc gga cta  
 90 Gly Leu Ala Lys Asn Lys Thr Ala Ser Asp Trp Ile Ile Ser Gly Leu  
 95  
 451 caa gct ttt ctc tcc cga cca atc agc ctc atc aat agg gaa caa caa  
 105 Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile Asn Arg Gln Gln  
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 499 atc tac ccc ttc cct acc aaa gaa ccc tca gag agt ctc cac gaa ata  
 120 Ile Tyr Pro Phe Pro Thr Lys Gln Pro Ser Gln Ser Leu His Gln Ile  
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 547 cga caa ctc acc aag cag ctc ctc cct cac cgc cgt att cgc cgt gga  
 140 Arg Gln Leu Thr Lys Gln Leu Pro His Arg Arg Ile Arg Arg Gly  
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 593 atc cac ttc cga tac ctc ctc gag tgg aca aag cct taacacagccc  
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 Gln Ser Tyr Asp Ala Ile Thr Phe Ile Ala Ser Leu His His Met Asn  
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 55





90	95	100
caa gct ttt ctc tcc cga cca atc agc ctc atc aat agg gaa caa caa	451	451
Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile Asn Arg Gln Gln		
105	110	115
atc tac ccc ttc cct acc aaa gaa gcc tca gag agt ctc cac gaa ata	499	499
Ile Tyr Pro Phe Pro Thr Lys Gln Pro Ser Gln Ser Leu His Gln Ile		
120	125	130
cga caa ctc acc aag cag ctc ctc cct cac cgc cgt atc cgc cgt gga	547	547
Arg Gln Leu Thr Lys Gln Leu Leu Pro His Arg Arg Ile Arg Arg Gly		
135	140	145
atc cac ttc cga tac ctc gag tgg aca aag cct taacaagcccc	593	593
Ile His Phe Arg Tyr Leu Leu Gln Trp Thr Lys Pro		
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 35 40 45  
 Gln Ser Tyr Asp Ala Ile Thr Phe Ile Ala Ser Leu His His Met Asn  
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 Ala Gln Gln Gly Leu Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly  
 65 70 75  
 Lys Leu Leu Ile Val Gly Leu Ala Lys Asn Lys Thr Ala Ser Asp Trp  
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 Ile Ile Ser Gly Leu Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile  
 100 105 110  
 Asn Arg Gln Gln Ile Tyr Pro Phe Pro Thr Lys Gln Pro Ser Gln  
 115 120 125  
 Ser Leu His Gln Ile Arg Gln Leu Thr Lys Gln Leu Pro His Arg  
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 Pro

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Gly Phe Gly Arg Val Leu Asp Val Gly Ala Gly Thr Gly Lys Leu Thr  
163 20  
agt gag cta aca gct gat cag gtc cta gcc ctt gat cca agc atg gac  
Ser Gln Leu Thr Ala Asp Gln Val Leu Ala Leu Asp Pro Ser Met Asp  
211 35  
atg ttg cgg gtg ttg cgc tcc gcg ctt ccg gcg ggt ccc tgc tgg caa  
Met Leu Arg Val Phe Arg Ser Ala Leu Pro Ala Val Pro Cys Trp Gln  
259 50  
gcg aca gca gaa cac aca gga ata cgt gac aac gcc ggt gat ctg att  
Ala Thr Ala Gln His Thr Gly Ile Arg Asp Asn Ala Val Asp Leu Ile  
307 65  
acg tgc gca caa acg tgg cat tgg gtt gac gtt gac gtt acg gct gcc tca gcg  
Thr Cys Ala Gln Thr Trp His Trp Val Asp Val Thr Ala Ala Ser Ala  
355 80  
gaa ttt gat cgg gtt atg gca cct gag ggt gca gtc ctg gtc gtc gtc gtc  
Glu Phe Asp Arg Val Ile Ala Pro Gln Gly Ala Val Leu Leu Val Trp  
403 95  
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Asn Asn Leu Asp Thr Ser Ile Ala Trp Val His Arg Leu Ser Arg Ile  
451 115  
atg cat gcc ggc gat gta ctc aag ccg gga ttc acc cca gaa acc gca  
Met His Ala Gly Asp Val Leu Lys Pro Gly Phe Thr Pro Gln Thr Ala  
499 130  
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Ala Pro Trp Ile Ile Asp Arg Gln Ile Thr Trp Asn Gln His  
547 145  
ctc acc cct gaa gaa atc atc cag ctg gct cac acg agg tcc tac tgg  
Leu Thr Pro Gln Ile Ile Gln Leu Ala His Thr Arg Ser Tyr Trp  
595 160  
tta aac gcg tca gag aaa atc aaa gag cgt gtt gat cag aac ctt cag  
Leu Asn Ala Ser Gln Lys Ile Lys Val Asp Gln Asn Leu Gln  
643 175  
180

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gactatcac gatgtccgac ctggatatcc ggctgagccc gtg gag tta gcc cgt  
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115  
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Gly Phe Gly Arg Val Leu Asp Val Gly Ala Gly Thr Gly Lys Leu Thr  
163 20  
agt gag cta aca gct gat cag gtc cta gcc ctt gat cca agc atg gac  
Ser Gln Leu Thr Ala Asp Gln Val Leu Ala Leu Asp Pro Ser Met Asp  
211 35  
atg ttg cgg gtg ttg cgc tcc gcg ctt ccg gcg ggt ccc tgc tgg caa  
Met Leu Arg Val Phe Arg Ser Ala Leu Pro Ala Val Pro Cys Trp Gln  
259 50  
gcg aca gca gaa cac aca gga ata cgt gac aac gcc ggt gat ctg att  
Ala Thr Ala Gln His Thr Gly Ile Arg Asp Asn Ala Val Asp Leu Ile  
307 65  
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Thr Cys Ala Gln Thr Trp His Trp Val Asp Val Thr Ala Ala Ser Ala  
355 80  
gaa ttt gat cgg gtt atg gca cct gag ggt gca gtc ctg gtc gtc gtc gtc  
Glu Phe Asp Arg Val Ile Ala Pro Gln Gly Ala Val Leu Leu Val Trp  
403 95  
aat aac ctg gac acc tcc atc gcg tgg gta cac cga ctg acg ctg agt cgc att  
Asn Asn Leu Asp Thr Ser Ile Ala Trp Val His Arg Leu Ser Arg Ile  
451 115  
atg cat gcc ggc gat gta ctc aag ccg gga ttc acc cca gaa acc gca  
Met His Ala Gly Asp Val Leu Lys Pro Gly Phe Thr Pro Gln Thr Ala  
499 130  
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Ala Pro Trp Ile Ile Asp Arg Gln Ile Thr Trp Asn Gln His  
547 145  
ctc acc cct gaa gaa atc atc cag ctg gct cac acg agg tcc tac tgg  
Leu Thr Pro Gln Ile Ile Gln Leu Ala His Thr Arg Ser Tyr Trp  
595 160  
tta aac gcg tca gag aaa atc aaa gag cgt gtt gat cag aac ctt cag  
Leu Asn Ala Ser Gln Lys Ile Lys Val Asp Gln Asn Leu Gln  
643 175  
180

tgg tat ctc tac gag cat ctg ggt ttc agt ccc gac aat cca gtg gaa  
 Trp Tyr Leu Tyr Gln His Leu Gly Phe Ser Pro Asp Asn Pro Val Gln  
 185 190 195  
 ctc ccc tat cgc tgt gat gca ttt tta ctt tca cgt tcc ggt acc ctg  
 Leu Pro Tyr Arg Cys Asp Ala Phe Leu Leu Ser Arg Ser Gly Thr Leu  
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 Asp Pro Ser Met Asp Met Leu Arg Val Phe Arg Ser Ala Leu Pro Ala  
 35 40 45  
 Val Pro Cys Trp Gln Ala Thr Ala Gln His Thr Gly Ile Arg Asp Asn  
 50 55 60  
 Ala Val Asp Leu Ile Thr Cys Ala Gln Thr Trp His Trp Val Asp Val  
 65 70 75 80  
 Thr Ala Ala Ser Ala Gln Phe Asp Arg Val Ile Ala Pro Gln Gly Ala  
 85 90 95  
 Val Leu Leu Val Trp Asn Asn Leu Asp Thr Ser Ile Ala Trp Val His  
 100 105 110  
 Arg Leu Ser Arg Ile Met His Ala Gly Asp Val Leu Lys Pro Gly Phe  
 115 120 125  
 Thr Pro Gln Thr Ala Ala Pro Trp Ile Ile Asp Arg Gln Ile Arg Thr  
 130 135 140  
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 Thr Arg Ser Tyr Trp Leu Asn Ala Ser Gln Lys Ile Lys Gln Arg Val  
 165 170 175  
 Asp Gln Asn Leu Gln Trp Tyr Leu Tyr Gln His Leu Gly Phe Ser Pro  
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 115 Met Glu Asn Pro Ser  
 163 ttg cgc gag ctt gat cac cga aac atc tgg cac ccg tat gcc ggc ccg  
 20 Leu Arg Glu Leu Asp His Arg Asn Ile Trp His Pro Tyr Ala Ala Pro  
 211 ggc gtg cgc aat aga ctc gtc acc aaa acc gat gga gtg ttt ttg acg  
 35 Gly Val Arg Asn Arg Leu Val Thr Lys Thr Asp Gly Val Phe Leu Thr  
 259 ctg gaa gat ggc agc acc gtg att gac gcg atg agc tcc tgg tgg tgg  
 50 Leu Glu Asp Gly Ser Thr Val Ile Asp Ala Met Ser Ser Trp Trp Ser  
 307 gca att cat gga cac gga cac ccc cga ctg aaa gct gcc gcc caa aaa  
 65 Ala Ile His Gly His Gly His Pro Arg Leu Lys Ala Ala Glu Lys  
 355 caa atc gac acc atg agt cac gtc atg ttt ggc gga cta acc cac gag  
 80 Gln Ile Asp Thr Met Ser His Val Met Phe Gly Leu Thr His Glu  
 403 ccc gcc att aag ctc acc cac aaa ctc ctc aat ctc act gga aat tcc  
 95 Pro Ala Ile Lys Leu Thr His Lys Leu Leu Asn Leu Thr Gly Asn Ser  
 451 ttt gac cac gtc ttt tat tcc gat tcc ggc tgc ggc tca gtg gag gtc  
 110 Phe Asp His Val Phe Tyr Ser Asp Ser Gly Ser Val Ser Val Glu Val  
 499 gcc atc aaa atg gca ctg cag gcc tcc aaa gga caa ggc cac ccg gaa  
 120 Ala Ile Lys Met Ala Leu Glu Ala Ser Lys Gly Gln Gly His Pro Glu  
 547 cgg aca aaa ctc ctc acc tgg cgg tcc ggc tac ggc tgc Tyr His Gly Asp Thr Phe  
 135 Arg Thr Lys Leu Leu Thr Trp Arg Ser Gly Tyr His Gly Asp Thr Phe  
 595 acc gcg atg agc gtg tgc gac cca gaa aat ggc atg cat agc ctc tgg  
 155 Thr Ala Met Ser Val Cys Asp Pro Glu Asn Gly Met His Ser Leu Trp  
 180 Lys Gly Thr Leu Pro Glu Gln Ile Phe Ala Pro Ala Pro Val Arg

115 163 211 259 307 355 403 451 499 547 595 643

691	ggg tca tcg ccg cag gcg att tcc gag tac ctg cgc agc atg gaa ttg	Gly Ser Ser Pro Gln Ala Ile Ser Gln Tyr Leu Arg Ser Met Gln Leu	185	190	195
739	ctt atc gac gac gag ggc gtc tcc gca atc atc atc gaa ccg atc gtc caa	Leu Ile Asp Gln Ala Val Ser Ala Ile Ile Ile Gln Pro Ile Val Gln	200	205	210
787	ggc gct gga ggc atg cgc ttt cac gat gtc gca ctc atc gaa gga gtc	Gly Ala Gly Met Arg Phe His Asp Val Ala Leu Ile Gln Gly Val	215	220	225
835	ggc aca ctg tgc aag aag cac gat cgt ttc ttg atc gtc gat gaa att	Ala Thr Leu Cys Lys His Asp Arg Phe Leu Ile Val Asp Gln Ile	230	235	240
883	ggc act ggt ttc ggc cgc acc ggt gaa cta ttt gcc acc tta agc aat	Ala Thr Gly Phe Gly Arg Thr Gln Leu Phe Ala Thr Leu Ser Asn	245	250	255
931	ggc cta caa cca gac atc atg tgt gtc ggc aag gcc ctc acc ggt gga	Gly Leu Gln Pro Asp Ile Met Cys Val Gly Lys Ala Leu Thr Gly Gly	260	265	270
979	ttc atg tcc ttc ggc gct act tta tgc acg gac aag gtc gct caa tta	Phe Met Ser Phe Ala Thr Leu Cys Thr Asp Lys Val Ala Gln Leu	275	280	285
1027	atc agc acc cca aat ggc gga ggt ggc ctg atg cac ggc ccc act ttt	Ile Ser Thr Pro Asn Gly Gly Gly Ala Leu Met His Gly Pro Thr Phe	290	295	300
1075	atg gct aat cct ctg ggc tgt ggc ggt tgc cat gct tca tta gaa atc	Met Ala Asn Pro Leu Ala Cys Ala Val Ser His Ala Ser Leu Gln Ile	305	310	315
1123	att gag acc ggc atg tgg cag aaa cag gta aaa aga atc gaa gcc gaa	Ile Gln Thr Thr Gly Met Trp Gln Lys Val Lys Arg Ile Gln Ala Gln	320	325	330
1171	ctt atc gca ggc ctt tcc cca cct caa cct caa ctc gln his leu pro gly	Leu Ile Ala Gly Leu Ser Pro Leu Gln His Leu Pro Gly Val Ala Asp	335	340	345
1219	gtc cgg gtt ctc ggc ggc att ggt gtc atc gaa atg gaa gaa aat gtc	Val Arg Val Leu Gly Ala Ile Gly Val Ile Gln Met Gln Asn Val	350	355	360
1267	aat gtc gaa gaa gct act cag gct gca tta gat cac ggt gtc tgg atc	Asn Val Gln Gln Ala Thr Gln Ala Leu Asp His Ggt Gly Val Trp Ile	365	370	375
1315	cgc ccc ttg gga cgc ttg ctc tat gtc atg cct cca tat atc acc acg	Arg Pro Phe Gly Arg Leu Leu Tyr Val Met Pro Pro Tyr Ile Thr Thr	380	385	390
1363	tca gag cag tgc gca cag atc tgc act gcg ctt cat gct gca gtt aaa	Ser Gln Gln Cys Ala Gln Ile Cys Thr Ala Leu His Ala Val Lys	395	400	405
			410	415	420

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Gly Lys

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Gly Val Phe Leu Thr Leu Glu Asp Gly Ser Thr Val Ile Asp Ala Met

Ser Ser Trp Trp Ser Ala Ile His Gly His Gly His Pro Arg Leu Lys

Ala Ala Ala Glu Lys Glu Ile Asp Thr Met Ser His Val Met Phe Gly

Gly Leu Thr His Glu Pro Ala Ile Lys Leu Thr His Lys Leu Leu Asn

Leu Thr Gly Asn Ser Phe Asp His Val Phe Tyr Ser Asp Ser Gly Ser

Val Ser Val Glu Val Ala Ile Lys Met Ala Leu Glu Ala Ser Lys Gly

Glu Gly His Pro Glu Arg Thr Lys Leu Leu Thr Trp Arg Ser Gly Tyr

His Gly Asp Thr Phe Thr Ala Met Ser Val Cys Asp Pro Glu Asn Gly

Met His Ser Leu Trp Lys Gly Thr Leu Pro Glu Glu Ile Phe Ala Pro

Ala Pro Pro Val Arg Gly Ser Ser Pro Glu Ala Ile Ser Glu Tyr Leu

Arg Ser Met Glu Leu Leu Ile Asp Glu Ala Val Ser Ala Ile Ile Ile

Glu Pro Ile Val Glu Glu Ala Gly Gly Met Arg Phe His Asp Val Ala

Leu Ile Glu Gly Val Ala Thr Leu Cys Lys Lys His Asp Arg Phe Leu

Ile Val Asp Glu Ile Ala Thr Gly Phe Gly Arg Thr Gly Glu Leu Phe

Ala Thr Leu Ser Asn Gly Leu Glu Pro Asp Ile Met Cys Val Gly Lys





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355	cct ctt gcg cca aat ctg gca gcc cga cga gag ggg gtc gag cca ata	70	Pro Leu Ala Pro Asn Leu Ala Arg Arg Glu Gly Val Glu Pro Ile
403	cag ttt gat cag att atc tgc tgg ctt cgt ggt ttt gac gac cca gat	90	Gln Phe Asp Gln Ile Ile Ser Trp Leu Arg Gly Phe Asp Asp Pro Asp
451	cgc atc att gtg gtg gag ggc gct ggt ggc ctg ctg ctg gtc aga tta ggg	105	Arg Ile Ile Val Val Glu Gly Ala Gly Gly Leu Leu Val Arg Leu Gly
499	gaa gat ttc acc ctg gca gat gtc gcc tcc gct ttg aat gca ccc tta	120	Glu Asp Phe Thr Leu Ala Asp Val Ala Ser Ala Leu Asn Ala Pro Leu
547	gtg att gtg aca acc gga ttg gga ttg gga agc ctc aac gct gct gaa tta	140	Val Ile Val Thr Ser Thr Gly Leu Gly Ser Leu Asn Ala Ala Glu Leu
595	agc gtc gag gca gca aac cgc cga gga ctc aca gtc ttg gga gtc ctc	155	Ser Val Glu Ala Ala Asn Arg Arg Gly Leu Thr Val Leu Gly Val Leu
643	ggc ggt tgc atc cct caa aat cct gat cta gct acg atg ctt aat ctc	170	Gly Gly Ser Ile Pro Gln Asn Pro Asp Leu Ala Thr Met Leu Asn Leu
691	gaa gaa ttt gag aga gtc acc ggc gtc gtc ccc ttt tgg gga gct ttg ccg	185	Glu Glu Phe Glu Arg Val Thr Gly Val Pro Phe Trp Gly Ala Leu Pro
739	gaa gga ttg tca cgg gtg gag ggg ttc gtc gaa aag caa tct ttt ccg	200	Glu Gly Leu Ser Arg Val Glu Gly Phe Val Glu Lys Glu Ser Phe Pro
795	gcc ctt gat gcc ttt aag aaa cgg ccg gca agg tgatcgtgaa cacggtgcct	215	Ala Leu Asp Ala Phe Lys Pro Pro Ala Arg
	tcg		
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	<211> 224		
	<212> PRT		
	<213> Corynebacterium glutamicum		
	<400> 642		
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		5	
		10	
	Phe Ser Thr Ala Val Leu Val Arg Tyr Leu Ala Asp Gln Gly His Asp	20	
		25	
	Val Leu Pro Val Lys Leu Val Gln Thr Gly Glu Leu Pro Gly Glu Gly	35	
		40	
		45	



259	atc cca gac	ttg atg gaa	tta ggc cac	cag gtt	cgg ttg aag	tgt	250
	Ile Pro Asp	Leu Met	Glu Leu	Ala His	Gln Val	Arg Lys	Trp Cys
307	ggg gaa gaa	atc gaa gac	atc gaa gac	atc gaa gac	atc gaa gac	atc gaa gac	50
	Gly Gln Gln	Ile Gln Ile	Gln Val	Gly Ile	Ser Leu	Lys Thr	Gly Gly
355	tgc cct gaa	gat tgc tca	cag tct	ggg ttg	ttt gaa	tcg	85
	Cys Pro Gln	Asp Cys	His Phe	Gly Leu	Phe Gln	Ser	
403	cgg gtt cgt	tcg ttg	tggtg	atc	cgg gac	ggt	100
	Pro Val Arg	Ser Val	Trp Leu	Asn Leu	Val Gln	Ala Ala	
451	aaa cag acc	gca aaa	act ggc	gct acc	gaa ttc	tgt atc	gac gca
	Lys Gln Thr	Ala Lys	Thr Gly	Ala Thr	Gln Phe	Cys Ile	Val Ala Ala
499	gtc aag ggg	cct gat	gag agg	ctc atg	acc cag	ctg gag	gaa gac
	Val Lys Gly	Pro Asp	Gln Arg	Leu Met	Thr Gln	Leu Gln	Ala Val
547	ctc gcg att	cac tct	gaa gtt	gaa att	gaa gtt	gaa gtt	145
	Leu Ala Ile	His Ser	Gln Val	Ile Gln	Val Ala	Ala Ser	Ile Gly
595	acg tta aat	aag gaa	cag gtt	gat cgc	ctc gct	gct ggc	gtg cac
	Thr Leu Asn	Lys Gln	Val Asp	Arg Leu	Ala Ala	Gly Val	His
643	cgc tac aac	cat aat	ttg gaa	act ggc	cgt tcc	tat ttc	cct gaa
	Arg Tyr Asn	His Asn	Leu Thr	Ala Arg	Ser Tyr	Phe Pro	Gln Val
691	gtc acc act	cat aca	tggtg	gaa gag	cgc cgc	gaa act	ttg cgt
	Val Thr Thr	His Thr	Trp Gln	Arg Gln	Thr Leu	Arg Leu	Val
739	gca gaa gct	gga atg	gaa gtt	tgt tcc	ggc gga	atc tta	gga atg
	Ala Gln Ala	Gly Met	Glu Val	Cys Ser	Gly Ile	Leu Gly	Met Gly
787	gaa act tta	gag cag	cgc ggc	gag ttg	gac gtt	cag cgt	gag cgt
	Gln Thr Thr	Leu Gln	Arg Ala	Gln Phe	Val Gln	Leu Ala	Gln Leu
835	gat ccg cac	gaa gtc	ccc atg	aac ttc	ctt gat	cct cgc	gac acc
	Asp Pro His	Gln Val	Pro Met	Asn Phe	Leu Asp	Pro Arg	Gly Thr
883	cca ttg gcc	gat agt	gaa ttg	atg gac	agc cgt	gac gct	ctg cgt
	Pro Phe Ala	Asp Arg	Gln Leu	Met Asp	Ser Arg	Ala Leu	Arg Ser
931	att ggt gcg	ttc cgc	ctt gcg	atg cct	acc atg	ctt cgt	ttt gct
	Ile Gly Ala	Phe Arg	Leu Met	Pro His	Thr Met	Leu Arg	Ala

[illegible]

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<400> 644
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<400> 644  
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	60	50	40	35	20	25	30
Arg Leu Lys Trp Cys Gly Gln Ile Glu Val Gln Gly Ile Ile Ser							
Leu Pro Gln Gln Ile Pro Asp Leu Met Gln Leu Ala His Gln Val							
Glu Gln Gly Ile Gly Leu Asn Gln Gln Gln Leu Met Gln Val Leu Thr							

[illegible]

Leu	65	Thr	65	Gly	70	Cys	85	Pro	90	Gln	95	Asp	95	His	75	Pro	80	Gln	85	Ser	90	Val	95	Arg	95	Ser	95	Val	95	Trp	95	Leu	95	Asp	95	Ile	95	Pro	95	Asn	95
-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----

Sequence	Count
Gly Leu Phe Gly Leu Asp Ile Pro Asn	95
Leu Val Gln Ala Lys Thr Gly Ala Thr Gln Phe	100
Ala Lys Thr Arg Ser Val Trp Leu Asp Ile Pro Asn	85
Ala Lys Thr Arg Ser Val Trp Leu Asp Ile Pro Asn	90
Ala Lys Thr Gly Ala Thr Gln Phe	105
Leu Val Gln Ala Lys Thr Gly Ala Thr Gln Phe	110

Leu	Val	Glu	Ala	Ala	Lys	Gln	Thr	Ala	Phe	110						
Cys	Ile	Val	Ala	Ala	Val	Lys	Gly	Pro	Asp	Glu	Arg	Leu	Met	Thr	Gln	125

130	Leu	Glu	Glu	Ala	Val	Leu	Ala	135
125	Cys	Ile	Val	Ala	Ala	Val	Lys	120
140							Gly	
							Pro	
							Asp	
							Glu	
							Arg	
							Leu	
							Met	
							Thr	
							Gln	

Ala	Ala	Ser	Ile	Gly	Thr	Leu	Asn	Lys	Gln	Gln	Val	Asp	Arg	Leu	Ala
145					150				155						160
Leu	Glu	Glu	Ala	Val	Leu	Ala	Ile	His	Ser	Glu	Val	Glu	Ile	Glu	Val
130					135						140				

Ala Ala Ser Ile Gly Thr Leu Asn Lys Gln Val Asp Arg Leu Ala	145	150	155	160
Ala Ala Gly Val His Arg Tyr Asn His Asn Leu Gln Thr Ala Arg Ser	165	170	175	

[illegible]

Thr Leu Arg Leu Val Ala Gln Ala Gly Met Gln Val Cys Ser Gly Gly 195  
 Ile Leu Gly Met Gly Gln Thr Leu Gln Arg Ala Gln Phe Ala Val 210  
 Gln Leu Ala Gln Leu Asp Pro His Gln Val Pro Met Asn Phe Leu Asp 225  
 Pro Arg Pro Gly Thr Pro Phe Ala Asp Arg Gln Leu Met Asp Ser Arg 245  
 Asp Ala Leu Arg Ser Ile Gly Ala Phe Arg Leu Ala Met Pro His Thr 260  
 Met Leu Arg Phe Ala Gly Gly Arg Gln Leu Thr Leu Gly Asp Lys Gly 275  
 Ser Gln Gln Ala Leu Leu Gly Gly Ile Asn Ala Met Ile Val Gly Asn 290  
 Tyr Leu Thr Thr Leu Gly Arg Pro Met Gln Asp Asp Leu Asp Met Met 305  
 Asp Arg Leu Gln Leu Pro Ile Lys Val Leu Asn Lys Val Ile 320  
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 <213> Corynebacterium glutamicum  
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 <222> (101)..(1189)  
 <223> RXA00223  
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 ttgaaacact ttttatctgg accatgcagc caccacacca atg cgt gag gtg gcc 115  
 Met Arg Gln Val Ala 1  
 gca gct gcg tgg atg gaa aac gcg cag gca ttg aat ccc gcg agt cag 163  
 Ala Ala Ala Trp Met Gln Asn Ala Gln Ala Leu Asn Pro Ala Ser Gln 20  
 Tac ggt tcg ggg cgt aag gcg agc agc gtc gcg gat tcg gct cgt gaa 211  
 Tyr Gly Ser Gly Arg Lys Ala Arg Ser Val Ala Asp Ser Ala Arg Gln 35  
 gaa att gct tct ctg ctg ggc tgt gaa cct atc gag gtc gtg ttc acc 259  
 Gln Ile Ala Ser Leu Leu Gly Cys Gln Pro Ile Gln Val Val Phe Thr 50  
 gcg tcc ggc acg gag gca gat aac ctc gct gtg cag ggg tca ttc cac 307  
 Ala Ser Gly Thr Gln Ala Asp Asn Leu Ala Val Gln Gly Leu Phe His 65

[illegible]

1075 cgt gcc agc cac gtc ctc ttg gcc atg gga att tcc gaa acc gac gcc  
 Arg Ala Ser His Val Leu Leu Ala Met Gly Ile Ser Glu Thr Asp Ala  
 310 315 320 325  
 1123 cgt ggt gcc atc cga ttc acc ctc gga aga acc acc act gaa gaa tcc  
 Arg Gly Ala Ile Arg Phe Thr Leu Gly Arg Thr Thr Glu Glu Ser  
 330 335 340  
 1171 atc aag gca gtg atc gcc gtg atc gaa gac gta gtg acc agg gct cgt  
 Ile Lys Ala Val Ile Ala Val Ile Glu Asp Val Thr Arg Ala Arg  
 345 350 355  
 1212 act gcg gga atg gct ttc tagcgaccgt aatcgcata gtg  
 Thr Ala Gly Met Ala Phe  
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 <212> PRT  
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 <400> 646

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 Asn Pro Ala Ser Gln Tyr Gly Ser Gly Arg Lys Ala Arg Ser Val Ala  
 20 25 30  
 Asp Ser Ala Arg Glu Glu Ile Ala Ser Leu Leu Gly Cys Glu Pro Ile  
 35 40 45  
 Glu Val Val Phe Thr Ala Ser Gly Thr Glu Ala Asp Asn Leu Ala Val  
 50 55 60  
 Gln Gly Leu Phe His Ala Ser Pro Leu Asn Arg Ile Ile Ser Thr Pro  
 65 70 75 80  
 Ile Glu His Pro Gly Ile Leu Glu Thr Val Lys Ala Leu Glu Leu Gly  
 85 90 95  
 Gly Ala Glu Ala Glu Leu Met Pro Ile Gly Pro Asp Gly Arg Val Ser  
 100 105 110  
 Ser Phe Glu Ala Leu Asp Lys Pro Ala Ala Val Ala Thr Met Met Trp  
 115 120 125  
 Ala Asn Asn Glu Thr Gly Ala Ile Gln Pro Val Ser Glu Phe Ile Ala  
 130 135 140  
 Ala Ala Gln Ala Ser Gly Thr Pro Thr His Ile Asp Ala Val Gln Val  
 145 150 155 160  
 Val Gly His Leu Pro Val Asn Phe Asp Glu Leu Gly Ala Thr Thr Leu  
 165 170 175  
 Ala Ala Ser Ala His Lys Phe Gly Gly Pro Arg Gly Val Gly Leu Leu  
 180 185 190  
 Leu Val Arg Arg Ser Pro Ala Pro Ser Ala Val Leu His Gly Gly Gly  
 195 200 205

Gln Glu Arg Gly Ile Arg Pro Gly Thr Leu Asp Val Ala Gly Ala Ala  
 210 215 220  
 Ala Thr Ala Ala Ala Leu Arg Glu Ala Val Ala Glu Leu Asp Gly Glu  
 225 230 235 240  
 Ala Thr Arg Leu Arg Gly Leu Lys Lys Met Leu Leu Asp Ala Ile Leu  
 245 250 255  
 His Thr Ile Pro Asn Val Leu Val His Thr Thr Glu Pro Ser Leu Pro  
 260 265 270  
 Gly His Leu His Leu Ser Phe Pro Gly Ala Glu Gly Asp Ser Leu Ile  
 275 280 285  
 Met Leu Leu Asp Ser Leu Arg Ile Glu Ala Ser Thr Gly Ser Ala Cys  
 290 295 300  
 Ser Asn Gly Val Asn Arg Ala Ser His Val Leu Leu Ala Met Gly Ile  
 305 310 315 320  
 Ser Glu Thr Asp Ala Arg Gly Ala Ile Arg Phe Thr Leu Gly Arg Thr  
 325 330 335  
 Thr Thr Glu Glu Ser Ile Lys Ala Val Ile Ala Val Ile Glu Asp Val  
 340 345 350  
 Val Thr Arg Ala Arg Thr Ala Gly Met Ala Phe  
 355 360

attctgtgca tgcacttgac ctaggactcg atatttcta atg ctc tac ctt gat  
 115 Met Leu Tyr Leu Asp  
 1 Asn Ala Ala Thr Thr Ser Val Arg Asn Glu Ala Leu Glu Ala Met Trp  
 163 aat gca gcc acc acc agt gtg cgc aat gaa gca ctt gag gcc atg tgg  
 15 20  
 cct tat ctc acc gga ggc ttc ggc aat ccg tca agt ccc cat gag gtg  
 211 Pro Tyr Leu Thr Gly Ala Phe Gly Asn Pro Ser Ser Pro His Glu Val  
 25 30 35  
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 40 45 50  
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 <223> RXN00262  
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355	tca gaa gcc aac aac ctc gct atc aaa gga ggc tgc tta gct aat cct	Ser Gln Ala Asn Asn Ala Asn Pro	85
403	cgt ggc cgc cgc ctc atc acc acc cgc atc gag cat gac agt gtc cta	Arg GLY Arg His Leu Ile Thr Pro Val Leu	100
451	gaa act gct gct gct gct gct gct gct gct gct gct gct gct gct gct	Gln Thr Ala Ala Tyr Leu Gln Ile Thr Tyr	115
499	cta tcc ccc gat cac act ggg cta atc tcc cgc gag ggt ctc cgc aaa	Leu Ser Pro Asp His Thr Gln Ile Ser Pro Gln GLY Leu Arg Lys	120
547	gca gtc agc agc acc acc acc acc acc acc acc acc acc acc acc acc	Ala Val Arg Pro Asp Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr	135
595	gag gtg gga acc acc acc acc acc acc acc acc acc acc acc acc acc	Gln Val GLY Thr Ile Gln Pro Ile Ala Gln Leu Ala Ala Val Ser Ser	150
643	acg cct ttt cac acc gat gca gta gta gta gta gta gta gta gta gta	Thr Pro Phe His Thr Asp Ala Val Gln Ala Ala His Leu Thr Thr Asp	170
691	ttg gga ggt gac ggc tca agt ttg ttg ttg ttg ttg ttg ttg ttg ttg	Leu GLY Val Asp Ala Leu Ser Leu Ser GLY His Lys Phe GLY Ala Pro	185
739	aaa ggg att gga gtg tca tgg tca aag ctt ccc ctg gag cgc gta atc	Lys GLY Ile GLY Val Leu Trp Ser Lys Leu Pro Leu Gln Pro Val Ile	200
787	cat ggc ggc ggc ggc cag gaa aaa ggg cgg cgt agt ggc acg gaa aac gtt	His GLY GLY GLY GLY Gln Gln Lys Arg Arg Ser GLY Thr Gln Asn Val	215
835	gcg ggg gct atc gcc ttt gcc act gcc ttg gaa ttg gaa ttg ggc agg gaa	Ala GLY Ala Ile Ala Phe Ala Thr Ala Leu Gln Leu Ala Arg Ala Gln	230
883	tcc tat cca gat ctt ggc gaa ttc atc gag gaa gtt ctc act atc ccg	Ser Tyr Pro Asp Leu GLY Phe Ile Gln Val Leu Thr Ile Pro	250
931	gga gca cac ctc act gga cat cct agc atg cgc att gat gga cac gca	Gly Ala His Leu Thr GLY His Pro Arg Met Arg Ile Asp GLY His Ala	265
979	tct ttt ctc ttc gac agc ata gga tct gaa act gtt ctt ctg gaa ttg	Ser Phe Leu Phe Asp Ser Ile GLY Ser Gln Thr Val Leu Gln Leu	280
1027	gaa cgc caa ggc att gtg tgc tcc cct ggt tct gcc tgt ggt tcc gga		290

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<210> 648
<211> 358
<212> PRT
<213> Corynebacterium glutamicum
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Ser Pro His	Gln Val	Gly Arg	Leu Ala	Ser Ala	Gly Leu	Gln Asp	Ala	45
Arg Thr	Arg Val	Ala Arg	Ile Gly	Gly Arg	Pro Thr	Gln Val	Thr	60
Phe Thr	Ser Gly	Gly Ser	Gln Ala	Asn Asn	Leu Ala	Ile Lys	Gly Ala	75
Cys Leu Ala	Asn Pro	Arg Gly	Arg His	Leu Ile	Thr Thr	Pro Ile	Gln	90
His Asp	Ser Val	Leu Gln	Thr Ala	Tyr Leu	Gln Arg	Phe His	Asp	110
Phe Gln Ile	Thr Tyr	Leu Ser	Pro Asp	His Thr	Gly Leu	Ile Ser	Pro	125
Gln Gly	Leu Arg	Lys Ala	Val Arg	Pro Asp	Thr Thr	Leu Ile	Ser Ile	140
Gly Tyr	Ala Asn	Asn Gln	Val Gly	Thr Ile	Gln Pro	Ile Ala	Gln Leu	155
Ala Ala	Val Ser	Ser Thr	Pro Phe	His Thr	Asp Ala	Val Gln	Ala Ala	170
His Leu	Thr Phe	Asp Leu	Gly Val	Asp Ala	Leu Ser	Leu Ser	Gly His	185
Met Leu Tyr	Leu Asp	Asn Ala	Ala Thr	Thr Ser	Val Arg	Asn Gln	Ala	190



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303	ggt tat gcc aac aat gag gtg gga acc att cag ccg ata gct gag ttg	60	glt tyr ala asn asn gln val glt thr ile gln pro ile ala gln leu	75
351	gcg gcg gta agc agt acg cct ttt cac acc gat gca gtg caa gct gca	80	ala ala val ser ser thr pro phe his thr asp ala val gln ala ala	90
399	cat tta acc ttt gac ttg gga gtt gac gcg tta agt ttg tcg ggt cat	95	his leu thr phe asp leu glt val asp ala leu ser leu ser glt his	105
447	aaa ttc ggt gcg cct aaa ggg att gga gtg tta tgg tca aag ctt ccc	110	lys phe gly ala pro lys gly ile gly val leu trp ser lys leu pro	120
495	ctg gag ccg gta atc cat ggc ggc ggc cag gaa aaa ggg cgg cgt agt	125	leu gln pro val ile his gly gly gln gln lys gly arg arg ser	135
543	ggc acg gaa aac gtt gcg ggg gct atc gcc ttt gcc act gcc ttg gaa	140	gly thr gln asn val ala gly ala ile ala phe ala thr ala leu gln	155
591	ttg gcc agg gcg gaa tcc tat cca gat ctt ggc gaa ttc atc gag gaa	160	leu ala arg ala gln ser tyr pro asp leu gly gln phe ile gln gln	170
639	ggt ctc act atc ccg gga gca cac ctg act gga cat cct agg atg cgc	175	val leu thr ile pro gly ala his leu thr gly his pro arg met arg	185
687	att gat gga cac gca tct ttt ctc ttc gac agc ata gga tct gaa act	190	ile asp gly his ala ser phe leu phe asp ser ile gly ser gln thr	200
735	gtt ctt ctg gaa ttg gaa cgc caa ggc att gtg tgc tcc cct ggt tct	205	val leu leu gln leu gln arg gln gly ile val cys ser pro gly ser	215
783	gcc tgt ggt tcc gga gag gta tcc cat gtg ttg ctg gcg ttg ggg ctt	220	ala cys gly ser gly gln val ser his val leu leu ala leu gly leu	235
831	gag gag gat caa gca acg gct gtg cgc tgt act ttt agt aca aca	240	glu gln asp gln ala arg thr ala val arg cys thr phe ser thr thr	250
879	cac agc cgt gaa gat gcg ctc gtg gca gcc tct gct ctt aaa tcc gcg	255	his ser arg glu asp ala leu val ala ala ser ala leu lys ser ala	265
920	gtc gcc tta atc aga ggg tgacgcctagt cagaggttta cgg	270	val ala leu ile arg gly	
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 <212> PRT  
 <213> Corynebacterium glutamicum

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 Leu Ser Pro Asp His Thr Gly Leu Ile Ser Pro Gln Gly Leu Arg Lys  
 35 40 45  
 Ala Val Arg Pro Asp Thr Thr Leu Ile Ser Ile Gly Tyr Ala Asn Asn  
 50 55 60  
 Gln Val Gly Thr Ile Gln Pro Ile Ala Gln Leu Ala Val Ser Ser  
 65 70 75 80  
 Thr Pro Phe His Thr Asp Ala Val Gln Ala Ala His Leu Thr Phe Asp  
 85 90 95  
 Leu Gly Val Asp Ala Leu Ser Leu Ser Gly His Lys Phe Gly Ala Pro  
 100 105 110  
 Lys Gly Ile Gly Val Leu Trp Ser Lys Leu Pro Leu Gln Pro Val Ile  
 115 120 125  
 His Gly Gly Gly Gln Gln Lys Gly Arg Ser Gly Thr Gln Asn Val  
 130 135 140  
 Ala Gly Ala Ile Ala Phe Ala Thr Ala Leu Gln Leu Ala Arg Ala Gln  
 145 150 155 160  
 Ser Tyr Pro Asp Leu Gly Gln Phe Ile Gln Gln Val Leu Thr Ile Pro  
 165 170 175  
 Gly Ala His Leu Thr Gly His Pro Arg Met Arg Ile Asp Gly His Ala  
 180 185 190  
 Ser Phe Leu Phe Asp Ser Ile Gly Ser Gln Thr Val Leu Gln Leu  
 195 200 205  
 Gln Arg Gln Gly Ile Val Cys Ser Pro Gly Ser Ala Cys Gly Ser Gly  
 210 215 220  
 Gln Val Ser His Val Leu Leu Ala Leu Gly Leu Gln Asp Gln Ala  
 225 230 235 240  
 Arg Thr Ala Val Arg Cys Thr Phe Ser Thr Thr His Ser Arg Gln Asp  
 245 250 255  
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 260 265 270  
 Gly

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>221> CDS
>222> (101)..(1273)
>223> RXN00435
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Val Gly Phe Asp Val

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5

211 ctt aat tca cat caa att ccg cag gtc ccg gag cgg gta gta ggc tga gga  
Leu Asn Ser His Gln Ile Pro Gln Val Pro Gln Arg Val Ala Ser Gly

25 30 35

307 cag cgc att gcg gtg gat cag ttg gag gct gct cgc gag gca gtt gcg  
Gln Pro Ile Ala Val Asp Gln Leu Gln Ala Ala Arg Gln Ala Val Ala

403 cag ttg gct cat acg tgc gcg cgc ggt ttg ggt ggg ttc gta cgt  
Gln phe leu ala his thr leu ala arg gly leu gly gly phe val arg

90  
95  
100

gag cga ttc cgc tcc ctc gag ggc gtt ttt agc tgg gcc gag ccc gat 499  
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[illegible]

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	Arg Val Ala Ser Gly Val Ala Ala Phe Arg Thr His Ala Gln Ile	35
	Ser Gln Val Thr Ser Gln Pro Ile Ala Val Asp Gln Leu Gln Ala Ala	50
	Arg Gln Ala Val Ala Ser Leu Ala Gly Val Asp Pro Asp Cys Val Val	65
	Leu Gly Pro Thr Arg Gln Phe Leu Ala His Thr Leu Ala Arg Gly Leu	85
	Gly Gly Phe Val Arg Arg Lys Ala Gly Val Val Leu Ser Arg Ala Asp	100
	Ala Asp Trp Leu Thr Ala Pro Phe Arg Ser Leu Asp Gly Val Phe Ser	115
	Trp Ala Gln Pro Asp Leu Gly Thr Gly Met Leu Pro Asp Trp Gln Tyr	130
	Gln Lys Leu Val Asp Gly Ser Thr Arg Leu Val Val Leu Ser Ala Ala	145
	His Pro Leu Leu Gly Thr Val Ala Pro Val Val Gly Lys Ile Val Asp Lys	165
	Val Arg Ala Arg Ser Arg Ala Trp Val Leu Val Asp Ala Thr Thr Tyr	180
	Ala Ala Tyr Arg Pro Leu Arg Leu Asp Gln Trp Gln Ala Asp Ile Val	195
	Met Leu Asp Leu Gly Gln Leu Gly Gly Pro Gln Ile Ser Ala Leu Ile	210
	Phe Arg Asp Thr Ser Met Phe Pro Arg Leu Asp Arg Thr Val Pro Leu	225
	Gln Leu Pro Ala Ser Ser Leu Pro His Gly Leu Leu Gly Gly Val Pro	245
	Asn Leu Val Arg His Leu Gly Asn Leu Asp Gln Asn Ala Pro Ser Val	260
	Val Gln Ala Met Gly Gln Met Ala Lys Phe His Lys Gly Leu Phe Gln	275
	His Leu Val Gln Ser Leu Gln Gly Leu His Ala Val His Ile Val Gly	290
	Ile Ser Gly Asp Ala Ala Gly Gln Asp Ala Pro Phe Leu Asp Arg Val	305





1000 900 800 700 600 500 400 300 200 100 0

130	135	140
ccc gca gat atg gtg tac cgc cga ttg gac aat cgt ttg atc act	Pro Ala Asp Met Val Tyr Arg Arg Leu Val Asp Asn Arg Leu Ile Thr	480
145	150	155
acc gtc agc cct gct gac ccg ctg ctc gaa gca atg ggt gtg act gaa	Thr Val Ser Pro Ala Asp Pro Leu Leu Gln Ala Met Gly Val Thr Gln	528
165	170	175
gct ggc gga tcg atc atc gga cta agc ccg ttg agc acc tac tat	Ala Gly Gly Ser Ile Thr Ile Gly Leu Ser Pro Phe Ser Thr Tyr Tyr	576
180	185	190
gaa gtc gat cag ctg acc agg gtc ctg gca tcg ctt gcc taaacgcgcaa	Gln Val Asp Gln Leu Thr Arg Val Leu Ala Ser Leu Ala	625
195	200	205
gcacgagctt gcc		638

<210> 654  
<211> 205  
<212> PRT  
<213> Corynebacterium glutamicum  
<400> 654

Val Asp Ala Thr Thr Tyr Ala Ala Tyr Arg Pro Leu Arg Leu Asp Gln  
1  
5  
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15  
20  
25  
30  
35  
40  
45  
50  
55  
60  
65  
70  
75  
80  
85  
90  
95  
100  
105  
110  
115  
120  
125  
130  
135  
140  
145  
150  
155  
160  
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Ala Gly Gly Ser Ile Thr Ile Gly Leu Ser Pro Phe Ser Thr Tyr Tyr

180 190 185 195 200 205  
 Gln Val Asp Gln Leu Thr Arg Val Leu Ala Ser Leu Ala

<210> 655  
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 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (101)..(535)  
 <223> FRXA02801

<400> 655  
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115 gttggaaggaa atgctgtggc ggttgaaagg agtgcccttc gtg ggt ttc gat gtg  
 Val Gly Phe Asp Val  
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 20  
 15  
 10  
 163 gcc agg gtt cgg ggg ctt tat acc tct ttg ggc gat ggc tgg acg tac  
 Ala Arg Val Arg Gly Leu Tyr Thr Ser Leu Gly Asp Gly Trp Thr Tyr  
 20

211 ctt aat tca cat caa atc ccg cag gtt ccg gag cgg gtg gcg tgg gga  
 Leu Asn Ser His Gln Ile Pro Gln Val Pro Gln Arg Val Ala Ser Gly  
 35  
 259 gtt gcg gcg gct ttc cgc acc cat ggc cag att tct gag gtt acg tgg  
 Val Ala Ala Phe Arg Thr His Ala Gln Ile Ser Gln Val Thr Ser  
 50

307 cag cgg att cgg gtt gtt gat cag ttg gag gct gct cgc gag gca gtt gcg  
 Gln Pro Ile Ala Val Asp Gln Leu Gln Ala Ala Arg Gln Ala Val Ala  
 65  
 355 tgg ttg gcg ggt gtt gtt gat ccg gac tgt gtt gtt ctt gtt ctt ggt  
 Ser Leu Ala Gly Val Asp Pro Cys Val Val Leu Gly Pro Thr Arg  
 80  
 403 cag ttt ttg gct cat aca ttg gcg cgc ggt ttg ggt ggg ttt gta cgt  
 Gln Phe Leu Ala His Thr Leu Ala Arg Gly Leu Gly Gly Phe Val Arg  
 100

451 cga aaa gcg ggc gtt gtt ttg ttg cgc ggc ggc gac gac tgg ctg acc  
 Arg Lys Ala Gly Val Val Leu Ser Arg Ala Asp Ala Asp Trp Leu Thr  
 115  
 499 gcg cgg ttc cgc tcc ctc gac ggc ggt ttt agc tgg gcc gag ccc gat  
 Ala Pro Phe Arg Ser Leu Asp Gly Val Phe Ser Trp Ala Gln Pro Asp  
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535 ttg ggc acc ggc atg ctg ccg gat tgg cag tac cag  
 Leu Gly Thr Gly Met Leu Pro Asp Trp Gln Tyr Gln  
 145  
 140

<210> 656



[illegible]



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 115 120 125  
 Val Val Ile Thr Glu Leu Glu His His Ala Asn Leu Val Pro Trp Glu  
 130 135 140  
 Glu Leu Cys Arg Arg Thr Gly Ala Thr Leu Lys Trp Tyr Lys Val Thr  
 145 150 155  
 Glu Asp Gly Arg Ile Asp Leu Asp Ser Leu Glu Leu Asp Glu Thr Val  
 165 170 175  
 Lys Val Val Ala Phe Thr His Glu Ser Asn Val Thr Gly Ala Val Ala  
 180 185 190  
 Asp Val Pro Glu Leu Val Arg Arg Ala Lys Ala Val Gly Ala Leu Thr  
 195 200 205  
 Val Leu Asp Ala Cys Glu Ser Val Pro His Met Pro Val Asn Phe His  
 210 215 220  
 Glu Leu Asp Val Asp Phe Ser Ala Phe Ser Gly His Lys Met Leu Gly  
 225 230 235  
 Pro Ala Gly Val Gly Val Val Tyr Ala Lys Ser Pro Ile Leu Asp Glu  
 245 250 255  
 Leu Pro Pro Phe Leu Thr Gly Gly Ser Met Ile Glu Val Val Thr Met  
 260 265 270  
 Glu Gly Ser Thr Tyr Ala Ala Pro Glu Arg Phe Glu Ala Gly Thr  
 275 280 285  
 Glu Met Thr Ser Glu Val Val Gly Leu Gly Ala Val Asp Met Leu  
 290 295 300  
 Asn Glu Ile Gly Met Glu Ala Ile Ala Ala His Glu His Ala Leu Thr  
 305 310 315  
 Ala Tyr Ala Leu Glu Lys Leu Thr Ala Ile Lys Gly Leu Thr Ile Ala  
 325 330 335  
 Gly Pro Leu Thr Ala Glu Glu Arg Gly Gly Ala Ile Ser Phe Gly Val  
 340 345 350  
 Glu Gly Ile His Pro His Asp Leu Gly Glu Val Leu Asp Asp Glu Gly  
 355 360 365  
 Val Asn Ile Arg Val Gly His His Cys Ala Trp Pro Val His Arg Ser  
 370 375 380  
 Met Asn Val Glu Ser Thr Ala Arg Ala Ser Phe Tyr Leu Tyr Asn Thr  
 385 390 395  
 Phe Glu Glu Ile Asp Arg Leu Ala Ala Ile Glu Lys Ala Lys Glu  
 405 410 415

Phe Phe Gly Val Gln  
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<210> 659

<211> 570

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(547)

<223> RXA02517

<400> 659

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115 Met Asn Leu Gln  
1  
5  
163 atg tac cag gag gtg atc ctg gac cac tac aaa aac cca cag cac aag  
Met Tyr Gln Val Ile Leu Asp His Tyr Lys Asn Pro Gln His Lys  
20  
15  
211 ggc ctt cgg gat cct ttc gat gct gag gtt cac gac cac gtc aac cct tct  
Gly Leu Arg Asp Pro Phe Asp Ala Gln Val His His Val Asn Pro Ser  
35  
30  
259 tgt ggc gac gaa ttg act ctg cgc gtg aag ctg tct gag gac ggc tcc  
Cys Gly Asp Gln Leu Thr Leu Arg Val Lys Leu Ser Gln Asp Gly Ser  
40  
45  
307 acc gtg gag gac gtc tcc tac gaa gca gtt ggt tgc tca atc agc cag  
Thr Val Gln Asp Val Ser Tyr Gln Ala Val Gly Cys Ser Ile Ser Gln  
65  
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355 ggc tcc acg tcc gtc atg ggc gag gac gtt ggt ggc caa ccc gtc gac  
Ala Ser Thr Ser Val Met Ala Gln Ile Val Gly Gln Pro Val Asp  
75  
80  
403 aag ggc ctg gaa aag ctg aca gaa ttt gag aag atg atc gtc tcc cgc  
Lys Ala Leu Gln Lys Leu Thr Gln Phe Gln Lys Met Ile Val Ser Arg  
90  
95  
451 ggt cag ttt gtt ggc gat gaa gat ctc atc gga gat ggc gtc gtc ttc  
Gly Gln Phe Val Gly Asp Gln Ile Gly Asp Gly Val Ala Phe  
115  
130  
499 tcc gga gtc gcc aag tac cgc gca cgc gtg aag tgc gcg ctg ctt ggg  
Ser Gly Val Ala Lys Tyr Pro Ala Arg Val Lys Cys Ala Leu Leu Gly  
120  
125  
547 tgg aag gct ttc cag gcg gca acc gct gac gct gtc gcg cac gca cat  
Trp Lys Ala Phe Gln Ala Thr Ala Asp Ala Val Ala His Ala His  
135  
140  
145 tagcccgctg tattaatgg agg

570

<210> 660



[illegible]

[illegible]

Met Gly Phe Ala Val Met Ser Gly Pro Leu Val Arg Ser Ser Tyr  
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 Arg Ala Gly Arg Leu Tyr Ala Gln Ala Met Gln Phe Arg Gly Gln Gln  
 295 300 305  
 atc cca gca cac ctc gcg cac ctg aag gat act tcc gga gga tcc acc  
 310 315 320 325  
 Ile Pro Ala His Leu Ala His Leu Lys Asp Thr Ser Gly Gly Ser Thr  
 330 335 340  
 ggc cag gaa gca tct aca ctt ctg gag cgt tac ggt gct tcc gaa gac  
 1123  
 Ala Gln Gln Ala Ser Thr Leu Leu Gln Arg Tyr Gly Ala Ser Gln Asp  
 345  
 acc cca gtg gtg tcc tcc aac taagcccgaa gtttttaac cgc  
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 Thr Pro Val Val Ser Phe Asn

<210> 662  
 <211> 348  
 <212> PRT  
 <213> Corynebacterium glutamicum  
 <400> 662

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 Val Lys Asn Gly Pro Gln Tyr Gln Asp Met Lys Gln Arg Val Ala Gly  
 35 40 45  
 Ala Ser Leu His Thr Val Cys Gln Gln Ala Gly Cys Pro Asn Ile His  
 50 55 60  
 Gln Cys Trp Gln Ser Arg Gln Ala Thr Phe Leu Ile Gly Gly Ala Asn  
 65 70 75 80  
 Cys Ser Arg Arg Cys Asp Phe Cys Met Ile Asn Ser Ala Arg Pro Gln  
 85 90 95  
 Pro Leu Asp Arg Gly Gln Pro Leu Arg Val Ala Gln Ser Val Arg Gln  
 100 105 110  
 Met Gln Leu Asn Tyr Ser Thr Ile Thr Gly Val Thr Arg Asp Asp Leu  
 115 120 125  
 Asp Asp Gln Gly Ala Trp Leu Tyr Ser Gln Val Val Arg Lys Ile His  
 130 135 140  
 Gln Leu Asn Pro His Thr Gly Val Gln Asn Leu Val Pro Asp Phe Ser  
 145 150 155 160  
 Gly Lys Lys Asp Leu Leu Gln Gln Val Phe Gln Ser Arg Pro Gln Val  
 165 170 175  
 Phe Ala His Asn Val Gln Thr Val Pro Arg Ile Phe Lys Arg Ile Arg  
 180 185 190

1167 1123 1075 1027 280 285 290 295 300 305 310 315 320 325 330 335 340 345

Pro Ala Phe Arg Tyr Gln Arg Ser Leu Asp Val Ile Arg Gln Ala Arg 195  
 200  
 205  
 Asp Phe Gly Leu Val Thr Lys Ser Asn Leu Ile Leu Gly Met Gly Gln 210  
 215  
 220  
 Thr Lys Gln Gln Ile Thr Gln Ala Leu Gln Asp Leu His Asp Ala Gly 225  
 230  
 235  
 240  
 Cys Asp Ile Ile Thr Ile Thr Gln Tyr Leu Arg Pro Gly Pro Leu Phe 245  
 250  
 255  
 His Pro Ile Gln Arg Trp Val Lys Pro Gln Gln Phe Leu Gln His Ala 260  
 265  
 270  
 Asp Ala Ala Lys Gln Met Gly Phe Ala Ala Val Met Ser Gly Pro Leu 275  
 280  
 285  
 Val Arg Ser Ser Tyr Arg Ala Gly Arg Leu Tyr Ala Gln Ala Met Gln 290  
 295  
 300  
 Phe Arg Gly Gln Gln Ile Pro Ala His Leu Ala His Leu Lys Asp Thr 305  
 310  
 315  
 320  
 Ser Gly Gly Ser Thr Ala Gln Gln Ala Ser Thr Leu Leu Gln Arg Tyr 325  
 330  
 335  
 Gly Ala Ser Gln Asp Thr Pro Val Val Ser Phe Asn 340  
 345

aaaccgccac tcccttcca ctgggagtg gcggtttgt cgttcctgc atgcagtgtg 60  
 115  
 163  
 211  
 259

tgactatca accctgttag ggctagggtg gatattcatc atg act gca cca aga  
 Met Thr Ala Pro Arg  
 1  
 5  
 gat cct ttt ttc ccc gca gat ctt tct atc cgc gcg tct gca gag ccc  
 Asp Pro Phe Phe Pro Ala Asp Leu Ser Ile Arg Ala Ser Ala Gln Pro  
 10  
 15  
 20  
 25  
 30  
 35  
 att gaa att cag cag ttg ggt ttg atc gat tat caa gag gcc tgg gat  
 Ile Gln Ile Gln Arg Leu Gly Leu Ile Asp Tyr Gln Gln Ala Trp Asp  
 40  
 45  
 50  
 tat caa gca gag ctt gct acc cgt agg gct aat gat gaa atc cct gat  
 Tyr Gln Ala Gln Leu Ala Thr Arg Arg Ala Asn Asp Gln Ile Pro Asp

[illegible]

Ala Ser Ala Gln Pro Ile Gln Ile Gln Arg Leu Gly Leu Ile Asp Tyr  
20 25 30

Gln Gln Ala Trp Asp Tyr Gln Ala Thr Arg Ala Asn  
35 40 45

Asp Gln Ile Pro Asp Gln Leu Ile Leu Gln His Pro Ser Val Tyr  
50 55 60

Thr Ala Gly Lys Arg Thr Gln Pro Gln Asp Leu Pro Thr Asn Gly Leu  
65 70 75 80

Pro Val Ile Asn Ala Asp Arg Gly Arg Ile Thr Trp His Gly Pro  
85 90 95

Gly Gln Leu Val Ile Tyr Pro Ile Ile Lys Leu Ala Asp Pro Ile Asp  
100 105 110

Val Val Asp Tyr Val Arg Arg Leu Gln Gln Ala Leu Ile Gln Val Val  
115 120 125

Gly Asp Met Gly Val Ala Gly Ala Gly Arg Ile Asp Gly Arg Ser Gly  
130 135 140

Val Trp Val Pro Ala His Asp Gly Trp Val Asp Ser Lys Val Ala Ala  
145 150 155 160

Ile Gly Ile Arg Ile Thr Arg Gly Val Ala Met His Gly Val Ala Ile  
165 170 175

Asn Cys Asn Asn Thr Leu Asp Phe Tyr Gln His Ile Ile Pro Cys Gly  
180 185 190

Ile Ala Asp Ala Gly Leu Ser Thr Leu Ser Arg Gln Leu Lys Arg Asp  
195 200 205

Val Ser Val Gln Gln Leu Val Gln Pro Ser Ile Arg Ala Leu Asp Asp  
210 215 220

Ala Leu Ala Gly Arg Leu Val Val Ser Asp His Ser Phe Gly Ser Ala  
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Pro Asp Pro Thr Lys Asn Leu Pro Lys Arg Gly  
245 250

<210> 665

<211> 1179

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1156)

<223> RXA02106

<400> 665

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aagcaaatc tcttagcaa atcgggtac tgtggggc atg aac cat tt 115



330	235	240	245	883	931	979	1027	1075	1123	1176	aag	1179																							
gct gca cag aaa cgt cgc agt ggc gca gtc ctc cac cag gtc acc atg	Ala Ala Gln Lys Arg Arg Ser Gly Ala Val Leu His His Val Thr Met	250	255	260	tcc tat gac atc gat gcg gac atg atg acc cag gtc ctg cgc atc gga	Ser Tyr Asp Ile Asp Ala Asp Met Met Thr Gln Val Leu Arg Ile Gly	265	270	275	280	aag gtg aag att tcc gac aag ggt ctt cgc agc gca aag aag cgc gtt	Lys Val Lys Ile Ser Asp Lys Gly Leu Arg Ser Ala Lys Lys Arg Val	285	290	295	gat cct ctg cgc cgc caa acg gca tca cgt gag caa atc atc gac	Asp Pro Leu Arg Arg Gln Thr Gly Ala Ser Arg Gln Ile Ile Asp	300	305	310	acc cta aag tcc aca ttc agt gct agg tac ggc gcg caa gaa gta gag	Thr Leu Lys Ser Thr Phe Ser Ala Arg Tyr Gly Ala Gln Val Gln	315	320	325	ctc agc gat gaa gat ttc gcg gca ggc cac gac cta gta aaa acc aaa	Leu Ser Asp Gln Asp Phe Ala Ala Gly His Asp Leu Val Lys Thr Lys	330	335	340	tac gcc acc gag gag tag act aag cga gtc caa tagttctcat ggatctgcac	Tyr Ala Thr Gln Gln Trp Thr Lys Arg Val Gln	345	350	1176
<210> 666	<211> 352	<212> PRT	<213> Corynebacterium glutamicum	<400> 666	Met Asn Asn His Phe Gln Leu Lys Val Pro Gly Gly Lys Leu Val Val	1	5	10	15	Val Asp Val Thr Thr Asp Leu Asp Ser Ile Ala Asp Val Lys Ile Ser	20	25	30	Gly Asp Phe Phe Leu Gln Pro Asp Gln Ala Phe Phe Ala Leu Gly Arg	35	40	45	Ala Leu Gln Gly Ala Ser Val Gly Asp Asn Thr Asp Arg Leu Gln Ala	50	55	60	Lys Leu Asp Ala Ala Leu Ala Gln Tyr Asp Asp Val Gln Leu His Gly	65	70	75	80	Phe Ser Thr Ala Asp Ile Ala Leu Ala Val Arg Arg Ala Val Thr Gly	85	90	95	Ala Gln Asp Phe Thr Asp Tyr Gln Trp Gln Ile Leu His Pro Gly Val	100	105	110	Leu Pro Thr Pro Leu Asn Val Ala Leu Asp Gln Leu Leu Asp Gln



115 Val Ala Ser Gly Gln Arg Gly Pro Thr Met Arg Ile Trp Asp Trp Asp  
 130 135 140  
 145 Asp Arg Ala Thr Val Ile Gly Ser Phe Gln Ser Tyr Val Asn Gln Ile  
 150 155  
 160 Asn Gln Gln Gly Val Asn Gln His Gly Val Thr Val Val Arg Arg Met  
 165 170 175  
 180 Ser Gly Gly Gly Ala Met Phe Met Gln Gly Gly Asn Cys Ile Thr Tyr  
 185 190  
 195 Ser Leu Tyr Ala Pro Gln Ser Leu Val Ala Gly Leu Ser Tyr Gln Gln  
 200 205  
 210 Ser Tyr Gln Tyr Leu Asp Arg Trp Val Ile Ala Leu Lys Thr His  
 215 220  
 225 Asp Val Asp Ala Trp Tyr Val Pro Ile Asn Asp Ile Thr Ser Thr Gly  
 230 235 240  
 245 Gly Lys Ile Gly Gly Ala Ala Gln Lys Arg Arg Ser Gly Ala Val Leu  
 250 255  
 260 His His Val Thr Met Ser Tyr Asp Ile Asp Ala Asp Met Met Thr Gln  
 265 270  
 275 Val Leu Arg Ile Gly Lys Val Lys Ile Ser Asp Lys Gly Leu Arg Ser  
 280 285  
 290 Ala Lys Lys Arg Val Asp Pro Leu Arg Arg Gln Thr Gly Ala Ser Arg  
 295 300  
 305 Gln Gln Ile Ile Asp Thr Leu Lys Ser Thr Phe Ser Ala Arg Tyr Gly  
 310 315 320  
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 340 Leu Val Lys Thr Lys Tyr Ala Thr Gln Gln Trp Thr Lys Arg Val Gln  
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<210> 667  
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115 ttcggtttaa acgacacgac ttgcgagagag tcttaataata atg gcg ttc tcc gta  
Met Ala Phe Ser Val 1  
5

163 gag atg ccc gag ctg ggc gaa tca gta acc gaa ggc acg atc acc cag  
Glu Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly Thr Ile Thr Gln 20

211 tgg ttg aag tct gtt ggt gac act gtt gag gta gat gag cgg ttg ctc  
Trp Leu Lys Ser Val Gly Asp Thr Val Glu Val Asp Glu Pro Leu Leu 35

259 gag gtc tca act gac aag gtc gac acc gag att ccc tct cct gtc gcc  
Glu Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro Ser Pro Val Ala 50

307 ggt gtc atc cta gag att aag gct gaa gag gat gac acc gtc gac gtc  
Gly Val Ile Leu Glu Ile Lys Ala Glu Glu Asp Thr Val Asp Val 65

355 ggc ggt gtc att gca ata atc ggc gat gct gat gag act cct gcc aac  
Gly Gly Val Ile Ala Ile Ile Gly Asp Ala Asp Glu Thr Pro Ala Asn 85

403 gaa gct cct gcc gac gag gca gca gct cct gcc gaa gag gaa gaa cca  
Glu Ala Pro Ala Asp Glu Ala Pro Ala Glu Glu Glu Pro 100

<210> 668

<211> 101

<212> PRT

<213> Corynebacterium glutamicum

<400> 668

Met Ala Phe Ser Val Glu Met Pro Glu Leu Gly Glu Ser Val Thr Glu 1  
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25 30

Asp Glu Pro Leu Leu Glu Val Ser Thr Asp Lys Val Asp Thr Glu Ile 35  
40 45

Pro Ser Pro Val Ala Gly Val Ile Leu Glu Ile Lys Ala Glu Asp 50  
55 60

Asp Thr Val Asp Val Gly Gly Val Ile Ala Ile Ile Gly Asp Ala Asp 65  
70 75 80

Glu Thr Pro Ala Asn Glu Ala Pro Ala Asp Glu Ala Pro Ala Pro Ala 85  
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Glu Glu Glu Pro 100

<210> 669

<211> 1305

<212> DNA

<213> Corynebacterium glutamicum

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Met Ala Phe Ser Val 1  
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<400> 670  
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Pro Ser Lys Val Ser Asp Gln Lys Arg 50  
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<210> 673  
<211> 1005  
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<221> CDS  
<222> (101)..(982)  
<223> RXA02717  
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Met Pro Pro Arg Asp 1  
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gat gca gct gaa gag cgt ctt tac cgc gca gca gag gtc ttc cat gac 163  
Asp Ala Ala Gln Arg Leu Tyr Arg Ala Ala Gln Val Phe His Asp 20  
ctc ggt gca tgc ttt gtc tcc gtg act tat ggt gct ggc gga tca acc 211  
Leu Gly Ala Ser Phe Val Ser Val Thr Tyr Gly Ala Gly Ser Thr 35  
cgt gag aga acc tca cgt att gct cga cga tta gcg aaa caa cgc ttg 259  
Arg Gln Arg Thr Ser Arg Ile Ala Arg Arg Leu Ala Lys Gln Pro Leu 50  
acc act cgt gtc cac ctg acc ctg gtt aac cac act cgc gaa gag atg 307  
Thr Thr Leu Val His Leu Thr Leu Val Asn His Thr Arg Gln Gln Met 65  
aag gca att ctt cgg gaa tac cta gag ctg gga tta aca aac ctg ttg 355  
Lys Ala Ile Leu Arg Gln Tyr Leu Gln Leu Gly Leu Thr Asn Leu Leu 85  
gcg ctt cga gga gat cgc cct gga gag cca tta ggc gat tgg gtg agc 403  
Ala Leu Arg Gly Asp Pro Gly Asp Pro Leu Gly Asp Trp Val Ser 100  
acc gat gga gga ctg aac tat gcc tct gag ctc atc gat ctt att aag 451  
Thr Asp Gly Gly Leu Asn Tyr Ala Ser Gln Leu Ile Asp Leu Ile Lys 115  
tcc act cct gag ttc cgg gaa ttc gag ctc gac ctc ggt atc gcc tcc ttc ccc 499  
Ser Thr Pro Gln Phe Arg Gln Phe Asp Leu Gly Ile Ala Ser Phe Pro 130  
gaa ggg cat ttc cgg gca aaa act cta gaa gaa gac acc aaa tac act 547  
Gln Gly His Phe Arg Ala Lys Thr Leu Gln Asp Thr Lys Tyr Thr 145  
ctg gcg aag cgt gga gga gca gag tac tcc atc acg cag atg ttc 595  
Leu Ala Lys Leu Arg Gly 155  
150

643	ttt gat gtc gaa gac tac ctg cga ctt cgt gat cgc ctt gtc gtc gaa gac	phe asp val glu asp tyr leu arg leu arg asp arg leu val ala ala	170	175	180
691	gac ccc att cat ggt ggc aag cca atc att cct ggc atc atg ccc att	asp pro ile his gln ala lys pro ile pro gly ile met pro ile	185	190	195
739	acg agc ctg cgg tct gtc cgt cga cag gtc gaa ctc tct ggt gtc caa	thr ser leu arg ser val arg gln val glu leu ser gly ala gln	200	205	210
787	ctg ccg agc caa cta gaa gaa tca ctt gtt cga gct gca aac ggc aat	leu pro ser gln leu glu ser leu val arg ala ala asn gly asn	215	220	225
835	gaa gaa ggc aac aaa gac gag atc cgc aag gtc ggc att gaa tat tcc	glu glu ala asn lys asp glu ile arg lys val gly ile glu tyr ser	230	235	240
883	acc aat atg gca gag cga ctc att gcc gaa ggt gcg gaa gat ctg cac	thr asn met ala glu arg leu ile ala glu gly ala glu asp leu his	250	255	260
931	ttc atg acg ctt aac ttc acc cgt gca acc caa gaa gtc tgc tac aac	phe met thr leu asn phe thr arg ala thr gln glu val leu tyr asn	265	270	275
979	ctt ggc atg gcg cct gct tgg gga gca gag cac ggc caa gac gcg gtc	leu gly met ala pro ala trp gly ala glu his gly gln asp ala val	280	285	290
1005	cgt taagccctct taggaatcat gaa	arg			
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<213> Corynebacterium glutamicum					
<400> 674					
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20	Glu Val Phe His Asp Leu Gly Ala Ser Phe Val Ser Val Thr Tyr Gly		20	25	30
35	Ala Gly Gly Ser Thr Arg Glu Arg Thr Ser Arg Ile Ala Arg Arg Leu		35	40	45
50	Ala Lys Gln Pro Leu Thr Thr Leu Val His Leu Thr Leu Val Asn His		50	55	60
65	Thr Arg Glu Glu Met Lys Ala Ile Leu Arg Glu Tyr Leu Glu Leu Gly		65	70	75
80	Leu Thr Asn Leu Leu Ala Leu Arg Gly Asp Pro Gly Asp Pro Leu		80	85	90
95			95		



Gly Asp Trp Val Ser Thr Asp Gly Gly Leu Asn Tyr Ala Ser Gln Leu 100  
105

Ile Asp Leu Ile Lys Ser Thr Pro Gln Phe Arg Gln Phe Asp Leu Gly 115  
120

Ile Ala Ser Phe Pro Gln Gly His Phe Arg Ala Lys Thr Leu Gln Gln 130  
135

Asp Thr Lys Tyr Thr Leu Ala Lys Leu Arg Gly Gly Ala Gln Tyr Ser 145  
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Ile Thr Gln Met Phe Phe Asp Val Gln Asp Tyr Leu Arg Leu Arg Asp 165  
170

Arg Leu Val Ala Ala Asp Pro Ile His Gly Ala Lys Pro Ile Ile Pro 180  
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Gly Ile Met Pro Ile Thr Ser Leu Arg Ser Val Arg Gln Val Gln 195  
200

Leu Ser Gly Ala Gln Leu Pro Ser Gln Leu Gln Ser Leu Val Arg 210  
215

Ala Ala Asn Gly Asn Gln Ala Asn Lys Asp Gln Ile Arg Lys Val 225  
230

Gly Ile Gln Tyr Ser Thr Asn Met Ala Gln Arg Leu Ile Ala Gln Gly 245  
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Ala Gln Asp Leu His Phe Met Thr Leu Asn Phe Thr Arg Ala Thr Gln 260  
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Met Ser Gln Thr Lys  
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Gln Gln Leu Arg Thr Lys Leu Arg Gln Ala Arg Thr Asn Met Asp Gln 20  
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 Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala Tyr Val Pro Val 40  
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 Arg Thr Gln Pro Gly Gly Arg Leu Leu Leu Leu Asp Ala Leu His Ala Gln 65  
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 Thr Ser Ala Leu Ile Leu Pro Val Ser Leu Gln Asp Arg Arg Leu Asp 85  
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 tgg gct ctt tat gaa ggc cca acc agc ctt gtt cct ggc gca ttt ggc 403  
 Trp Ala Leu Tyr Gln Gly Pro Thr Ser Leu Val Pro Gly Ala Phe Gly 100  
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 Ile Gln Gln Pro Gly Gly Thr Arg Leu Gly Pro Gln Ala Leu Asn Phe 110  
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 tgc gac ctt gtc atc gcc ccc gca ctg gca tgc acc ccc agt gga atc 499  
 Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys Thr Pro Ser Gly Ile 130  
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 agg cta ggt aaa ggt ggc ggt ttc tac gac cgc gct cta gcc acc gga 547  
 Arg Leu Gly Lys Gly Gly Gly Phe Tyr Asp Arg Ala Leu Ala Thr Gly 145  
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 Ala Asn Val Ser Tyr Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala 35  
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 Ala Tyr Val Pro Val Arg Thr Gln Pro Gly Gly Arg Leu Leu Asp 50  
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 Ala Leu His Ala Gln Thr Ser Ala Leu Ile Leu Pro Val Ser Leu Gln

GenBank accession number: F01001.1  
Protein name: Corynebacterium glutamicum  
Gene name: gltA  
Accession number: F01001.1

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Pro Gly Ala Phe Gly Ile Gln Gln Pro Gly Gly Thr Arg Leu Gly Pro  
Gln Ala Leu Asn Phe Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys  
Thr Pro Ser Gly Ile Arg Leu Gly Lys Gly Gly Gly Phe Tyr Asp Arg  
Ala Leu Ala Thr Gly Val Lys Ala Asp Val Ile Thr Leu Leu Phe Asn  
Gly Gln Ile Arg Asp Ile  
165  
677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000  
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Met Ser Gln Thr Lys  
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cag gaa ctg cgc acg aag ctt cgg gaa gcg cgc acc aat atg gat gag  
Gln Gln Leu Arg Thr Lys Leu Arg Gln Ala Arg Thr Asn Met Asp Gln  
10 15 20  
gct tct cgc acg cga gaa aac gca gcc atc atc ggc aac gtt tct tat  
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25 30 35  
tac atc cgc tca aag cag cca aaa agg att gcc gct tac gtg ccg gtg  
Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala Ala Tyr Val Pro Val  
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cgt acc gaa cct ggt ggg cga ttg ctt ctt gac gcc ctc cac gcc gaa  
Arg Thr Gln Pro Gly Gly Arg Leu Leu Leu Asp Ala Leu His Ala Gln  
55 60 65  
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Thr Ser Ala Leu Ile Leu Pro Val Ser Leu Gln Asp Arg Arg Leu Asp  
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Trp Ala Leu Tyr Gln Gly Pro Thr Ser Leu Val Pro Gly Ala Phe Gly  
90 95 100  
403

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 Ile Gln Glu Pro Gly Thr Arg Leu Gly Pro Glu Ala Leu Asn Phe  
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 Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys Thr Pro Ser Gly Ile  
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 Arg Leu Gly Lys Gly Gly Phe Tyr Asp Arg Ala Leu Ala Thr Gly  
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&lt;210&gt; 678

&lt;211&gt; 165

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 678

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Ala Asn Val Ser Tyr Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala  
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Ala Tyr Val Pro Val Arg Thr Glu Pro Gly Gly Arg Leu Leu Asp  
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Ala Leu His Ala Glu Thr Ser Ala Leu Ile Leu Pro Val Ser Leu Glu  
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 75  
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Asp Arg Arg Leu Asp Trp Ala Leu Tyr Glu Gly Pro Thr Ser Leu Val  
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 90  
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Pro Gly Ala Phe Gly Ile Gln Glu Pro Gly Gly Thr Arg Leu Gly Pro  
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 105  
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Glu Ala Leu Asn Phe Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys  
 115  
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Thr Pro Ser Gly Ile Arg Leu Lys Gly Gly Gly Phe Tyr Asp Arg  
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Gly Glu Ile Arg Asp  
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&lt;211&gt; 579

&lt;212&gt; DNA

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 Met Ile Gly Ala Ile 1  
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tg gca caa ggc cgt gac ggc atc atc ggc gac ggc acc gac atg ccc 163  
 Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp Gly Thr Asp Met Pro 20

tgc cac atc ccc gaa gac ctc aaa cac ttc aag aaa acc acc atg ggc 211  
 Trp His Ile Pro Gln Asp Leu Lys His Phe Lys Lys Thr Thr Met Gly 35

cag ccg gtc atc atg ggt cgt cgc acg tgg gag tct ttg ccg ttc aag 259  
 Gln Pro Val Ile Met Gly Arg Arg Thr Trp Gln Ser Leu Pro Phe Lys 50

ccg ctc ccc ggc cgc gag aac ttc atc ttc tcc tca cgc gag ccc ggc 307  
 Pro Leu Pro Gly Arg Gln Asn Phe Ile Leu Ser Ser Arg Gln Pro Gly 65

gac tgg tcc gcc ggc ggc aca gtc gtc acc gaa atc cct aaa agc ggc 355  
 Asp Trp Ser Ala Gly Thr Val Val Thr Gln Ile Pro Lys Ser Gly 85

tgg atc atg ggc ggc ggc gag gtc tac aag ggc acc gtc ggc agc ggc 403  
 Trp Ile Met Gly Gly Gln Val Tyr Lys Ala Thr Val Gly Ser Ala 100

gac gtc tta gaa ata acg ctt atc gac gcc acc ttc gat gtc tcc act 451  
 Asp Val Leu Gln Ile Thr Leu Ile Asp Ala Thr Phe Asp Val Ser Thr 115

ccc gtc ttc tac gca ccc gaa atc ccg ggc aac ttc aac ctc gat gac gaa 499  
 Pro Val Tyr Ala Pro Gln Ile Pro Ala Asn Phe Asn Leu Asp Asp Gln 130

tcc gag tgg ttt acc tca ggc gag tat cgt tac aag ttc cag cgc tac 547  
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cga agt tct cct gaa gtt cgt aat cgt ccg agc gct gcg cct gaa gag 163  
Pro Ser Ser Ser Pro Gln Val Arg Asn Arg Pro Ser Ala Ala Pro Gln Gln  
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cgt cag ttg gtc ctc act ttg ggc tgc cct gac tcc act gga atg gtg 211  
Arg Gln Phe Val Leu Thr Phe Gly Cys Pro Asp Ser Thr Gly Ile Val 35  
gca aag tgc tgc tgc cta gct gag cgt gag ggt tgg att act gag 259  
Ala Lys Leu Ser Ser Phe Leu Ala Gln Arg Gly Gly Trp Ile Thr Gln 50  
gct gga tat ttc acg gat cct gat tgc aat tgg ttc ttg act cgt cag 307

Met Ile Gly Ala Ile Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp 1  
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Lys Thr Thr Met Gly Gln Pro Val Ile Met Gly Arg Thr Trp Gln 35  
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Ser Leu Pro Phe Lys Pro Leu Pro Gly Arg Gln Asn Phe Ile Leu Ser 50  
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Ser Arg Gln Pro Gly Asp Trp Ser Ala Gly Gly Thr Val Val Thr Gln 65  
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Ile Pro Lys Ser Gly Trp Ile Met Gly Gly Gln Val Tyr Lys Ala 85  
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Thr Val Gly Ser Ala Asp Val Leu Gln Ile Thr Leu Ile Asp Ala Thr 100  
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Phe Asp Val Ser Thr Pro Val Tyr Ala Pro Gln Ile Pro Ala Asn Phe 115  
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Asn Leu Asp Asp Gln Ser Gln Trp Phe Thr Ser Gly Gln Tyr Arg Tyr 130  
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Lys Phe Gln Arg Tyr Ile Lys Val 145  
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Gly Trp Ile Thr Gln Ala Gly Tyr Phe Thr Asp Pro Asp Ser Asn Trp	50
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Phe Phe Thr Arg Gln Ala Ile Arg Ala Gln Ser Ile Asp Thr Thr Ile	60
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Glu Gln Leu Arg Gln Gln Phe Ala Pro Leu Ala Gln Gln Phe Gly Pro	85
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Arg Ala Lys Trp Ser Phe Thr Asp Thr Ala Gln Val Lys Lys Ala Val	100
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Leu Leu Val Ser Lys Gln Gly His Cys Leu His Asp Leu Leu Gly Arg	115
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Val Ala Gln Asn Asp Tyr Pro Met Gln Val Val Ala Val Val Gly Asn	130
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His Gln Asn Leu Arg Tyr Ile Ala Gln Asn His Asn Val Pro Phe Phe	145
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His Val Pro Phe Pro Lys Asp Ala Val Gly Lys Arg Lys Ala Phe Asp	160
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Gln Val Ala Gln Ile Val Asn Gly Tyr Asp Pro Asp Ala Ile Val Leu	180
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Ala Arg Phe Met Gln Ile Leu Pro Pro Asp Leu Cys Gln Met Trp Ala	195
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Gly Arg Val Leu Asn Ile His His Ser Phe Leu Pro Ser Phe Met Gly	210
	215
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Ala Arg Pro Tyr His Gln Ala Tyr Ser Arg Gly Val Lys Leu Ile Gly	225
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Ala Thr Cys His Tyr Ala Thr Gly Asp Leu Asp Asp Gly Pro Ile Ile	245
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Gln Gln Asp Val Ile Arg Val Thr His Lys Asp Thr Pro Thr Gln Met	260
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295

305



[illegible]

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 Tyr Gly Asn Arg Thr Val Val Phe Asp  
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cgc 582

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 His Val Pro Phe Pro Lys Asp Ala Val Gly Lys Arg Lys Ala Phe Asp  
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 Gln Val Ala Gln Ile Val Asn Gly Tyr Asp Pro Asp Ala Ile Val Leu  
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 Ala Arg Phe Met Gln Ile Leu Pro Pro Asp Leu Cys Gln Met Trp Ala  
 65  
 70  
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 80  
 Gly Arg Val Leu Asn Ile His His Ser Phe Leu Pro Ser Phe Met Gly  
 85  
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 95  
 Ala Arg Pro Tyr His Gln Ala Tyr Ser Arg Gly Val Lys Leu Ile Gly  
 100  
 105  
 110  
 Ala Thr Cys His Tyr Ala Thr Gly Asp Leu Asp Asp Gly Pro Ile Ile  
 115  
 120  
 125  
 Gln Gln Asp Val Ile Arg Val Thr His Lys Asp Thr Pro Thr Gln Met  
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 135  
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 Gln Arg Leu Gly Arg Asp Ala Gln Lys Gln Val Leu Ala Arg Gly Leu  
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 Val Phe Asp

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 Val Thr Ala Ile Lys 1

163 ctt gat gga aac tta tac cgc ggg gaa atc ttc gcc gac ttg gaa cag  
 Leu Asp Gly Asn Leu Tyr Arg Gly Gln Ile Phe Ala Asp Leu Gln 20

211 cgc gtt gct gct gct gct gct gct gct gct gct gct gct gct gct gct gct  
 Arg Val Ala Ala Leu Lys Gln Lys Gly Ile Val Pro Gly Leu Ala Thr 35

259 gtg ctg gct gct gct gct gct gct gct gct gct gct gct gct gct gct gct  
 Val Leu Val Gly Asp Pro Ala Ser His Ser Tyr Val Lys Met Lys 50

307 cat cgt gac tgt gag cag att ggt gtg aac tgc atc cgt aag gat ctg  
 His Arg Asp Cys Gln Ile Gly Val Asn Ser Ile Arg Lys Asp Leu 65

355 cct gct gat gct gat gct gat gct gat gct gat gct gat gct gat gct gat  
 Pro Ala Asp Val Thr Gln Gln Leu Phe Ala Val Ile Asp Gln Leu 85

403 aac aac gat gat gat tct tgc act ggt tac att gtg cag ctt cct ttg cct  
 Asn Asn Asp Asp Ser Cys Thr Gly Tyr Ile Val Gln Leu Pro Leu Pro 100

451 aag cac ttg gac gaa aac gct gct gct gct gct gct gct gct gct gct gct  
 Lys His Leu Asp Gln Asn Ala Val Leu Gln Arg Ile Asp Pro Ala Lys 115

499 gat gct gat gat gct gct gct gct gct gct gct gct gct gct gct gct gct  
 Asp Ala Asp Gly Leu His Pro Val Asn Leu Gly Lys Leu Val Leu Asn 130

547 gag cca gct cca cca ctg cca tgc acc cgc aat ggt tcc atc agc ttg ttg  
 Gln Pro Ala Pro Leu Pro Cys Thr Pro Asn Gly Ser Ile Ser Leu Leu 145

595 cgt cgt ttc ttc ggc gct gag ctt gat ggc ggc aag gtt gtt gtt gtt gtt gtt  
 Arg Arg Phe Gly Val Gln Leu Asp Gly Ala Lys Val Val Val Ile Gly 165

643 cgt ggc gct acc gtt ggt ggt cgc cca att ggc ctg atg ctg acc cgc cgt  
 Arg Gly Val Thr Val Gly Arg Pro Ile Gly Leu Met Leu Thr Arg Arg 180

691 tcc gag aac tcc acg gtt act ttg tgc cac act ggc acg aag gat ctg  
 Ser Gln Asn Ser Thr Val Thr Leu Cys His Thr Gly Thr Lys Asp Leu 195

739 gct gcg gag acc cgt gct gct gac gct gct gct gct gct gct gct gct gct  
 Ala Ala Gln Thr Arg Ala gct gct gct gct gct gct gct gct gct gct gct 195

200 787 cgc cac atg ctg acc gca gac atg gtc aag cca ggc gca ggc gtc gtc ctc gac gtc cac  
 Pro His Met Leu Thr Ala Asp Met Val Lys Pro Gly Ala Val Leu 215  
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 Asp Val Gly Val Ser Arg Lys Asp Gly Lys Leu Gly Asp Val His 245  
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 Pro Asp Val Trp Glu Val Ala Gly Ala Val Ser Pro Asn Pro Gly Gly 275  
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 Val Gly Pro Leu Thr Arg Ala Phe Leu Val His Asn Val Val Glu Arg 295  
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 Tyr Val Lys Met Lys His Arg Asp Cys Glu Gln Ile Gly Val Asn Ser 50  
 Ile Arg Lys Asp Leu Pro Ala Asp Val Thr Gln Glu Leu Phe Ala 65  
 Val Ile Asp Glu Leu Asn Asn Asp Asp Ser Cys Thr Gly Tyr Ile Val 85  
 Gln Leu Pro Leu Pro Lys His Leu Asp Glu Asn Ala Val Leu Glu Arg 100  
 Ile Asp Pro Ala Lys Asp Ala Asp Gly Leu His Pro Val Asn Leu Gly 115  
 Lys Leu Val Leu Asn Glu Pro Ala Pro Leu Pro Cys Thr Pro Asn Gly 130  
 Ser Ile Ser Leu Leu Arg Arg Phe Gly Val Glu Leu Asp Gly Ala Lys 145  
 Val Val Val Ile Gly Arg Gly Val Thr Val Gly Arg Pro Ile Gly Leu 165  
 Val Val Val Ile Gly Arg Gly Val Thr Val Gly Arg Pro Ile Gly Leu 175



451	ggt aag tcc ggc aag gtc act ggc ctg tcc aag ctg gcg cgt tta gcg	105	Gly Lys Ser Gly Lys Val Thr Gly Leu Ser Lys Leu Ala Arg Leu Ala	115
499	gat atg ttt gct aag cga cct cag gtc cag gag cgc ttg acc tcc caa	120	Asp Met Phe Ala Lys Arg Pro Gln Val Gln Arg Leu Thr Ser Gln	130
547	att gcg gat gct ctc gtc gaa aag ctt gat gcc cag gcc gtc gcc gtc	140	Ile Ala Asp Ala Leu Val Gln Lys Leu Asp Ala Gln Ala Val Ala Val	145
595	gtg att gaa gct gag cac ctg tgc atg gcc atg cgc gga atc cgt aag	155	Val Ile Gln Ala Gln His Leu Cys Met Ala Met Arg Gly Ile Arg Lys	165
643	cct ggt gct gtc acc acc acg tct gcg gtc cgc ggc ggt ttt aag aac	170	Pro Gly Ala Val Thr Thr Thr Ser Ala Val Arg Gly Phe Lys Asn	180
688	aac gct gcc tcc cgc gct gag gtc tcc tcc ctg att cgg ggc cac	185	Asn Ala Ala Ser Arg Ala Gln Val Phe Ser Leu Ile Arg Gly His	195
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35	Gln Gly Leu Leu Gln Thr Pro Ala Arg Val Ala Arg Ala Tyr Lys Gln	40		45
50	Thr Phe Ala Gly Leu His Gln Asp Pro Thr Thr Val Leu Gln Lys Thr	55		60
65	Phe Ser Gln Gly His Gln Gln Leu Val Leu Val Arg Gln Ile Pro Ile	70		75
80				85
85	Tyr Ser Met Cys Gln His His Leu Val Pro Phe Phe Gly Val Ala His	90		95
100	Ile Gly Tyr Ile Pro Phe Phe Gly Val Ala His Ile Gly Tyr Ile Pro	95		100

130 140 135

Gln Ala Val Ala Val Ile Gln Ala Gln His Leu Cys Met Ala Met 145 150 155 160

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Met Ala Asp Arg Ile 1

gaa ctt aaa ggc ctt gaa tgc ttc gga cac cac ggt gtg ttc gac ttt 163

Glu Leu Lys Gly Leu Gln Cys Phe Gly His His Gly Val Phe Asp Phe 20

gaa aaa gag caa ggc caa ggc ctt ctt att gtg gat gtc acc tgc tgg atg 211

Glu Lys Gln Gln Gly Gln Pro Phe Ile Val Asp Val Thr Cys Trp Met 35

gat ttc gat gcc gca ggt gcc agc gat gac ctt tcc gac acc gta gat 259

Asp Phe Asp Ala Ala Gly Ala Ser Asp Asp Leu Ser Asp Thr Val Asp 50

tac ggc ggc ttg gca ttg ttg gtt gct gaa atc gtg gaa ggc cca tcc 307

Tyr Gly Ala Leu Ala Leu Leu Val Ala Gln Ile Val Gln Gly Pro Ser 65

agg gat ttg atc gag acg gtg gcc acg gaa tct gcg gat gct gtg atg 355

Arg Asp Leu Ile Gln Thr Val Ala Thr Gln Ser Ala Asp Ala Val Met 85

gct aaa ttt gat ggc ctt cat gcg gtg gaa gta acc atc cat aag ccc 403

Ala Lys Phe Asp Ala Leu His Ala Val Gln Val Thr Ile His Lys Pro 100

aaa gca ccg atc cca cgt act ttt gct gac gtc gcg gtg gct gcc cga 451

Lys Ala Pro Ile Pro Arg Thr Phe Ala Asp Val Ala Val Val Ala Arg 115

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<213> Corynebacterium glutamicum

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35 40 45

Ser Asp Thr Val Asp Tyr Gly Ala Leu Ala Leu Val Ala Glu Ile  
50 55 60

Val Glu Gly Pro Ser Arg Asp Leu Ile Glu Thr Val Ala Thr Glu Ser  
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Ala Asp Ala Val Met Ala Lys Phe Asp Ala Leu His Ala Val Glu Val  
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Met Asn Val Ser Ser  
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Leu Thr Ile Pro Gly Arg Cys Leu Val Met Gly Ile Val Asn Val Thr  
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 Arg Val Asp Ala Ser Val Gln Arg Asp Arg Val Val Pro Val Ile Lys  
 65 70 75 80  
 Ala Leu His Asp Ala Gly Ile His Thr Ser Val Asp Thr Met Arg Ala  
 85 90 95  
 Ser Val Ala Gln Ala Ala Gly Ala Gly Val Ser Met Ile Asn Asp  
 100 105 110  
 Val Ser Gly Gly Leu Ala Asp Pro Gln Met Phe Ser Val Met Ala Gln  
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 Ala Gln Ile Pro Val Cys Leu Met His Trp Arg Thr Leu Gln Phe Gly  
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 Asp Ala Ala Gly Gln Ala Asp His Gly Gly Asp Val Val Ala Asp Val  
 145 150 155 160  
 His Ala Val Leu Asp Asp Leu Val Ala Arg Ala Thr Ala Ala Gly Val  
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 Ala Gln Asn Gln Ile Val Leu Asp Pro Gly Leu Gly Phe Ala Lys Ser  
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 Gly Val Arg Lys Asp Arg Gly Leu Asp Val Thr Pro Ile Asp Ala Asp  
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 Met Ser Ser Leu Pro 1  
 Val Ile Met Ala Ile Val Asn Arg Thr Pro Asp Ser Phe Tyr Asp Lys 20  
 ggt gcg aca ttg gag gac acc gct gcg cta aac agg gca gcg gag gtc 211  
 Gly Ala Thr Phe Gln Asp Thr Ala Ala Leu Asn Arg Ala Ala Gln Val 35  
 att gaa caa ggc gcc ggc att gtc gat atc ggt ggg gtg aaa gcc ggc 259  
 Ile Gln Gln Gly Ala Gly Ile Val Asp Ile Gly Gly Val Lys Ala Gly 50  
 ccg ggg gat ttc ttg tcg gcg gag gaa gag atc gac gcg gtg gtc cca 307  
 Pro Gly Asp Phe Val Ser Ala Gln Gln Ile Asp Arg Val Val Pro 65  
 atc atc gct gcg gtg cga gaa cgt ttt cct gac att gat atc tct gtt 355  
 Ile Ile Ala Ala Val Arg Gln Arg Phe Pro Asp Ile Asp Ile Ser Val 85  
 gat acc ttg gcg gcg tcg gct gat gtc gca gtc gca gtc ggc cat gga gca 403  
 Asp Thr Trp Arg Ala Ser Val Ala Asp Val Ala Val Ala His Gly Ala 100  
 acg ctg atc aat gat gac act ttg gcc ggc cat gat cat gat gag ttg gtg cag 451  
 Thr Leu Ile Asn Asp Thr Trp Ala Gly His Asp His Gln Leu Val Gln 115  
 gta gca ggg cag cac aag gtg ggt tat gtc tgc tcg cac acc gcc ggc ggg 499  
 Val Ala Gly Gln His Lys Val Gly Tyr Val Cys Ser His Thr Gly Gly 130  
 gtg atc cca aga acg cga cca tat cgg gtg cat ttc gat gac atc gtc 547  
 Val Ile Pro Arg Thr Arg Pro Tyr Arg Val His Phe Asp Ile Val 145

595	gac gat gta att acg gag acc acc aaa ttg gca gag caa gct gct cgt	150	Ala Asp Val Ile Thr Gln Thr Thr Lys Leu Ala Gln Ala Val Arg	165
643	gac gag gta cca gag gaa cgg gta ttg ttg att gat ccc acc cat gat ttc	170	Ala Gly Val Pro Gln Arg Val Phe Ile Asp Pro Thr His Asp Phe	180
691	ggg aaa aac acc ttc cac gga ctg gag ctt tta cga cgg atc gat gag	185	Gly Lys Asn Thr Phe His Gly Leu Gln Leu Arg Arg Ile Asp Gln	195
739	gtg gtt gct gcc acg ggc ttg cgg gta ctg atg gcc ttg agt aat aag gat	200	Val Val Ala Thr Gly Trp Pro Val Leu Met Ala Leu Ser Asn Lys Asp	210
787	ttc att ggg gaa act ttg gaa aag ggc gtc gat aag cgt gct gct ggc	220	Phe Ile Gly Gln Thr Leu Gln Arg Gly Val Asp Lys Arg Val Ala Gly	225
835	acg ctt gct gcc act gcc ttg ggc ggc ggc ggc ggc ggc ggc ggc ggc	235	Thr Leu Ala Ala Thr Ala Trp Ala Ala Arg Gly Val Ala Ala Phe	245
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100	Val Ala Ala His Gly Ala Thr Leu Ile Asn Asp Thr Trp Ala Gly His Asp	105		110
115	His Gln Leu Val Gln Val Ala Gly Gln His Lys Val Gly Tyr Val Cys	120		125
130	Ser His Thr Gly Gly Val Ile Pro Arg Thr Arg Pro Tyr Arg Val His	135		140

Phe Asp Ile Val Ala Asp Val Ile Thr Gln Thr Thr Lys Leu Ala 145  
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 Gln Gln Ala Val Arg Ala Gly Val Pro Gln Gln Arg Val Phe Ile Asp 165  
 170 175  
 Pro Thr His Asp Phe Gly Lys Asn Thr Phe His Gly Leu Gln Leu 180  
 185 190  
 Arg Arg Ile Asp Gln Val Val Ala Thr Gly Trp Pro Val Leu Met Ala 195  
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 Met Ile Gly Ala Ile 1  
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 tgg gca caa ggc cgt gac ggc atc atc ggc gac ggc acc gac atg ccc 163  
 Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp Gly Thr Asp Met Pro 20  
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 tgg cac atc ccc gaa gac ctg aaa cac ttc aag aaa acc acc atg ggc 211  
 Trp His Ile Pro Gln Asp Leu Lys His Phe Lys Lys Thr Thr Met Gly 35  
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 cag ccg gtc atc atg ggt cgt cgc acg tgg gag tct ttg ccg ttc aag 259  
 Gln Pro Val Ile Met Gly Arg Arg Thr Trp Gln Ser Leu Pro Phe Lys 50  
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 ccg ctt ccc ggc cgc gag aac ttc att ctc tcc tca cgc gag ccc ggc 307  
 Pro Leu Pro Gly Arg Gln Asn Phe Ile Leu Ser Ser Arg Gln Pro Gly 65  
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 gac tgg tcc ggc ggc ggc aca gtc gtc acc gaa atc cct aaa agc ggc 355  
 Asp Trp Ser Ala Gly Thr Gly Thr Val Val Thr Gln Ile Pro Lys Ser Gly 80  
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 tgg atc atg ggc ggc ggc gag gtc tac aag gcc acc gtc ggc agc gcc 403

Trp Ile Met Gly Gly Gln Val Tyr Lys Ala Thr Val Gly Ser Ala  
 90 95 100  
 451 gac gtt tta gaa ata acg ctt atc gac gcc acc ttc gat gtt tcc act  
 Asp Val Leu Gln Ile Thr Leu Ile Asp Ala Thr phe Asp Val Ser Thr  
 105 110 115  
 499 ccc gtc tac gca ccc gaa atc ccg gcg aac ttc aac ctg gat gac gaa  
 Pro Val Tyr Ala Pro Gln Ile Pro Ala Asn phe Asn Leu Asp Asp Gln  
 120 125 130  
 547 tcc gag tgg ttt acc tca ggc gag tat cgt tac aag ttc cag cgc tac  
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 Lys Thr Thr Met Gly Gln Pro Val Ile Met Gly Arg Arg Thr Trp Gln  
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 Ser Leu Pro phe Lys Pro Leu Pro Gly Arg Gln Asn phe Ile Leu Ser  
 50 55 60  
 Ser Arg Gln Pro Gly Asp Trp Ser Ala Gly Gly Thr Val Val Thr Gln  
 65 70 75 80  
 Ile Pro Lys Ser Gly Trp Ile Met Gly Gly Gly Gln Val Tyr Lys Ala  
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 Thr Val Gly Ser Ala Asp Val Leu Gln Ile Thr Leu Ile Asp Ala Thr  
 100 105 110  
 Phe Asp Val Ser Thr Pro Val Tyr Ala Pro Gln Ile Pro Ala Asn phe  
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 Lys phe Gln Arg Tyr Ile Lys Val  
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<210> 697  
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 asp ala thr asn val ile asn ala ala val ser val ile thr pro val  
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	Gln Gln Asp Leu Ala Gly Ala Val Gln Leu Ala Ile Gln Leu Ala Gln	470
	gac acc gat gta cag tcc gga tca ggt gtt gtg atc acc ggt tca atc	475
1488	Asp Thr Asp Val Gln Ser Gly Ser Gly Val Ile Thr Gly Ser Ile	480
	gtg acc gcc ggc gat gcg acg cgt ttt gga aag gaa cct gca	485
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 Met Gln Met Thr Asp Ala Trp Ser Gln Ala Gln Gly Gly Pro Lys Met  
 Ile His Pro Arg Asp Phe Val Arg Ile Tyr Gln Ile Lys Pro Tyr  
 Pro His Leu Gln Leu Val Thr Gln Arg Ile Ala Ile Asp Gly Lys Pro  
 Gln Ser Leu Leu Arg Ala Phe His Arg Arg Thr Gly Arg Thr Thr Ser  
 Ile His Val Ala Gly Thr Asn Gly Lys Thr Ser Thr Thr Arg Met Ile  
 Ser Tyr Met Met Asp Leu Met Gly Gln Pro Gln Asn Ser Phe Pro Ala  
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Ser Ile Gly Ser Asn Met Asp Arg Tyr Ala Leu Leu Asn Thr Val  
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Thr Pro Pro Trp Gly Ile Glu Asp Glu Asp Glu Phe Leu Asn Ala Val  
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ctc gtt gtt gag gtt gag gaa gaa acc ccc atc gag ttg ctc gcg cgt ggc 307  
Leu Val Val Val Glu Glu Thr Pro Ile Glu Leu Leu Arg Arg Gly  
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caa aaa ctc gaa gaa gcc gcc gag cgg gtc cgc gtc cgc aaa tgg ggg 355  
Gln Lys Leu Glu Glu Ala Glu Arg Val Arg Val Arg Lys Trp Gly  
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cca cgc acc ctc gat gttg gat atc gttg cag atc att aaa gat ggg gaa 403  
Pro Arg Thr Leu Asp Val Asp Ile Val Glu Ile Ile Lys Asp Gly Glu  
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gag atc ctt tct gag gat ccc gaa ctg acc ttg cca ctc ctc tgg gct 451  
Glu Ile Leu Ser Glu Asp Pro Glu Leu Thr Leu Pro His Pro Trp Ala  
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Trp Glu Arg Ala Phe Val Leu Ile Pro Trp Leu Glu Ala Glu Pro Asp  
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gcc gtc ctg cag cgc acc acc att gca gaa cat gttg gat aat ctt gat 547  
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 1747 gcc cca aag ctt cgc acc atg gag atc atc gat gag ctt gag gca gct

Ala Pro Lys Leu Arg Thr Met Gln Ile Ile Asp Gln Leu Gln Ala Ala  
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1795 Pro Arg Gly Ile Tyr Ser Gly Gln Gly Tyr Phe Ser Leu Asp Gly  
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1843 Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu Val Ile Gln Asn  
570 575 580  
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585 590 595  
gag gct gag tgg gag gaa atc cgc gtt aaa tca cgg cct ctg ctg aat  
1939 Gln Ala Gln Trp Gln Gln Ile Arg Val Lys Ser Arg Pro Leu Leu Asn  
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Asn Asp Gln Gln Ile Asp Gln Met Leu Phe Asp Ala Val Ile Leu Ser  
35 40 45  
Pro Gly Pro Gly His Ala Gly Val Ala Ala Asp Phe Gly Ile Cys Ala  
50 55 60  
Gly Val Ile Gln Arg Ala Arg Val Pro Ile Leu Gly Val Cys Leu Gly  
65 70 75 80  
His Gln Gly Ile Ala Leu Ala Tyr Gly Gly Asp Val Asp Leu Ala Pro  
85 90 95  
Arg Pro Val His Gly Gln Val Ser Gln Ile Thr His Asp Gly Ser Gly  
100 105 110  
Leu Phe Ala Gly Ile Pro Gln Thr Phe Gln Ala Val Arg Tyr His Ser  
115 120 125  
Met Val Ala Thr Arg Leu Pro Gln Ser Leu Lys Ala Thr Ala Thr Ser  
130 135 140  
Asp Asp Gly Leu Ile Met Ala Leu Ala His Gln Val Leu Pro Gln Trp  
145 150 155 160  
Gly Val Gln Phe His Pro Gln Ser Ile Gly Gln Phe Gly His Gln

165	Arg Gly Ala Leu Pro Thr Thr Val Lys Thr Ser Lys Leu Phe Asp Val	485
170	Arg Ala Glu Asn Leu Met Ile Val Asp Leu Val Arg Asn Asp Leu Ala	465
175	Gln Gln Asp Gln Gln Ile Ile Ala Glu Leu Arg Ser Asn Pro Lys Asp	450
	Val Gln Ser Lys Pro Ile Lys Gly Thr Arg Pro Arg Gly Arg Thr Ala	435
	Leu Ser Ser Ser Pro Gln Arg Phe Ile Thr Ile Asp Ser Ala Gly Tyr	420
	Asn Pro Thr Ala Tyr Gly Ala Tyr Leu Gln Leu Gly Asp Thr Ser Ile	405
	Thr Thr Asp Val Ala Pro Leu Ala Ala Tyr Leu Ala Leu Arg Gly Ala	385
	Thr Arg Gly Gln Ser Tyr Gln Ile Cys Leu Thr Thr Lys Leu Gln Gly	370
	Ser Lys Asp Asp Gln Tyr Leu Asp Lys Ile Arg Arg Ala Gln Gln Ile	355
	Ala Pro Arg Ile Pro Ala Ser Gly His Leu Ala Leu Gln Val Arg Asp	340
	Gln Asp Gln Trp Phe Gln Gln Thr Ile Lys Lys Leu His Asn Leu Val	325
	Ala Ile Ala Val Gln Ser Asp Gln Val Arg Leu Leu Ala Leu Gly Gln	310
	Ala His Thr Ser Ser Ser Leu Pro Asp Ala His Leu Ile Phe Ala Asp Arg	295
	Val Gly Tyr Val Gly Tyr Gln Leu Lys Ala Gln Ala Gly Ala Arg Ala	275
	Leu Ala Ala Asn Ser Val Ala Pro Gly Gln Gly Phe Arg Leu Gly Trp	260
	Thr His Asn Val Gly Gln Gly Asp Phe Thr Trp Leu Lys Gln Asp	245
	Gly Thr Ser Tyr Leu Gly Asp Ala Ser Gly Pro Leu Ala Arg Thr Lys	230
	Thr Phe Phe Ala His Ser Ser His Ala Phe Trp Leu Asp Asp Ala Gln	215
	Thr Gln Lys Thr Ile Pro Leu Ser Val Asp Ser Ala Val Phe Gln	200
	Ile Ile Lys Asn Phe Leu Asn Leu Ala Arg Thr Tyr Arg Trp Gln Leu	185
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Gln Thr Tyr Ala Thr Val His Gln Leu Val Ser Thr Val Ser Ala Gln  
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 Leu Gly Pro Arg Ser Pro Ile Gln Cys Val Arg Ala Phe Pro Gly  
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 Gly Ser Met Thr Gly Ala Pro Lys Leu Arg Thr Met Gln Ile Ile Asp  
 530 535 540  
 Gln Leu Gln Ala Ala Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr  
 545 550 555 560  
 Phe Ser Leu Asp Gly Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu  
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 Val Ile Gln Asn Asn His Val Gln Tyr Gly Val Gly Gly Ala Leu Leu  
 580 585 590  
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 115 Met Thr His Val Val  
 1 Met  
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 163 Leu Ile Asp Asn His Asp Ser Phe Val Tyr Asn Leu Val Asp Ala Phe  
 20 15 10  
 gcc gtg gcc ggt tat aag tgc acg gtg ttc cgc aat acg gtg cca gtg  
 211 Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg Asn Thr Val Pro Val  
 25 30 35  
 gaa acc att ttg gca gcc aac ccg gac ctg atc tgc ctt tca cct gga  
 259 Gln Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile Cys Leu Ser Pro Gly  
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 307 Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met Ala Leu Ile Gln Arg  
 55 60 65  
 aca ctc gcc cag att cct tta cta ctg ggt att tgc ctc gcc tac cag gca  
 355 Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys Leu Gly Tyr Gln Ala

[illegible]



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451	gaa caa atg aac gca gca gct gca gta tgc gct ctg ctt gat cca gac	Glu Gln Met Asn Ala Ala Ala Ala Ser Ala Leu Leu Asp Pro Asp	105	110	115
499	aac cag gtt gat ctc ctc gac att cac ggc ggc ggc ggc ggc ggc	Asn Gln Val Asp Leu Leu Asp Ile His Gly Gly Ala Thr Leu Met Asp	120	125	130
547	gtc act gtt gtc ggc gga aac acc cgc gcg gga atc tac tcc cag atc	Val Thr Val Val Gly Gly Asn Thr Arg Ala Gly Ile Tyr Ser Gln Ile	135	140	145
595	gca gcc gtc gtc acc tgc acc gaa ggc tcc ggc aac tgc atc acc gct gag	Ala Ala Val Thr Cys Thr Gln Gly Ser Ala Asn Cys Ile Thr Ala Glu	150	155	160
643	gat ttg cag cag gtt gcc tcc acc gtc tgc cct gca gaa ttg ggt gtc	Asp Leu Gln Val Val Ala Ser Thr Val Ser Pro Ala Glu Leu Gly Val	170	175	180
691	cca gat tgg gca atc gct gct gta gaa gct cgc gga acc gat cca aag	Pro Asp Trp Ala Ile Ala Val Gln Ala Arg Gly Thr Asp Pro Lys	185	190	195
739	cgc ctc gaa ggc ctg atc atg cct ggc caa tac gtc gtc gat cca tcc	Arg Leu Gln Gly Leu Ile Met Pro Gly Gln Tyr Val Val Asp Pro Ser	200	205	210
787	aac gac gcc cag gga atc ctc acc gat ctc atc acg cga tca gca aac	Asn Asp Ala Gln Gly Ile Leu Thr Asp Leu Ile Thr Arg Ser Ala Asn	215	220	225
835	cat ttc caa gaa acc gac atc acg ggc cgt gca gat gcc atc gga ctt	His Phe Gln Gln Thr Asp Ile Thr Gly Arg Ala Asp Ala Ile Gly Leu	230	235	240
883	act cca tat gag ctg gtc acc gca gca tct tta atc gag cgc gaa gca	Thr Pro Tyr Gln Leu Val Thr Ala Ala Ser Leu Ile Gln Arg Glu Ala	250	255	260
931	cca gca gga gat ttt gat aag gtc gcc ggc gtc atc ttg aac cgt ctg	Pro Ala Gly Asp Phe Asp Lys Val Ala Arg Val Ile Leu Asn Arg Leu	265	270	275
979	gcc gag cca atg cag ctg caa ttc gac tcc acc gtc aac tac ggt ctg	Ala Gln Pro Met Gln Leu Gln Phe Asp Ser Thr Val Asn Tyr Gly Leu	280	285	290
1027	tct gaa caa gaa gta gca acc acc gac gaa gac cgt cag acc gtc acc	Ser Gln Gln Gln Val Ala Thr Thr Asp Gln Asp Arg Gln Thr Val Thr	295	300	305
1075	cca tgg aac act tac gcc atg gac ggc ctg cca cca acc ccc atc gcc	Pro Trp Asn Thr Tyr Ala Met Asp Gly Leu Pro Gln Thr Pro Ile Ala	310	315	320
325					

1123	gca gta tcc acc gaa gca ctc caa gcc atg gaa aac cct gca gaa gga	330	Ala Val Ser Thr Gln Ala Leu Gln Ala Met Gln Asn Pro Ala Gln Gly	340
1171	aac tgg ctg tac ttg gtc acc atc gac acc gat gga acc acc gtc ttc	345	Asn Trp Leu Tyr Phe Val Thr Ile Asp Thr Asp Gly Thr Val Phe	355
1219	aac gac acc ttc gaa gag cac gaa gcc gac att gag caa gct ttg aac	360	Asn Asp Thr Phe Gln His Gln Ala Asp Ile Gln Gln Ala Leu Asn	370
1266	agt ggc gtc cta gac agc aac cga taagatcag cgaataaat tgg	380	Ser Gly Val Leu Asp Ser Asn Arg	

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	Val Val Gln Leu Val Gln Ile Pro Gln Gly Ser Ser Ile Ser Gln Leu	50
	Gly Pro Gln Leu Gln Arg Asp Ile Val Ala Thr Asn Ser Ala Phe	65
	Gln Thr Ala Ala Ser Asn Asn Pro Asn Ala Gly Ser Val Gln Pro Gly	85
	Phe Tyr Arg Leu Gln Gln Met Asn Ala Ala Ala Val Ser Ala	100
	Leu Leu Asp Pro Asp Asn Gln Val Asp Leu Leu Asp Ile His Gly Gly	115
	Ala Thr Leu Met Asp Val Thr Val Val Gly Gly Asn Thr Arg Ala Gly	130
	Ile Tyr Ser Gln Ile Ala Ala Val Thr Cys Thr Gln Gly Ser Ala Asn	145
	Cys Ile Thr Ala Gln Asp Leu Gln Val Ala Ser Thr Val Ser Pro	165
	Ala Gln Leu Gly Val Pro Asp Trp Ala Ile Ala Ala Val Gln Ala Arg	180
	Gly Thr Asp Pro Lys Arg Leu Gln Gly Leu Ile Met Pro Gly Gln Tyr	195

Val Val Asp Pro Ser Asn Asp Ala Gln Gly Ile Leu Thr Asp Leu Ile 210  
 Thr Arg Ser Ala Asn His Phe Gln Gln Thr Asp Ile Thr Gly Arg Ala 225  
 Asp Ala Ile Gly Leu Thr Pro Tyr Gln Leu Val Thr Ala Ala Ser Leu 245  
 Ile Gln Arg Gln Ala Pro Ala Gly Asp Phe Asp Lys Val Ala Arg Val 260  
 Ile Leu Asn Arg Leu Ala Gln Pro Met Gln Leu Gln Phe Asp Ser Thr 275  
 Val Asn Tyr Gly Leu Ser Gln Gln Val Ala Thr Asp Gln Asp 290  
 Arg Gln Thr Val Thr Pro Trp Asn Thr Tyr Ala Met Asp Gly Leu Pro 305  
 Gln Thr Pro Ile Ala Val Ser Thr Gln Ala Leu Gln Ala Met Gln 325  
 Asn Pro Ala Gln Gly Asn Trp Leu Tyr Phe Val Thr Ile Asp Thr Asp 340  
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 Met Ile Gly Ala Ile 1  
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 tgg gca caa ggc cgt gac ggc atc atc ggc gac ggc acc gac atg ccc 163  
 Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp Gly Thr Asp Met Pro 20  
 tgg cac atc ccg gaa gac ctc aaa cac ttc aag aaa acc acc atg ggc 211  
 Trp His Ile Pro Gln Asp Leu Lys His Phe Lys Lys Thr Thr Met Gly 35  
 cag ccg gtc atc atg ggt cgt cgc acg tgg gag tct ttg ccg ttc aag 259

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579	atc aag gtt taaggagcaa acaacatgag caa	Ile Lys Val	150
547	tcc gag tgg ttt acc tca ggc gag tat cgt tac aag ttc cag cgc tac	Ser Gln Trp Phe Thr Ser Gly Gln Tyr Arg Tyr Lys Phe Gln Arg Tyr	135 140 145
499	ccc gtc tac gca ccc gaa atc ccg gcg aac ttc aac ctc gat gac gaa	Pro Val Tyr Ala Pro Gln Ile Pro Ala Asn Phe Asn Leu Asp Asp Gln	120 125 130
451	gac gtt tta gaa ata acg ctt atc gac gcc acc ttc gat gtt tcc act	Asp Val Leu Gln Ile Thr Leu Ile Asp Ala Thr Phe Asp Val Ser Thr	105 110 115
403	tgg atc atg ggc ggc gag gtc tac aag gcc acc gtc ggc agc gcc	Trp Ile Met Gly Gly Gln Val Tyr Lys Ala Thr Val Gly Ser Ala	90 95 100
355	gac tgg tcc gcc ggc ggc aca gtc gtc acc gaa atc cct aaa agc ggc	Asp Trp Ser Ala Gly Gly Thr Val Val Thr Gln Ile Pro Lys Ser Gly	70 75 80 85
307	ccg ctt ccc ggc cgc gag aac ttc att ctc tcc tca cgc gag ccc ggc	Pro Leu Pro Gly Arg Gln Asn Phe Ile Leu Ser Ser Arg Gln Pro Gly	55 60 65
	Gln Pro Val Ile Met Gly Arg Arg Thr Trp Gln Ser Leu Pro Phe Lys		40 45 50
	Gly Thr Asp Met Pro Trp His Ile Pro Gln Asp Leu Lys His Phe Lys		20 25 30
	Lys Thr Thr Met Gly Gln Pro Val Ile Met Gly Arg Arg Thr Trp Gln		35 40 45
	Ser Leu Pro Phe Lys Pro Leu Pro Gly Arg Gln Asn Phe Ile Leu Ser		50 55 60
	Ser Arg Gln Pro Gly Asp Trp Ser Ala Gly Gly Thr Val Val Thr Gln		65 70 75 80
	Ile Pro Lys Ser Gly Trp Ile Met Gly Gly Gly Gln Val Tyr Lys Ala		85 90 95
	Thr Val Gly Ser Ala Asp Val Leu Gln Ile Thr Leu Ile Asp Ala Thr		100 105 110
	Phe Asp Val Ser Thr Pro Val Tyr Ala Pro Gln Ile Pro Ala Asn Phe		115 120 125

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Lys Phe Gln Arg Tyr Ile Lys Val  
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115 Met Ser Thr Ser Val  
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163 Thr Ser Pro Ala His Asn Asn Ala His Ser Ser Gln Phe Leu Asp Ala  
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211 Leu Ala Asn His Val Leu Ile Gln Asp Gln Ala Met Gln Thr Gln Leu  
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caa ggc ttt gac ctg gac gtg gaa aag gat ttc ctt gat ctg gag ggg  
259 Gln Gln Phe Asp Leu Asp Val Gln Lys Asp Phe Leu Asp Leu Gln  
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tgt aat gag att ctg aac gac acc cgc cct gat gtg ttg agg cag att  
307 Cys Asn Gln Ile Leu Asn Asp Thr Arg Pro Asp Val Leu Arg Gln Ile  
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cac arg gcc tac ttt gag ggc gga gct gat ttg gtt gag acc aat act  
355 His Arg Ala Tyr Phe Gln Ala Gln Asp Leu Val Gln Thr Asn Thr  
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85

ttt ggt tgc aac ctg ccg aac ttg gac gat tat gat atc gat gct gct  
403 Phe Gln Cys Asn Leu Pro Asn Leu Ala Asp Tyr Asp Ile Ala Asp Arg  
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95  
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451 Cys Arg Gln Leu Ala Tyr Lys Gln Thr Ala Val Ala Arg Gln Val Ala  
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gat gag atg ggg ccg ggc cga aac ggc atg cgg cgt ttc gtg gtt ggt  
499 Asp Gln Met Gln Pro Gln Arg Asn Gln Met Arg Arg Phe Val Val Gln  
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125  
130

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547 Ser Leu Gln Pro Gln Thr Lys Leu Pro Ser Leu Gln His Ala Pro Tyr  
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140  
145



595	gca gat ttg cgt ggg cac tac aag gaa gca gcg ctt ggc atc atc gac	150	Ala Asp Leu Arg Gly His Tyr Lys Gln Ala Ala Leu Gly Ile Ile Asp	165
643	ggt ggt ggc gat ggc ttt ttg att gag act gct cag gac ttg ctt cag	170	Gly Gly Gly Asp Phe Leu Ile Gln Thr Ala Gln Asp Leu Gln	180
691	gtc aag gct gcg ggt cca ggt ggt cca gat ggc atg gct gaa ctt gat	185	Val Lys Ala Ala Val His Gly Val Gln Asp Ala Met Ala Gln Leu Asp	195
739	aca ttc ttg ccc att att tgc cac gtc acc gta gag acc acc ggc acc	200	Thr Phe Leu Pro Ile Ile Cys His Val Thr Val Gln Thr Gly Thr	210
787	atg ctc atg ggt tct gag atc ggt gcc ggc ttg aca gcg ctt cag cca	220	Met Leu Met Gly Ser Gln Ile Gly Ala Ala Leu Thr Ala Leu Gln Pro	225
835	ctg ggt atc gac atg att ggt ctt gac ttg aac tgc gcc acc ggc cca gat	235	Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala Thr Gly Pro Asp Gln	245
883	atg agc gag cac ctt gct tac ctt ggc atc gag cag gcc gat att cct gtc	250	Met Ser Gln His Leu Arg Tyr Leu Ser Lys His Ala Asp Ile Pro Val	260
931	tcg gtc atg cct aac gca ggt ctt cct gtc ctt gtc ctt gtc ggt aac ggt	270	Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu Gly Lys Asn Gly Ala	275
979	gaa tac cca ctt gag gct gag gat ttg ggc cag ggc ctt gct gga ttc	285	Glu Tyr Pro Leu Gln Ala Asp Leu Ala Gln Ala Leu Gly Phe	290
1027	gtc ttc gaa tat ggc ctt tcc atg ttg ggt ggt ggt ggt ggt ggt ggt	300	Val Ser Gln Tyr Gly Leu Ser Met Val Gly Gly Cys Cys Gly Thr Thr	305
1075	cct gag cac atc cgt ggc gtc cgc gat ggc gtc gtc gtc gtc gtc gtc	315	Pro Gln His Ile Arg Ala Val Val Gly Val Pro Gln	325
1123	cag gaa acc tcc aca ctt gag acc aag atc cct gca ggc cct gtt gag cag	330	Gln Gln Thr Ser Thr Leu Thr Lys Ile Pro Ala Gly Pro Val Gln Gln	340
1171	gcc tcc cgc gag ggt gag aaa gag gac tcc gtc gcg tcg ctt tac acc	345	Ala Ser Arg Gln Val Gln Lys Gln Asp Ser Val Ala Ser Leu Tyr Thr	355
1219	tcg gtc cca ttg tcc cag gaa acc ggc att tcc atg atc ggt gag cgc	360	Ser Val Pro Leu Ser Gln Gln Thr Gly Ile Ser Met Ile Gly Gln Arg	370
1267	acc aac tcc aac ggt tcc aag gca ttc cgt gag gca atg ctt tct ggc	380	Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Gln Ala Met Leu Ser Gly	385
1315	gat ttg gaa aag tgt gtc gat att gcc aag cag caa acc cgc gat ggt			

1363	gca cac atg ctg gat ctt tgt gtg gat tac gtg gga cga gac ggc acc	Ala His Met Leu Asp Leu Cys Val Asp Tyr Val Gly Thr	410	415	420
1411	gac gat atg atg ggc acc tgg gca gca ctt ctt gct acc acc gtc act tgg	Ala Asp Met Ala Thr Leu Ala Leu Ala Thr Ser Ser Thr Leu	425	430	435
1459	cca atc atg att gac tcc acc gag cca gag gtt att cgc aca ggc ctt	Pro Ile Met Ile Asp Ser Thr Gln Pro Gln Val Ile Arg Thr Gly Leu	440	445	450
1507	gag cac tgg ggt gga cga agc atc gtt aac tcc gtc aac ttt gaa gac	Gln His Leu Gly Gly Arg Ser Ile Val Asn Ser Val Asn Phe Gln Asp	455	460	465
1555	ggc gat ggc cct gag tcc cgc tac cag cgc atc atg aaa ctg gta aag	Gly Asp Gly Pro Gln Ser Arg Tyr Gln Arg Ile Met Lys Leu Val Lys	470	475	480
1603	cag cac ggt ggc ggt ggt ggt ggt ggt ggt ggt ggt ggt ggt ggt	Gln His Gly Ala Val Val Val Val Val Val Val Val Val Val Val	490	495	500
1651	gca cgt acc gct gag cac aag gtt cgc atc gct aaa cga ctg att gac	Ala Arg Thr Ala Gln His Lys Val Arg Ile Ala Lys Arg Leu Ile Asp	505	510	515
1699	gat atc acc acc ggc agc tac ggc ctg gat atc aaa gac atc gtt gtt gac	Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys Asp Ile Val Val Asp	520	525	530
1747	tgc ctg acc ttc ccc att tct act ggc cag gaa gaa acc agg cga gat	Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Gln Thr Arg Arg Asp	535	540	545
1795	ggc att gaa acc acc gaa ggc atc ggc ggc ggc ggc ggc ggc ggc ggc	Gly Ile Gln Thr Ile Gln Ala Ile Arg Gln Leu Lys Lys Leu Tyr Pro	550	555	560
1843	gaa atc cac acc acc ctg ggt ctg tcc aat att tcc att tcc ggc ctg aac	Gln Ile His Thr Thr Leu Gly Leu Ser Asn Ile Ser Phe Gly Leu Asn	570	575	580
1891	cct gct gca cgc cag gtt ctt aac tct gtt ttc ctg aat gag tgc att	Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe Leu Asn Gln Cys Ile	585	590	595
1939	gag gct ggt ctg gac tct ggc att ggc cac agc tcc aag att ttg cgc	Gln Ala Gly Leu Asp Ser Ala Ile Ala His Ser Ser Lys Ile Leu Pro	600	605	610
1987	atg aac cgc att gat gat cgc cag cgc gaa gtt ggc ttg gat atg gtc	Met Asn Arg Ile Asp Asp Arg Gln Arg Gln Val Ala Leu Asp Met Val	615	620	625
2035	tat gat cgc cgc acc gag gat tac gat cgc cgc cgc cgc cgc cgc cgc	Tyr Asp Arg Arg Thr Gln Asp Tyr Asp Pro Leu Gln Phe Met Gln			

630  
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 Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln Met Gln Leu Pro Phe  
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 Val Leu Gln Ser Ala Thr Met Lys Thr Ala Val Ala Tyr Leu Glu  
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 Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys Gly Asp Val His Asp  
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 Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser Asn Asn Gly Tyr Asp  
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 gtg gtg aac ttg ggc atc aag cag cca ctg tcc ggc atg ttg gaa gca  
 Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser Ala Met Leu Glu Ala  
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 820  
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 Ala Glu Glu His Lys Ala Asp Val Ile Gly Met Ser Gly Leu Leu Val  
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Met Gly Thr	35	Gln Leu Gln Gly Phe	40	Asp Leu Asp Val Gln Lys Asp Phe	45
Leu Asp Leu Gln Gly Cys Asn Gln Ile Leu Asn Asp Thr Arg Pro Asp	50		55		60
Val Leu Arg Gln Ile His Arg Ala Tyr Phe Gln Ala Gly Ala Asp Leu	65		70		75
Val Gln Thr Asn Thr Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr	85		90		95
Asp Ile Ala Asp Arg Cys Arg Gln Leu Ala Tyr Lys Gly Thr Ala Val	100		105		110
Ala Arg Gln Val Ala Asp Gln Met Gly Pro Gly Arg Asn Gly Met Arg	115		120		125
Arg Phe Val Val Gly Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu	130		135		140
Gly His Ala Pro Tyr Ala Asp Leu Arg Gly His Tyr Lys Gln Ala Ala	145		150		155
Leu Gly Ile Ile Asp Gly Gly Gly Asp Ala Phe Leu Ile Gln Thr Ala	165		170		175
Gln Asp Leu Leu Gln Val Lys Ala Ala Val His Gly Val Gln Asp Ala	180		185		190
Met Ala Gln Leu Asp Thr Phe Leu Pro Ile Ile Cys His Val Thr Val	195		200		205
Gln Thr Thr Gly Thr Met Leu Met Gly Ser Gln Ile Gly Ala Ala Leu	210		215		220
Thr Ala Leu Gln Pro Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala	225		230		235
Thr Gly Pro Asp Gln Met Ser Gln His Leu Arg Tyr Leu Ser Lys His	245		250		255
Ala Asp Ile Pro Val Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu	260		265		270
Gly Lys Asn Gly Ala Gln Tyr Pro Leu Gln Ala Gln Asp Leu Ala Gln	275		280		285
Ala Leu Ala Gly Phe Val Ser Gln Tyr Gly Leu Ser Met Val Gly Gly	290		295		300
Cys Cys Gly Thr Thr Pro Gln His Ile Arg Ala Val Arg Asp Ala Val	305		310		315
Val Gly Val Pro Gln Gln Thr Ser Thr Leu Thr Lys Ile Pro Ala	325		330		335
Gly Pro Val Gln Gln Ala Ser Arg Gln Val Gln Lys Gln Asp Ser Val	340		345		350



Ala Gln Arg Ile Ile Asp Gly Asp Lys Asn Gly Leu Gln Asp Leu 675  
 680 685  
 Gln Ala Gly Met Lys Gln Lys Ser Pro Ile Ala Ile Ile Asn Gln Asp 690  
 695 700  
 Leu Leu Asn Gly Met Lys Thr Val Gly Gln Leu Phe Gly Ser Gly Gln 705  
 710 715 720  
 Met Gln Leu Pro Phe Val Leu Gln Ser Ala Gln Thr Met Lys Thr Ala 725  
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 Val Ala Tyr Leu Gln Pro Phe Met Gln Gln Ala Gln Ala Thr Gly 740  
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 Ser Ala Gln Ala Gln Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys 755  
 760 765  
 Gly Asp Val His Asp Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser 770  
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 Asn Asn Gly Tyr Asp Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser 785  
 790 795 800  
 Ala Met Leu Gln Ala Ala Gln Gln His Lys Ala Asp Val Ile Gly Met 805  
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 1 Met Ser Thr Ser Val  
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 163 act tca cca gcc cac aac aac gca cat tcc tcc gaa ttt ttg gat gcg  
 15 Thr Ser Pro Ala His Asn Asn Ala His Ser Ser Ser Gln Phe Leu Asp Ala  
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 211 ttg gca aac cat gtg ttg atc ggc gac ggc ggc atg ggc acc cag ctc  
 25 Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala Met Gly Thr Gln Leu  
 30 35  
 259 caa ggc ttt gac ctg gac gtg gaa aag gat ttc ctt gat ctg gag ggg  
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[illegible]

[illegible]



[illegible]

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 Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser Ala Met Leu Gln Ala 805  
 gcg gaa gaa cac aaa gca gac gtc atc ggc atg tgc gga ctc ctt gtc 2563  
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 aag tcc acc gtc gtc 2578  
 Lys Ser Thr Val Val 825

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 Leu Asp Leu Gln Gly Cys Asn Gln Ile Leu Asn Asp Thr Arg Pro Asp 50  
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 Val Leu Arg Gln Ile His Arg Ala Tyr Phe Gln Ala Gly Ala Asp Leu 65  
 70 75  
 Val Gln Thr Asn Thr Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr 90  
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 Asp Ile Ala Asp Arg Cys Arg Gln Leu Ala Tyr Lys Gly Thr Ala Val 100  
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 Ala Arg Gln Val Ala Asp Gln Met Gly Pro Gly Arg Asn Gly Met Arg 115  
 120 125  
 Arg Phe Val Val Gly Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu 130  
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 Gly His Ala Pro Tyr Ala Asp Leu Arg Gly His Tyr Lys Gln Ala Ala 145  
 150 155  
 Leu Gly Ile Ile Asp Gly Gly Gly Asp Ala Phe Leu Ile Gln Thr Ala 165  
 170 175  
 Gln Asp Leu Leu Gln Val Lys Ala Ala Val His Gly Val Gln Asp Ala 180  
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 Met Ala Gln Leu Asp Thr Phe Leu Pro Ile Ile Cys His Val Thr Val 195  
 200 205



530 535 540

Glu Thr Arg Arg Asp Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu 545  
Lys Lys Leu Tyr Pro Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile 560

Ser Phe Gly Leu Asn Pro Ala Ala Arg Glu Val Leu Asn Ser Val Phe 575  
Leu Asn Glu Cys Ile Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser 590

Ser Lys Ile Leu Pro Met Asn Arg Ile Asp Arg Glu Arg Glu Val 605  
Ala Leu Asp Met Val Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu 620

Gln Glu Phe Met Gln Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys 635  
Ala Arg Ala Glu Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu 640

Ala Gln Arg Ile Ile Asp Gly Asp Lys Asn Gly Leu Glu Asp Leu 655  
Glu Ala Gly Met Lys Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp 670

Leu Leu Asn Gly Met Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln 685  
Met Gln Leu Pro Phe Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala 700

Val Ala Tyr Leu Glu Pro Phe Met Glu Glu Ala Glu Ala Thr Gly 715  
Ser Ala Gln Ala Glu Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys 730

Gly Asp Val His Asp Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser 745  
Asn Asn Gly Tyr Asp Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser 760

Ala Met Leu Glu Ala Ala Glu His Lys Ala Asp Val Ile Gly Met 775  
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Met Thr Ser Asn Phe  
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5  
163 tct tcc act gtc gct ggt ctt cct cgc atc gga gcg aag cgt gaa ctg  
Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly Ala Lys Arg Gln Leu  
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211 aag ttc gcg ctc gaa ggc tac tgg aat gga tca att gaa ggt cgc gaa  
Lys Phe Ala Leu Gln Gly Tyr Trp Asn Gly Ser Ile Gln Gly Arg Gln  
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259 ctt gcg cag acc gcc cgc caa ttg gtc aac act gca tcg gat tct ttg  
Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu  
40  
307 tct gga ttg gat tcc gtt ccg ttt gca gga cgt tcc tac tac gac gca  
Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala  
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355 atg ctc gat acc gcc gct att ttg ggt ggt ggt ggt ggt ggt ggt ggt  
Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Gln Arg Phe Asp  
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403 gac atc gct gat cat gaa aac gat ggt ctc cca ctg tgg att gac cgc  
Asp Ile Ala Asp His Gln Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg  
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Tyr Phe Gly Ala Ala Arg Gly Thr Gln Thr Leu Pro Ala Gln Ala Met  
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499 acc aag tgg ttt gat acc aac tac cac tac ctc gtc ccg gac ttg tct  
Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Gln Leu Ser  
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547 gcg gat aca cgt ttc gtt ttg gat gcg tcc gcg ctg att gag gat ctc  
Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Gln Asp Leu  
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595 cgt tgc cag cag gtt cgt ggc ggt aat gcc gcg cct gtt ctg gtt ggt  
Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly  
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643 cca ctg act ttc ctt tcc ctt gct cgc acc act gat ggt tcc aat cct  
Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro  
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691 ttg gat cac ctc gca ctg ttt gag gtc tac gag cgc atc aag  
Leu Asp His Leu Pro Ala Leu Phe Gln Val Tyr Gln Arg Leu Ile Lys  
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190  
195

739	tct ttc gat act gag tgg gtt cag atc gat gag cct ggc tgg gtc acc	Ser Phe Asp Thr Gln Trp Val Ala Leu Val Thr	200
787	gat gtt gct cct gag gtt ttg gag cag gtc cgc ggt ggt tac acc act	Asp Val Ala Pro Gln Val Arg Ala Gly Tyr Thr Thr	215
835	ttg gct aag cgc gat ggc ttg ttg gtc aat act tac ttc ggc tct ggc	Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly	230
883	gat cag gcg ctg aac act ctt gcg ggc atc ggc ctt ggc ggc atc ggc	Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly	250
931	ggt gac ttg gtc acc cat ggc gtc act gag ctt gct ggc tgg aag ggt	Val Asp Leu Val Thr His Gly Val Thr Gln Leu Ala Ala Trp Lys Gly	265
979	gag gag ctg ctg ggt ggt ggc ggc atc gtt gat ggt ggt aac att tgg cgc	Gln Gln Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg	280
1027	acc gac ctg tgt gct gct gct gct tcc ctg aag cgc ctg gca gct cgc	Thr Asp Leu Cys Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg	295
1075	ggc cca atc gca gtg tct acc tct tgt tca ctg ctg cag ctt cct tac	Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr	310
1123	acc ctg gag gct gag aac att gag cct gag gtc cgc gac tgg ctt ggc	Thr Leu Gln Ala Gln Asn Ile Gln Pro Val Arg Asp Trp Leu Ala	330
1171	ttc ggc tgc gag aag atc acc gag gtc aag ctg ctt ggc gac ggc cta	Phe Gly Ser Gln Lys Ile Thr Gln Val Lys Leu Leu Ala Asp Ala Leu	345
1219	ggc ggc aac atc gac ggc gct ggc ttc gat ggc ggc tcc gca gca att	Ala Gly Asn Ile Asp Ala Phe Asp Ala Ala Ser Ala Ala Ile	360
1267	gct tct cga cgc acc tcc cca cgc acc gca cca atc acg cag gaa ctc	Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Gln Leu	375
1315	cct ggc cgt agc cgt gga tcc ttc gac act cgt gtt acg ctg cag gag	Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Gln	390
1363	aag tca ctg gag ctt cca gct ctg cca acc acc acc acc att ggt tct ttc	Lys Ser Leu Gln Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe	410
1411	cca cag acc cca tcc att cgt tct gct cgc gct cgt ctg cgc aag gaa	Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Gln	425
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	730	tcc cta aag gtt ctc gtc gag tcc gct aag cag gct cgt gag aaa atc	735	2323
	745	Ser Leu Lys Val Leu Val Gln Ser Ala Lys Gln Ala Arg Gln Lys Ile	740	
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	35	Ile Gln Gly Arg Gln Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr	40	
	50	Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg	55	
	65	Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu	70	
	75	Pro Gln Arg Phe Asp Ile Ala Asp His Gln Asn Asp Gly Leu Pro	75	
	85		90	
	100	Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Gln Thr Leu	105	
	115	Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu	120	
	130	Val Pro Gln Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala	135	
	145	Leu Ile Gln Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg	150	
	165	Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr	170	
	180	Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Gln Val Tyr	185	
	190		190	





515 520 525

Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr  
530 535 540

Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr  
545 550 555 560

Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Gln Ile Asn Asp Leu Ile  
565 570 575

Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Gln Pro Ala Ile Arg Glu  
580 585 590

Leu Leu Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr Leu Gln Trp Ser  
595 600 605

Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln  
610 615 620

Ile His Thr His Met Cys Tyr Ser Gln Phe Asn Glu Val Ile Ser Ser  
625 630 635 640

Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser  
645 650 655

Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly  
660 665 670

Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala  
675 680 685

Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro  
690 695 700

Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp  
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Ala Arg Glu Lys Ile Gly Ala Thr Ile  
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<223> FRXA02085

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Met Thr Ser Asn Phe  
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163	tct tcc act gtc gct ggt ctt cct cgc atc gga gcg aag cgt gaa ctg	Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly Ala Lys Arg Glu Leu	20
211	aag ttc gcg ctc gaa ggc tac tgg aat gga tca att gaa ggt cgc gaa	Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser Ile Glu Gly Arg Glu	35
259	ctt gcg cag acc gcc cgc caa tgg gtc aac act gca tgg gat tct ttg	Leu Ala Gln Thr Ala Arg Gln Val Asn Thr Ala Ser Asp Ser Leu	50
307	tct gga tgg gat tcc gtt ccg ttt gca gga cgt tcc tac tac gac gca	Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala	65
355	atg ctc gat acc gcc gct att ttg ggt gtg ctg ccg gag cgt ttt gat	Met Leu Asp Thr Ala Ile Leu Gly Val Leu Pro Gln Arg Phe Asp	80
403	gac atc gct gat cat gaa aac gat ggt ctc cca ctg tgg att gac cgc	Asp Ile Ala Asp His Gln Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg	95
451	tac ttt ggc gct gct cgc ggt act gag acc ctg cct gca cag gca atg	Tyr Phe Gly Ala Ala Arg Gly Thr Gln Thr Leu Pro Ala Gln Ala Met	110
499	acc aag tgg ttt gat acc aac tac cac tac ctc gtc ccg gag ttg tct	Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Gln Leu Ser	125
547	gcg gat aca cgt ttc gtt ttg gat ggc tcc gcg cgt att gag gat ctc	Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Gln Asp Leu	145
595	cgt tgc cag cag gtt cgt ggc ggt aat ggc cgc cct gtc ctg gtt ggt	Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly	160
643	cca ctg act ttc ctt tcc ctt gct cgc acc act gat ggt tcc aat cct	Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Asp Gly Ser Asn Pro	175
691	ttg gat cac ctc cct gca ctg ttt gag gtc tac gag cgc ctc atc aag	Leu Asp His Leu Pro Ala Leu Phe Gln Val Tyr Gln Arg Leu Ile Lys	190
739	tct ttc gat act gag tgg gtt cag atc gat gag cct gcg ttg gtc acc	Ser Phe Asp Thr Gln Trp Val Gln Ile Asp Gln Pro Ala Leu Val Thr	210
787	gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act	Asp Val Ala Pro Gln Val Leu Gln Val Arg Ala Gly Tyr Thr Thr	225
835	ttg gct aag cgc gat ggc ggt ttg gtc aat act tac ttc ggc tct ggc	Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly	240
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[illegible]





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 455 460  
 Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Glu Tyr 465  
 470 475 480  
 Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val 485  
 490 495  
 Glu Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn 500  
 505 510  
 Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Glu Tyr Ala Glu 515  
 520 525  
 Ser Leu Thr Glu Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr 530  
 535 540  
 Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Glu Pro Leu Ala Thr Thr 545  
 550 555 560  
 Ala Asp Glu Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile 565  
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 Glu Ala Gly Ala Lys Ile Ile Glu Val Asp Glu Pro Ala Ile Arg Glu 580  
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 Val Glu Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile 40  
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 Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met Cys Tyr Ser Gln  
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 Phe Asn Gln Val Ile Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr  
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 Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys  
 65 70 75 80  
 Ser Ser Gly Phe Gln Leu Gly Val Gly Val Thr Asp Ile His  
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 Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala  
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 Ala Leu Gln Ser Val Asp Pro Arg Cys Ser Val Asp Pro Arg Cys  
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BGI-121CP  
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 BGI-121CP



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 Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Gln Leu 20  
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 Asp Ala Asn Ile Lys Arg Ser Asn Gly Gln Ile Gly Gln Gln Phe 35  
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 Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val 50  
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 Ala Val Arg Ser Thr Pro Gly Asn Ile Gln Leu Thr Ser Phe Ser Asp 115  
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 Arg Arg Asp Arg Ala Leu Phe Ser Gln Ala Tyr Gln Asp Pro Val Ser 130  
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 Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Gln Phe Thr Gly 145

123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

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691	gca cta tcc cca gga tct gca gct cga tct gca gaa gaa gaa gaa gaa	Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp	160
739	act gat gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa	Thr Asp Gln Val Val Val Val Val Val Val Val Val Val Val Val Val	170
787	tac aag atc atc atc acc gat gaa gaa gaa gaa gaa gaa gaa gaa gaa	Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala Pro	175
835	gac tgg gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa	Asp Leu Ala Ala Thr Asp Ala Ala Thr Asp Ala Ala Thr Asp Ala Ala	180
883	gat tac tgg gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa	Asp Tyr Leu Asp Thr Ile Gly Thr Arg Ile Asp Ala Ile Asn Ser Ala	185
931	gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc tgc tgg ggc	Val Lys Gly Leu Pro Lys Gln Thr Arg Leu His Ile Cys Trp Gly	190
979	tct tgg cac gga cca cac gtc act gac atc cca ttc ggt gac atc att	Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly Asp Ile Ile	195
1027	ggt gag atc ctg cgc gaa gag gtc ggt ggc ttc ttc ttc ttc ttc ttc	Gly Gln Ile Leu Arg Ala Gln Val Gly Gly Phe Ser Phe Gln Gly Ala	200
1075	tct cct cgt cac gca cac gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa	Ser Pro Arg His Ala His Gln Trp Arg Val Trp Gln Gln Asn Lys Leu	205
1123	cct gaa ggc tct gtt atc tac cct ggt ggt ggt ggt ggt ggt ggt ggt	Pro Gln Gly Ser Val Ile Tyr Pro Gly Val Val Val Val Val Val Val	210
1171	gct gtt gag cac cca cgc ctg gtt gtt gtt gtt gtt gtt gtt gtt gtt	Ala Val Gln His Pro Arg Leu Val Ala Asp Arg Ile Val Gln Phe Ala	215
1219	aag ctt gtt ggc cct gag aac gtc att ggc tcc act gac tgt ggt ctg	Lys Leu Val Gly Pro Gln Asn Val Ile Ala Ser Thr Asp Cys Gly Leu	220
1267	ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg gag tcc cta	Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu Gln Ser Leu	225

gta gag ggc gct cgc atc gca tca aag gaa ctg ttc taagctagac 1313  
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Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Gln Gly Gln 50  
Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn 65  
Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg 85  
Trp Ala Ser Gln Ala Val Arg Ser Thr Pro Gly Asn Ile Gln Leu 100  
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Gln Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn 130  
Pro Gln Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Gln Thr Gln 145  
Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr 165  
Asp Gly Phe Val Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr 180  
Asn Lys Phe Tyr Asp Thr Asp Gln Val Val Ala Cys Ala Asp 195  
Ala Leu Ser Gln Gln Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val 210  
Gln Leu Asp Ala Pro Asp Leu Ala Gln Ala Trp Asp Gln Ile Asn Pro 225  
Gln Pro Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp 245  
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Ala Ile Asn Ser Ala Val Lys Gln Thr Arg Leu 260  
 His Ile Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro 275  
 Phe Gly Asp Ile Ile Gly Gln Ile Leu Arg Ala Gln Val Gly Phe 290  
 Ser Phe Gln Gly Ala Ser Pro Arg His Ala His Gln Trp Arg Val Trp 305  
 Gln Gln Asn Lys Leu Pro Gln Gly Ser Val Ile Tyr Pro Gly Val Val 325  
 Ser His Ser Ile Asn Ala Val Gln His Pro Arg Leu Val Ala Asp Arg 340  
 Ile Val Gln Phe Ala Lys Leu Val Gly Pro Gln Asn Val Ile Ala Ser 355  
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 Lys Leu Gln Ser Leu Val Gln Gly Ala Arg Ile Ala Ser Lys Gln Leu 385  
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 agc ttg aag gat tac ttg gac ttg atc ggt aca cgc atc gat gcc atc 96  
 Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile 30  
 aac agt gca ttg aag ggc ctc cca aag gaa gac acc cgc ctg cac atc 144  
 Asn Ser Ala Val Lys Gly Leu Pro Lys Gln Thr Arg Leu His Ile 45  
 tgc ttg ggc tct ttg cac gga cca cac gtc act gac atc cca ttg ggt 192  
 Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly 60  
 gac atc atc ggt gag atc ctg cgc gca gag gtc ggt ggc ttg tcc ttc 240  
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atc agg acc acc cag gtc ggt tcc ttg ccc cgt acc cca gag cta ctt 163  
 Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu 20  
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gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211  
 Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Phe 35  
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ttc cag att ctc cag tct tct gta gat gac gtc atc aag cgc cag gtt 259  
 Phe Gln Ile Leu Gln Ser Ser Val Asp Val Ile Lys Arg Gln Val 50  
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gac ctg ggt atc gat atc ctt aac gag ggc gaa tac ggc cac gtc acc 307  
 Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Tyr Gly His Val Thr 65  
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tcc ggt gca gtc gat ttc gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355  
 Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg 85  
 70 75 80

ctg ggc gga ctc acc atg acc gat acc gac cgt tgg gca agc cag gaa 403  
 Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu 100  
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gca gtc cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat 451  
 Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp 115  
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cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct 499  
 Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser 130  
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ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga 547  
 Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly 145  
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cct att acc tac att ggc cag gaa gaa act cag acg gat gtc gat ctg 595

Pro Ile Thr Tyr Ile Gly Gln Gln Thr Gln Thr Asp Val Asp Leu 150  
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 Leu Lys Lys Lys Gly Met Asn Ala Gly Ala Thr 160  
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 Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp 175  
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 Thr Asp Gln Gln Val Val Ala Cys Ala Asp Ala Leu Ser Gln Gln 185  
 739  
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 Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala 195  
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 Thr Pro Gln Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Gln Ile 205  
 Gly Gln Gln Gln Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val 210  
 Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Gln Gly Gln 215  
 Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn 220  
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 Thr Ser Phe Ser Asp Arg Asp Arg Ala Leu Phe Ser Gln Ala Tyr 235  
 Gln Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn 240  
 Pro Gln Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Gln Thr Gln 245  
 Thr Asp Val Asp Leu Lys Lys Gly Met Asn Ala Gly Ala Thr 250  
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 Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr 255  
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 Leu Cys Ile Ala Asp Phe Ile Arg Pro Arg Glu Gln Ala Val Lys Asp 30  
 ggc caa gtc gac gtc atg cca ttc cag ctg gtc acc atg ggt aat cct 144  
 Gly Gln Val Asp Val Met Pro Phe Gln Leu Val Thr Met Gly Asn Pro 45  
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 Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu 60  
 tac ttg gaa gtt cac ggc atc ggc ttg cag ctg acc gaa gca ttg gcc 240  
 Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala 80  
 gag tac tgg cac tcc cga gtc arg Ser Arg Ser Glu Leu Lys Leu Asn Asp Gly 95  
 gaa tct gtc gct gat ttt gat cca gaa gag aag acc aag ttc ttc gac 336  
 Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp 110  
 ctg gat tac cgc ggc ggc cgc ttc ttc ttc ggt ttc ggt tac ggt tct tgc cct 384  
 Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro 125  
 gat ctg gaa gac gac aag ctg gaa ttg gaa ttg ctc gag cca ggc cgt 432  
 Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Glu Pro Gly Arg 140  
 atc ggc gtc gag ttg gag ttg tcc gag gaa ctc cag ctg cac cca gag cag tcc 480  
 Ile Gly Val Glu Leu Ser Glu Glu Leu His Pro Glu Gln Ser 160



aca gac gcg ttg gtc ctc tac cac cca gag gca aag tac ttt aac gtc  
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Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu  
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Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala  
 65 70 75 80

Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly  
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Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro  
 115 120 125

Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Glu Pro Gly Arg  
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Gln Ser Ile Gln Tyr Gly Pro Leu Gly Lys Gly His Asp Pro Leu Lys 20  
163

gat ccc atg aag ggt atc cga ggt gtc atg gcc ggc acc tta gac atg  
Asp Pro Met Lys Gly Ile Arg Gly Val Met Ala Gly Thr Leu Val Met 35  
211

gaa gca atc acc tta ggt ctt gtc ctc acc gtc atc ctg gcc gtc gac  
Gln Ala Ile Thr Leu Gly Leu Val Leu Thr Val Ile Leu Arg Val Asp 50  
259

gac ggc atc tac tgg acc acc ttc aac tgg gtc tat gta tca gca gtc  
Asp Gly Ile Tyr Thr Thr Phe Asn Trp Val Tyr Val Ser Ala Val 65  
307

gcg atc gca cac ttc gtc gct gca ttc ctg caa agt ttc agt tgg tcc  
Ala Ile Ala His Phe Val Ala Phe Leu Gln Arg Phe Ser Trp Ser 85  
355

atc ccg atg aac atc gtc ctg cag gtc ctt gca ctt gcc ggt ttc ttt  
Ile Pro Met Asn Ile Val Leu Gln Val Leu Ala Leu Ala Gly Phe Phe 100  
403

gtt cac ccc gcc ggc atg ggc ttc gcc gcc atc atc ttc atc ggc tgg  
Val His Pro Ala Met Gly Phe Ala Ile Ile Phe Ile Ala Trp 115  
451

gcg tac ctg ttc tac ctg cgc tct aat ctg att gat cgc atg aaa cgc  
Ala Tyr Leu Phe Tyr Leu Arg Ser Asn Leu Ile Asp Arg Met Lys Arg 130  
499

ggg ctg ctt acc acc cag cac agc taagcttaa ggcctccgg ggc  
Gly Leu Leu Thr Thr Gln His Ser 140  
546

<210> 728

<211> 141

<212> PRT

<213> Corynebacterium glutamicum

<400> 728

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His Asp Pro Leu Lys Asp Pro Met Lys Gly Ile Arg Gly Val Met Ala 20  
25 30

Gly Thr Leu Val Met Gln Ala Ile Thr Leu Gly Leu Val Leu Thr Val 35  
40 45

Ile Leu Arg Val Asp Asp Gly Ile Tyr Trp Thr Thr Phe Asn Trp Val 50  
55 60

Tyr Val Ser Ala Val Ala Ile Ala His Phe Val Ala Ala Phe Leu Gln 65  
 Arg Phe Ser Trp Ser Ile Pro Met Asn Ile Val Leu Gln Val Leu Ala 85  
 Leu Ala Gly Phe Phe Val His Pro Ala Met Gly Phe Ala Ala Ile Ile 100  
 Phe Ile Ile Ala Trp Ala Tyr Leu Phe Tyr Leu Arg Ser Asn Leu Ile 115  
 Asp Arg Met Lys Arg Gly Leu Leu Thr Thr Gln His Ser 130  
 135  
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 tccacacagac attgaaggctg tcaccacaagat ttaaggagtc gtg gct ttc atg cag 115  
 Val Ala Phe Met Gln 1  
 aaa acg tca cgc ggt tgg tgg atc gca acg gga ggt ttc ctc gcc gct 163  
 Lys Thr Ser Ala Gly Trp Leu Ile Ala Thr Gly Gly Phe Leu Ala Ala 20  
 gtg tcc gcc att tgg acg tgg cgt ttt tat gga tcc atg acc tct att 211  
 Val Ser Ala Ile Leu Thr Trp Arg Phe Tyr Gly Ser Met Thr Ser Ile 35  
 tcc atc acg gta tcc atc act ttt tgg tgg tgg gcc gtg gtg tgt ggt 259  
 Ser Ile Thr Val Ser Ile Thr Phe Trp Leu Leu Ala Val Val Cys Gly 50  
 ttc gca ggt gtg aag gtc caa ggt cgc ctc gat gag ggg ctc gtc atc ggc 307  
 Phe Ala Gly Val Lys Val Gln Gly Arg Leu Asp Gln Gly Leu Ile Gly 65  
 cag gac aaa tcc caa atg aac ccc gtc acc att gcc tat ctc ggc atg 355  
 Gln Asp Lys Ser Gln Met Asn Pro Val Thr Ile Ala Tyr Leu Ala Met 85  
 ctg ggt cga cgc ggt tgg ggc ggc gga att ttc ggc ggc ggt tat 403  
 Leu Gly Arg Ala Cys Ala Trp Gly Gly Ala Ile Phe Gly Gly Val Tyr 100  
 gtg gga att ggc agt tat gta atc cca cgc gcc ggt gag tgg tcc gca 451  
 Val Gly Ile Gly Ser Tyr Val Ile Pro Arg Ala Gly Gln Leu Ser Ala 115

gca tcg aat gat ctt ccg gga ggt att gcc tgt gcg ctg gga atc 499  
 Ala Ser Asn Asp Leu Pro Gly Val Ile Ala Cys Ala Leu Gly Gly Ile  
 gca ctc tca gct gcc gga ctt tat tta gag cga agc tgt gag gct ccg 547  
 Ala Leu Ser Ala Ala Gly Leu Tyr Leu Gln Arg Ser Cys Gln Ala Pro  
 cct ccc caa tct ggc gaa gcg atc agc tagattggaa ttcatggaatc 594  
 Pro Pro Gln Ser Gly Gln Ala Ile Ser  
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 aag 597

<400> 730  
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Gly Phe Leu Ala Ala Val Ser Ala Ile Leu Thr Trp Arg Phe Tyr Gly

Ser Met Thr Ser Ile Ser Ile Thr Val Ser Ile Thr Phe Trp Leu Leu

Ala Val Val Cys Gly Phe Ala Gly Val Lys Val Gln Gly Arg Leu Asp

Gln Gly Leu Ile Gly Gln Asp Lys Ser Gln Met Asn Pro Val Thr Ile

Ala Tyr Leu Ala Met Leu Gly Arg Ala Cys Ala Trp Gly Gly Ala Ile

Phe Gly Gly Val Tyr Val Gly Ile Gly Ser Tyr Val Ile Pro Arg Ala

Gly Gln Leu Ser Ala Ala Ser Asn Asp Leu Pro Gly Val Ile Ala Cys

Ala Leu Gly Gly Ile Ala Leu Ser Ala Ala Gly Leu Tyr Leu Gln Arg

Ser Cys Gln Ala Pro Pro Gln Ser Gly Gln Ala Ile Ser

<213> Corynebacterium glutamicum

<212> DNA

<211> 723

<210> 731

<220>

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&lt;223&gt; RXC01942

&lt;400&gt; 731

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 gtgatcaagg tcaacggcaa gaacggatca cctgggatcc atg ttg cgc att gga  
 Met Leu Arg Ile Gly  
 5  
 cta aca gga ggg atc ggc agc ggt aaa tct acc gtt ggc gat ctt ttg  
 Leu Thr Gly Ile Gly Ser Gly Lys Ser Thr Val Ala Asp Leu Leu  
 10 15 20  
 tca tct gaa gga ttt ctc atc gtc gac gcg gac caa gtt ggc cgc gat  
 Ser Ser Gln Gly Phe Leu Ile Val Asp Ala Asp Gln Val Ala Arg Asp  
 25 30 35  
 atc gtc gaa ccc gga caa ccg gca tta gca gag cta gct gaa gct ttt  
 Ile Val Gln Pro Gly Gln Pro Ala Leu Ala Gln Leu Ala Phe  
 40 45 50  
 ggc caa gac atc tta aaa ccc gac ggc act cta gac gcg gga tta  
 Gly Gln Asp Ile Leu Lys Pro Asp Gly Thr Leu Asp Arg Ala Gly Leu  
 55 60 65  
 gca gcc aaa gca ttt gtc agc gaa gaa caa aca gcg ctc aat gcc  
 Ala Ala Lys Ala Phe Val Ser Gln Gln Thr Ala Leu Leu Asn Ala  
 70 75 80  
 att acc cac cct cgt atc gcc gaa gag tca gct cgt cga ttc aac gaa  
 Ile Thr His Pro Arg Ile Ala Gln Gln Ser Ala Arg Arg Phe Asn Gln  
 90 95 100  
 gcc gaa gat caa ggc gcc aaa gtt gcg gtt tat gac atg cct ttg ctt  
 Ala Gln Asp Gln Gly Ala Lys Val Ala Val Tyr Asp Met Pro Leu Leu  
 105 110 115  
 gta gaa aaa ggc ctt gac cgc aag atg gac ctt gtc gta gtt gat  
 Val Gln Lys Gly Leu Asp Arg Lys Met Asp Leu Val Val Val Asp  
 120 125 130  
 gtt gac gta gag gaa cgc gtc cgc aga ctt gtc gaa aaa cgt ggc ctc  
 Val Asp Val Gln Arg Val Arg Arg Leu Val Gln Lys Arg Gly Leu  
 135 140 145  
 aca gag gac gac gtc cgc cgt cga atc gct tct caa gtc ccc gac gac  
 Thr Gln Asp Asp Val Arg Arg Ile Ala Ser Gln Val Pro Asp Asp  
 150 155 160  
 gtc aga ctt aaa gcc gct gac atc gtt gtc gac aat aac ggc acg cta  
 Val Arg Leu Lys Ala Asp Ile Val Val Asp Asn Asn Gly Thr Leu  
 170 175 180  
 gag gac ctt cat gct gaa gca agc aag ctc att gct gag att ctt agt  
 Gln Asp Leu His Ala Gln Ala Ser Lys Leu Ile Ala Gln Ile Leu Ser  
 185 190 195  
 cgc gtc aat tagcactaaa acatcgtcaa agt  
 Arg Val Asn  
 200

723

<210> 732  
<211> 200  
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<213> Corynebacterium glutamicum  
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Ala Glu Ile Leu Ser Arg Val Asn

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<223> RXN02802  
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agcaaacgcg cctcagcgc tccaccgact gggtcggcct gtg aaa aac ctc gac 115

163	atc gcc cgc tac cgc cgc caa att atg ctc ggc gaa atc ggc cag caa	Ile Ala Arg	10	atc gcc cgc tac cgc cgc caa att atg ctc ggc gaa atc ggc cag caa	Ile Ala Arg	20	Val Lys Asn Leu Asp	1
211	aaa caa caa caa tgc ctt ttc gac gct aag gtc tcc gtc atc ggc gca ggc	Lys Gln Gln Ser	25	aaa caa caa caa tgc ctt ttc gac gct aag gtc tcc gtc atc ggc gca ggc	Lys Gln Gln Ser	30		
259	ggc ctc cgc ggc tca ccc gcc ctc tac ctt gct ggc gct ggc ggc ggc	Gly Leu Gly Ser	40	ggc ctc cgc ggc tca ccc gcc ctc tac ctt gct ggc gct ggc ggc ggc	Gly Leu Gly Ser	50		
307	cac atc cac atc atc atc gac gat gac ctc gtc gac ctc tcc aac ctc cac	His Ile His Ile	55	cac atc cac atc atc atc gac gat gac ctc gtc gac ctc tcc aac ctc cac	His Ile His Ile	60		
355	cgc cag gtc atc cac acc acc gct ggc gtc gga acc gga acc aag gcc gag	Arg Gln Val Ile	70	cgc cag gtc atc cac acc acc gct ggc gtc gga acc gga acc aag gcc gag	Arg Gln Val Ile	80		
403	tcc gcg cgc gaa gca atg ctc gca ctc gac ctc aac cct tcc gtc aaa gtc acg	Ser Ala Arg Gln	90	tcc gcg cgc gaa gca atg ctc gca ctc gac ctc aac cct tcc gtc aaa gtc acg	Ser Ala Arg Gln	100		
451	ggt tct gtc agg cga ctc gac tgg tca aat gca ctt tct gag ctc gca gca	Val Ser Val Arg	105	ggt tct gtc agg cga ctc gac tgg tca aat gca ctt tct gag ctc gca gca	Val Ser Val Arg	115		
499	gat tcc gat gtc atc tgc gat ggc tcc gat aac ttc gac acc cga cac	Asp Ser Asp Val	120	gat tcc gat gtc atc tgc gat ggc tcc gat aac ttc gac acc cga cac	Asp Ser Asp Val	130		
547	ctc gca tcc tgg gcc gcc gca aaa ctt ggc atc ccc cac gtc tgg gca gca	Leu Ala Ser Trp	135	ctc gca tcc tgg gcc gcc gca aaa ctt ggc atc ccc cac gtc tgg gca gca	Leu Ala Ser Trp	145		
595	tcc atc ctc ggt ttc gac gcc caa ctc tcc gtc ttc cac gcc ggc cac	Ser Ile Leu Gly	155	tcc atc ctc ggt ttc gac gcc caa ctc tcc gtc ttc cac gcc ggc cac	Ser Ile Leu Gly	160		
643	ggc ccc atc tac gaa gac ctc ttc ccc acc ccc gcc cca cca ccc gga tcc	Gly Pro Ile Tyr	170	ggc ccc atc tac gaa gac ctc ttc ccc acc ccc gcc cca cca ccc gga tcc	Gly Pro Ile Tyr	175		
691	gtc cca tca tgt tcc caa gca ggc gtc ttc ggt cca gtc gtc ggc gta gta	Val Pro Ser Cys	185	gtc cca tca tgt tcc caa gca ggc gtc ttc ggt cca gtc gtc ggc gta gta	Val Pro Ser Cys	190		
739	atg ggc tcc gcg atg gcc atg gaa gcc ctc gaa gcc ctc gaa gcc gtc gtc	Met Gly Ser Ala	200	atg ggc tcc gcg atg gcc atg gaa gcc ctc gaa gcc ctc gaa gcc gtc gtc	Met Gly Ser Ala	210		
787	ggc aca ccc ttg atc gga aaa ctc ggc tac tac tcc tcc ctc gac ggc	Gly Thr Pro Leu	215	ggc aca ccc ttg atc gga aaa ctc ggc tac tac tcc tcc ctc gac ggc	Gly Thr Pro Leu	225		
835	acc tgg gaa tac atc ccc gtc gtc ggt tcc ggc ggc ggc ggc ggc ggc	Thr Trp Gln Tyr	220	acc tgg gaa tac atc ccc gtc gtc ggt tcc ggc ggc ggc ggc ggc ggc	Thr Trp Gln Tyr	225		

230	235	240	245
gtg ctt ggg tct gct ggt gtt tct ggg att tct ggc ggt ttt ggt gag	Val Leu Gly Ser Ala Gly Val Ser Gly Ile Ser Gly Phe Gly Gln	250	260
gtg ctc gat gtt cct cga gtt tcc ggc cgt gtt gac ggc ggt tct gct	Val Leu Asp Val Pro Arg Val Ser Ala Leu Val Asp Gly Val Ser Leu	265	275
atc gac gtc cgc gaa ccc tcc gaa ttc tcc ggc tac tcc atc ccc ggc	Ile Asp Val Arg Gln Pro Ser Gln Phe Ser Ala Tyr Ser Ile Pro Gly	280	290
gcg cac aac acc cca ctg tcc ggc atc cgc gaa ggc ggc atc cca ccc	Ala His Asn Thr Pro Leu Ser Ala Ile Arg Gln Gly Ala Ile Pro Pro	295	305
tcc gtt tcc gca ggt aaa gag gtt atc gtc tac tgc gca gct ggt gtc	Ser Val Ser Ala Gly Lys Gln Val Ile Val Tyr Cys Ala Ala Gly Val	310	325
cgc tcc gca caa gcc atc gca att tta gaa tcc gca ggc tac acc gga	Arg Ser Ala Gln Ala Ile Ala Ile Leu Gln Ser Ala Gly Tyr Thr Gly	330	340
atg agc agc ctc gac ggc gga atc gaa ggc tgg cta gat tcc cta ggg	Met Ser Ser Leu Asp Gly Gly Ile Gln Gly Trp Leu Asp Ser Leu Gly	345	355
taaaccaag gcgtgtgcc acc			
1194			
<210> 734			
<211> 357			
<212> PRT			
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Val Lys Asn Leu Asp Ile Ala Arg Tyr Arg Arg Gln Ile Met Leu Gly	1	5	10
Gln Ile Gly Gln Gln Lys Gln Ser Leu Phe Asp Ala Lys Val Ser	20	25	30
Val Ile Gly Ala Gly Gly Leu Gly Ser Pro Ala Leu Tyr Leu Ala	35	40	45
Gly Ala Gly Val Gly His Ile His Ile Asp Asp Leu Val Asp	50	55	60
Leu Ser Asn Leu His Arg Gln Val Ile His Thr Thr Ala Gly Val Gly	65	70	75
Thr Pro Lys Ala Gln Ser Ala Arg Gln Ala Met Leu Ala Leu Asn Pro	85	90	95
Ser Val Lys Val Thr Val Ser Val Arg Arg Leu Asp Trp Ser Asn Ala	100	105	110
Leu Ser Gln Leu Ala Asp Ser Asp Val Ile Leu Asp Gly Ser Asp Asn			



115 120 125  
 Phe Asp Thr Arg His Leu Ala Ser Trp Ala Ala Lys Leu Gly Ile  
 130 135 140  
 Pro His Val Trp Ala Ser Ile Leu Gly Phe Asp Ala Gln Leu Ser Val  
 145 150 155  
 Phe His Ala Gly His Gly Pro Ile Tyr Gln Asp Leu Phe Pro Thr Pro  
 165 170 175  
 Pro Pro Pro Gly Ser Val Pro Ser Cys Ser Gln Ala Gly Val Leu Gly  
 180 185 190  
 Pro Val Val Gly Val Met Gly Ser Ala Met Ala Met Gln Ala Leu Lys  
 195 200 205  
 Ile Ile Thr Gly Val Gly Thr Pro Leu Ile Gly Lys Leu Gly Tyr Tyr  
 210 215 220  
 Ser Ser Leu Asp Gly Thr Trp Gln Tyr Ile Pro Val Val Gly Ser Pro  
 225 230 235 240  
 Gln Val Leu Gln Arg Val Leu Gly Ser Ala Gly Val Ser Gly Ile Ser  
 245 250 255  
 Gly Gly Phe Gly Gln Val Leu Asp Val Pro Arg Val Ser Ala Leu Val  
 260 265 270  
 Asp Gly Val Ser Leu Ile Asp Val Arg Gln Pro Ser Gln Phe Ser Ala  
 275 280 285  
 Tyr Ser Ile Pro Gly Ala His Asn Thr Pro Leu Ser Ala Ile Arg Gln  
 290 295 300  
 Gly Ala Ile Pro Pro Ser Val Ser Ala Gly Lys Gln Val Ile Val Tyr  
 305 310 315 320  
 Cys Ala Ala Gly Val Arg Ser Ala Gln Ala Ile Ala Ile Leu Gln Ser  
 325 330 335  
 Ala Gly Tyr Thr Gly Met Ser Ser Ser Leu Asp Gly Gly Ile Gln Gly Trp  
 340 345 350  
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 <213> Corynebacterium glutamicum

<220>  
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 <222> (7)..(474)  
 <223> FRXA02802

<400> 735  
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 Met Ala Met Gln Ala Leu Lys Ile Ile Thr Gly Val Gly Thr Pro

Protein	Position	Sequence	Mass
Pro Arg Val Ser Ala Leu Val Asp Gly Val Ser Leu Ile Asp Val Arg	65		80
Ala Gly Val Ser Gly Ile Ser Gly Gly Phe Gly Gln Val Leu Asp Val	50		60
Ile Pro Val Val Gly Ser Pro Gln Val Leu Gln Arg Val Leu Gly Ser	35		45
Ile Gly Lys Leu Gly Tyr Tyr Ser Ser Leu Asp Gly Thr Trp Gln Tyr	20		30
Met Ala Met Gln Ala Leu Lys Ile Ile Thr Gly Val Gly Thr Pro Leu	1		15
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<211> 156			
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gctgtgtgcc acc			497
Leu Asp Gly Ile Gln Gly Trp Leu Asp Ser Leu Gly	145		155
ctc gac ggc gga atc gaa ggc tgg cta gat tcc cta ggg taaaccgaag			484
Gln Ala Ile Ala Ile Leu Gln Ser Ala Gly Tyr Thr Gly Met Ser Ser	130		140
caa gcc atc gca att tta gaa tcc gca ggc tac acc gga atg acc agc			435
Ala Gly Lys Gln Val Ile Val Tyr Cys Ala Ala Gly Val Arg Ser Ala	115		125
gca ggt aaa gag gtt atc gtc tac tgc gca gct ggt gtc cgc tcc gca			387
Thr Pro Leu Ser Ala Ile Arg Gln Gly Ala Ile Pro Pro Ser Val Ser	100		110
acc cca ctg tcc gcc atc cgc gaa ggc gcc atc cca ccc tcc gtt tcc			339
Arg Gln Pro Ser Gln Phe Ser Ala Tyr Ser Ile Pro Gly Ala His Asn	85		95
cgc gaa ccc tcc gaa ttc tcc gcc tac tcc atc ccc ggc ggc cac aac			291
Val Pro Arg Val Ser Ala Leu Val Asp Gly Val Ser Leu Ile Asp Val	65		75
glt cct cga gtt tcc ggc ctg ggt gac ggc ggt tct tgc ctc atc gac gtc			243
Ser Ala Gly Val Ser Gly Ile Ser Gly Phe Gly Gln Val Leu Asp	50		60
tct gct ggt gtt tgc ggg att tct ggc ggt ttt ggt gag gtt ctc gat			195
Tyr Ile Pro Val Val Gly Ser Pro Gln Val Leu Arg Val Leu Gly	35		45
tac atc ccc gtc gtc ggt tgc ggt tgc cgc gag ggt ctg gaa cgg gtt ctt ggg			147
Leu Ile Gly Lys Leu Gly Tyr Tyr Ser Ser Leu Asp Gly Thr Trp Gln	20		30
tgg atc gga aaa ctc ggc tac tac tcc tcc ctc gac ggc acc tgg gaa			99